

ALIGNMENTS

RESULT 1
S13586
triacylglycerol lipase (EC 3.1.1.3) precursor, bile salt-activated - human
M:Alternate names: bile salt-stimulated lipase; carboxyl ester lipase; lipamidase; panc
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Jun-1999
C:Accession: S13586; S34490; S12983; S34489; A37916; B42824; A42864; S13917; A31520; S12
R:Nilsson, J.; Blackberg, L.; Carlsson, P.; Eneback, S.; Hernell, O.; Bjurzell, G.
E:J. Biochem. 192, 543-550, 1993
A:Title: cDNA cloning of human-milk bile salt-stimulated lipase and evidence for its ide
A:Reference number: S13586; MUID:9106144; PMID:1696825
A:Accession: S13586
A:Molecule type: mRNA
A:Residues: 1-745 <N1>
A:Cross-references: EMBL:X54457; NID:g295C0; PIDN:CAA8325.1; PID:g29501
A:Accession: S34490
A:Molecule type: Protein
A:Residues: 55-63;361-378;387-403;436-446 <N12>
R:Hu, D.Y.; Kiese, J.A.
FEBS Lett. 276, 131-134, 1990
A:Title: Sequence identity between human pancreatic cholesterol esterase and bile salt-
A:Reference number: S12983; MUID:51092399; PMID:2265692
A:Accession: S12983
A:Molecule type: mRNA
A:Residues: 1-745 <HUI>
A:Cross-references: EMBL:M85201
R:Hu, D.Y.; Kissel, J.A.
Submitted to the EMBL Data Library, February 1992
A:Description: Molecular cloning and tentative identification of the catalytic triad of
A:Reference number: S34489
A:Accession: S34489
A:Molecule type: mRNA
A:Residues: 1-715 'CAPSVTLRLPQPMTPRKRLQSLGFSVP' <HUI2>
A:Cross-references: EMBL:M85201; NID:g180481; PIDN:AA5503.1; PID:g180482
R:Badu, T.; Downs, D.; Jackson, K.W.; Tang, J.; Wang, C.S.
Biochemistry 30, 500-510, 1991
A:Title: Structure of human milk bile salt activated lipase.
A:Reference number: A37916; MUID:91105134; PMID:1988041
A:Accession: A37916
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 4-745 <BAB>
A:Cross-references: GB:M54994; GB:J05301; NID:g187149; PIDN:AAA63211.1; PID:g187150
A:Note: It is uncertain whether Met-1 or Met-4 is the initiator
R:Ridberg, U.; Nilsson, J.; Stromberg, K.; Stenmar, G.; Sahlin, P.; Eneback, S.; Bjurzell
Genomics 13, 630-640, 1992
A:Title: Genomic organization, sequence analysis, and chromosomal localization of the hu
A:Reference number: A42824; MUID:92347858; PMID:1639390
A:Accession: B42824
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 433-498 <LID>
A:Cross-references: GB:M94579
A:Note: the authors translated the codon TAC for residue 7 as Thr
A:Note: sequence modified after extraction from NCBI database
R:Kumar, B.V.; Aleman-Gomez, G.A.; Colwell, N.; Lopez-Candales, A.; Bosner, M.S.; Spilbu
Biochemistry 31, 6077-6081, 1992
A:Title: Structure of the human pancreatic cholesterol esterase gene.
A:Reference number: A42864; MUID:92329425; PMID:1627550
A:Accession: A42864
A:Molecule type: DNA
A:Residues: 458-485 <KMC>
A:Cross-references: GB:S40178; NID:g251572; PIDN:AA82337.1; PID:g251573
A:Experimental source: PME 15, PTCF
A:Note: sequence extracted from NCBI backbone (NCBI:109184, NCBI:109185)
R:Christie, D.L.; Cleverly, D.R.; O'Connor, C.J.
FEBS Lett. 278, 193-194, 1991
A:Title: Human milk bile-salt stimulated lipase. Sequence similarity with rat lysophosph
A:Reference number: S13917; MUID:5112282; PMID:1991511
A:Accession: S13917

A>Status: preliminary
A:Molecule type: protein
A:Residues: 24-40;135-170;278-286;V',288-294;V',296;305-340;534-543 <CHR>
R:Wang, C.S.
Biochem. Biophys. Res. Commun. 155, 950-955, 1988
A:Title: Purification of carboxyl ester lipase from human pancreas and the amino acid
A:Reference number: A31520; MUID:88339990; PMID:3421974
A:Accession: A31520
A:Molecule type: protein
A:Residues: 24-33 <WAN>
R:Hu, D.Y.; Hayakawa, K.; Oizumi, J.
Biochem. J. 291, 65-69, 1993
A:Title: Lipomycin activity in normal and mutagenized pancreatic cholesterol estera
A:Reference number: S32318; MUID:93228634; PMID:8471055
A:Accession: S32318
A>Status: preliminary
A:Molecule type: protein
A:Residues: 54;X',56-75;77-79;369-377 <HUI>
R:Roudaut, S.; Xatallier, F.; Margotat, A.; Escribano, M.J.; Lombardic, D.
Biochim. Biophys. Acta 1264, 141-150, 1995
A:Title: Bile salt-dependent lipase transcripts in human fetal tissues.
A:Reference number: S59907; MUID:96038811; PMID:758248
A:Accession: S59907
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 26-729 <ROU>
R:Loomes, K.M.
Eur. J. Biochem. 230, 607-613, 1995
A:Title: Structural organisation of human bile-salt-activated lipase probed by limite
A:Reference number: S65641; MUID:95331299; PMID:7607235
A:Accession: S65641
A>Status: preliminary
A:Molecule type: protein
A:Residues: 24-30;31-32;109-110;456-459;545-552 <ZOO>
C:Genetics:
A:Gene: GDB:CEL
A:Cross-references: GDB:127527; OMIM:114840
A:Map position: 9q34.3-q34.3
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein
F:1-23/Domain: (or 4-23) signal sequence #status predicted <Sig>
F:24-745/Product: triacylglycerol lipase, bile salt-activated #status predicted <MAT>
F:53-536/Domain: cholinesterase homology <CHE>
F:210/Binding site: carboxylate (Asn) (covalent) #status predicted
F:217/458/Active site: Ser, His #status predicted
Query Match 1.5%; Score 12; DB 2; length 745;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 526 YWTFNFAKTGDPN 537
Db 490 YWTFNFAKTGDPN 501
RESULT 2
S5337
carboxylesterase (EC 3.1.1.1) Bi - southern house mosquito
C:Species: Culex pipiens quinquefasciatus (southern house mosquito)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jun-2000
A:Accession: S53371
R:Vaughan, A.; Rodriguez, M.; Hemingway, J.
Biochem. J. 305, 651-658, 1995
A:Title: The independent gene amplification of electrophoretically indistinguishable
A:Reference number: S53370; MUID:95134253; PMID:7530448
A:Accession: S53371
A:Molecule type: mRNA
A:Residues: 1-540 <VANU>
A:Cross-references: EMBL:Z32695; NID:g475069; PIDN:CAA83444.1; PID:g780238
A:Experimental source: strain MRES
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase

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OM protein - protein search, using sw model

Run on: November 5, 2003, 15:22:38 ; Search time 21 Seconds

(without alignments)
3736.640 Million cell updates/sec

Title: US-09-978-423a-375

Perfect score: 816
Sequence: 1 MENSVLWLTALAIKFTLI.....TFSGGCNSTNLPHGSHSTRV 816

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database: PIR 76:*

1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	1.5	745	2	triacylglycerol 11
2	11	1.3	540	2	carboxylesterase 1
3	10	1.2	348	2	CAMP-regulated D2
4	10	1.2	503	2	carboxylesterase 1
5	10	1.2	540	2	carboxylesterase 1
6	10	1.2	540	2	carboxylesterase 1
7	9	1.1	157	2	esterase B1 - souc
8	9	1.1	157	2	acetylchoinestera
9	9	1.1	503	2	lysyl-tRNA synthet
10	9	1.1	532	2	lysine-tRNA ligase
11	9	1.1	539	2	60k esterase (EC 3
12	9	1.1	540	2	carboxylesterase 1
13	9	1.1	549	2	carboxylesterase 1
14	9	1.1	554	2	carboxylesterase 1
15	9	1.1	554	2	carboxylesterase 1
16	9	1.1	557	2	hypothetical prote
17	9	1.1	561	2	esterase - Caenorh
18	9	1.1	561	2	carboxylesterase 1
19	9	1.1	561	2	carboxylesterase 1
20	9	1.1	561	2	carboxylesterase 1
21	9	1.1	562	2	carboxylesterase 1
22	9	1.1	562	2	carboxylesterase 1
23	9	1.1	565	2	esterase precursor
24	9	1.1	566	2	hypothetical prote
25	9	1.1	567	1	carboxylesterase 1
26	9	1.1	567	1	carboxylesterase 1
27	9	1.1	620	2	sterol esterase (E
28	9	1.1	956	2	acetylchoinestera
29	8	1.0	231	2	glicolactin precurs

30	8	1.0	281	2	hypothetical prote
31	8	1.0	289	2	hypothetical prote
32	8	1.0	380	2	probable cysteine
33	8	1.0	450	2	hypothetical prote
34	8	1.0	506	2	cysteine proteinas
35	8	1.0	518	1	multidrug-efflux t
36	8	1.0	539	2	hypothetical prote
37	8	1.0	540	2	carboxylesterase 1
38	8	1.0	544	2	triacylglycerol 11
39	8	1.0	544	2	triacylglycerol 11
40	8	1.0	544	2	triacylglycerol 11
41	8	1.0	544	2	triacylglycerol 11
42	8	1.0	544	2	triacylglycerol 11
43	8	1.0	544	2	triacylglycerol 11
44	8	1.0	544	2	triacylglycerol 11
45	8	1.0	563	1	triacylglycerol 11
46	8	1.0	563	1	triacylglycerol 11
47	8	1.0	578	2	protein 128C12.4b
48	8	1.0	596	1	acetylchoinestera
49	8	1.0	596	1	acetylchoinestera
50	8	1.0	599	2	sterol esterase (E
51	8	1.0	599	2	acetylchoinestera
52	8	1.0	602	2	sterol esterase (E
53	8	1.0	612	2	acetylchoinestera
54	8	1.0	637	2	sterol esterase (E
55	8	1.0	656	2	acetylchoinestera
56	8	1.0	658	2	hypothetical prote
57	8	1.0	672	2	hypothetical prote
58	8	1.0	730	2	hypothetical prote
59	8	1.0	782	1	probable organic s
60	8	1.0	837	2	mucin-like peptide
61	8	1.0	912	1	protein kinase C 1
62	8	1.0	918	1	protein kinase C 1
63	8	1.0	2145	2	glutamate synthase
64	7	0.9	23	2	trans-cinnamate 4-
65	7	0.9	28	2	sterol esterase (E
66	7	0.9	89	2	hypothetical prote
67	7	0.9	98	2	probable PE protei
68	7	0.9	103	2	hypothetical prote
69	7	0.9	133	2	ribosome binding f
70	7	0.9	141	2	choinesterase (EC
71	7	0.9	141	2	choinesterase (EC
72	7	0.9	141	2	choinesterase (EC
73	7	0.9	141	2	choinesterase (EC
74	7	0.9	141	2	choinesterase (EC
75	7	0.9	162	2	choinesterase (EC
76	7	0.9	166	2	choinesterase (EC
77	7	0.9	177	2	choinesterase (EC
78	7	0.9	180	2	choinesterase (EC
79	7	0.9	188	2	choinesterase (EC
80	7	0.9	199	2	choinesterase (EC
81	7	0.9	206	2	choinesterase (EC
82	7	0.9	208	2	choinesterase (EC
83	7	0.9	208	2	choinesterase (EC
84	7	0.9	208	2	choinesterase (EC
85	7	0.9	225	2	choinesterase (EC
86	7	0.9	225	2	choinesterase (EC
87	7	0.9	230	2	choinesterase (EC
88	7	0.9	240	2	choinesterase (EC
89	7	0.9	256	2	choinesterase (EC
90	7	0.9	259	2	choinesterase (EC
91	7	0.9	259	2	choinesterase (EC
92	7	0.9	259	2	choinesterase (EC
93	7	0.9	262	2	choinesterase (EC
94	7	0.9	270	2	choinesterase (EC
95	7	0.9	270	2	choinesterase (EC
96	7	0.9	274	2	choinesterase (EC
97	7	0.9	274	2	choinesterase (EC
98	7	0.9	280	2	choinesterase (EC
99	7	0.9	282	2	choinesterase (EC
100	7	0.9	291	2	choinesterase (EC

Query Match 1.3%; Score 11; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 240 GAFGDPKRYT 250
|||
Db 176 GAFGDPKRYT 186

RESULT 3
C26720
C:Species: Dictyostelium discoideum
C:Date: 19-Nov-1988 #sequence_revision 30-Jun-1991 #text_change 16-Dec-1998
C:Accession: C26720
R:Van, S.K.O.; Firtel, R.A.
Mol. Cell. Biol. 7, 458-469, 1987
A:Title: Cyclic AMP regulation of early gene expression in Dictyostelium discoideum: mod
A:Reference number: A26720; MUID:87172740; PMID:3031475
A:Accession: C26720
A:Molecule type: DNA
A:Residues: 1-348 <MAN>
A:Cross-references: GB:M15966
C:Superfamily: cholinesterase homology
F:52-343/Domain: cholinesterase homology <CHE>

Query Match 1.2%; Score 10; DB 2; Length 348;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 TINRGLTG 210
|||
Db 123 TINRGLTG 132

RESULT 4
S53372
C:Species: Culex pipiens quinquefasciatus (southern house mosquito)
C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999
R:Vaughan, A.; Rodriguez, M.; Hemingway, J.
Biochem. J. 305, 651-658, 1995
A:Title: The independent gene amplification of electrophoretically indistinguishable B e
A:Reference number: S53370; MUID:9534253; PMID:7530448
A:Accession: S53372
A:Molecule type: mRNA
A:Residues: 1-503 <VAU>
A:Cross-references: EMBL:Z32696
A:Experimental source: PeISS
R:Vaughan, A.; Rodriguez, M.; Hemingway, J.
Submitted to the EMBL Data Library, April 1994
A:Description: The independent gene amplification of indistinguishable esterase B elect
A:Reference number: S44212
A:Accession: S44212
A:Molecule type: mRNA
A:Residues: 1-503 <VAU>
A:Cross-references: EMBL:Z32696; NID:9475070; PID:9475071
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase

Query Match 1.2%; Score 10; DB 2; Length 503;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 AFGDPKRYT 250
|||
Db 140 AFGDPKRYT 149

RESULT 5
S53370
C:Species: Culex pipiens quinquefasciatus (southern house mosquito)
C:Date: 15-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 21-Jul-2000
C:Accession: S53370; MUID:9534253; PMID:7530448
A:Title: The independent gene amplification of electrophoretically indistinguishable
A:Reference number: S53370; MUID:9534253; PMID:7530448
A:Accession: S53370
A:Molecule type: mRNA
A:Residues: 1-540 <VAU>
A:Cross-references: EMBL:Z32694; NID:9475067; PID:CAA83643.1; PID:9475068
A:Experimental source: strain Pe:RR
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase

C:Species: Culex pipiens quinquefasciatus (southern house mosquito)
C:Date: 15-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 21-Jul-2000
C:Accession: S53370; S44211
R:Vaughan, A.; Rodriguez, M.; Hemingway, J.
Biochem. J. 305, 651-658, 1995
A:Title: The independent gene amplification of electrophoretically indistinguishable
A:Reference number: S53370; MUID:9534253; PMID:7530448
A:Accession: S53370
A:Molecule type: mRNA
A:Residues: 1-540 <VAU>
A:Cross-references: EMBL:Z32694; NID:9475067; PID:CAA83643.1; PID:9475068
A:Experimental source: strain Pe:RR
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase

Query Match 1.2%; Score 10; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 AFGDPKRYT 250
|||
Db 177 AFGDPKRYT 186

RESULT 6
A35986
C:Species: Culex pipiens quinquefasciatus (southern house mosquito)
C:Date: 16-Nov-1990 #sequence_revision 13-Jan-1993 #text_change 21-Jul-2000
C:Accession: A35986
R:Mouches, C.; Pauplin, Y.; Aarwal, M.; Lemieux, L.; Hetzog, M.; Abador, M.; Beyssat
Proc. Natl. Acad. Sci. U.S.A. 87, 2574-2578, 1990
A:Title: Characterization of amplification core and esterase B1 gene responsible for
A:Reference number: A35986; MUID:90207238; PMID:2120576
A:Accession: A35986
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-540 <MOU>
A:Cross-references: GB:M32228; NID:9156687; PID:AAA28289.1; PID:9156688
A:Note: the authors translated the codon CGT for residue 213 as Ala, and CGT for resi
C:Superfamily: cholinesterase; cholinesterase homology

Query Match 1.2%; Score 10; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 AFGDPKRYT 250
|||
Db 177 AFGDPKRYT 186

RESULT 7
T29347
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
R:Wu, X.; Le, T.T.
Submitted to the EMBL Data Library, April 1996
A:Description: The sequence of C. elegans cosmid F01G12.
A:Reference number: Z20611
A:Accession: T29347
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-157 <MTX>
A:Cross-references: EMBL:U53342; PID:AAA96212.1; GSPDB:GN00028; CESP:ace-1
A:Experimental source: strain Bristol N2; clone F01G12
C:Genetics:
A:Gene: CESP:ace-1
A:Map position: X
A:Insertions: 46/2; 110/1; 143/2
C:Superfamily: cholinesterase; cholinesterase homology

A: Molecule type: mRNA
A: Residues: 1-540 <LON>
A: Cross-references: GB:M20629; GB:X13587; NID:g203279; PIDN:AAA40871.1; PID:g203280
C: Superfamily: cholinesterase; cholinesterase homology
C: Keywords: carboxylic ester hydrolase; glycoprotein
F: 1-9/Domain: signal sequence #status predicted <SIG>
F: 13-540/Product: carboxylesterase #status predicted <CAT>
F: 41-529/Domain: cholinesterase homology <CHE>
F: 70,265,266,293,366,467/Binding site: carbohydrate (Asn) (covalent) #status predicted
F: 212,444/Active site: Ser, His #status predicted

Query Match 1.1%; Score 9; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 EDCLYNTY 133
Db 105 EDCLYNTY 113

RESULT 13
X0054
carboxylesterase (EC 3.1.1.1) E1 precursor, minor form - rat
C: Species: Rattus norvegicus (Norway rat)
C: Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Aug-1995
C: Accession: X0054
R: Takagi, Y.; Morohashi, K.; Kawabata, S.; Go, M.; Omura, T.
J. Biochem. 104, 801-806, 1988
A: Title: Molecular cloning and nucleotide sequence of cDNA of microsomal carboxylesterase
A: Reference number: X0054; MUID:89174514; PMID:2335453
A: Accession: X0054
A: Molecule type: mRNA
A: Residues: 1-549 <TAK>
A: Experimental source: liver
C: Superfamily: cholinesterase; cholinesterase homology
C: Keywords: carboxylic ester hydrolase; glycoprotein; microscope
F: 118/Domain: signal sequence #status predicted <SIG>
F: 19-549/Product: carboxylesterase E1 #status predicted <CAT>
F: 50-538/Domain: cholinesterase homology <CHE>
F: 79,274,302,375,476/Binding site: carbohydrate (Asn) (covalent) #status predicted
F: 221,453/Active site: Ser, His #status predicted

Query Match 1.1%; Score 9; DB 2; Length 549;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 EDCLYNTY 133
Db 114 EDCLYNTY 122

RESULT 14
A3960
carboxylesterase (EC 3.1.1.1) precursor - mouse
C: Species: Mus musculus (house mouse)
C: Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 18-Jun-1999
C: Accession: A3960
R: Ovnac, M.; Tepperman, K.; Medda, S.; Elliott, R.N.; Stephenson, D.A.; Grant, S.G.; Gar
Genomics 9, 344-354, 1991
A: Title: Characterization of a murine cDNA encoding a member of the carboxylesterase mul
A: Reference number: A3960; MUID:51169540; PMID:1845565
A: Accession: A3960
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-554 <OVN>
A: Cross-references: GB:M57960; NID:g192853; PIDN:AAA63297.1; PID:g192854
C: Superfamily: cholinesterase; cholinesterase homology
C: Keywords: carboxylic ester hydrolase
F: 50-540/Domain: cholinesterase homology <CHE>
F: 221,455/Active site: Ser, His #status predicted

Query Match 1.1%; Score 9; DB 2; Length 554;
Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 EDCLYNTY 133
Db 114 EDCLYNTY 122

RESULT 15
T31783
hypothetical protein F13H6.3 - Caenorhabditis elegans
C: Species: Caenorhabditis elegans
C: Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Jan-2000
C: Accession: T31783
R: Jones, K.; Wohldmann, P.
Submitted to the EMBL Data Library, July 1997
A: Description: The sequence of C. elegans cosmid F13H6.
A: Reference number: Z21085
A: Accession: T31783
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-554 <JON>
A: Cross-references: EMBL:AF016437; PIDN:AA56887.1; GSPDB:GN00023; CESP:F13H6.3
A: Experimental source: strain Bristol N2; clone F13H6
C: Genetics:
A: Gene: CESP:F13H6.3
A: Map position: 5
A: Introns: 31/3; 84/3; 113/3; 143/2; 225/1; 443/1; 486/2
C: Superfamily: cholinesterase; cholinesterase homology

Query Match 1.1%; Score 9; DB 2; Length 554;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 168 PVMVYIHGG 176
Db 118 PVMVYIHGG 126

RESULT 16
A56690
esterase - Caenorhabditis elegans
C: Species: Caenorhabditis elegans
C: Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 21-Jul-2000
C: Accession: A56690; S21556
R: Fedon, Y.; Cousin, X.; Toulant, J.P.; Thierry-Mieg, D.; Atpagau, M.
DNA Seq. 3, 347-355, 1993
A: Title: cDNA sequence, gene structure, and cholinesterase-like domains of an esteras
A: Reference number: A56690; MUID:94033620; PMID:8219278
A: Accession: A56690
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-557 <FED>
A: Cross-references: EMBL:X66104; NID:g6703; PIDN:CAA46899.1; PID:g6704
C: Genetics:
A: Introns: 31/3; 84/3; 113/3; 143/2; 225/1; 443/1; 486/2
C: Superfamily: cholinesterase; cholinesterase homology
F: 39-537/Domain: cholinesterase homology <CHE>

Query Match 1.1%; Score 9; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 168 PVMVYIHGG 176
Db 118 PVMVYIHGG 126

RESULT 17
S62788
carboxylesterase (EC 3.1.1.1) ES-4 precursor, liver - rat
N: Alternate names: hydrolase B
C: Species: Rattus norvegicus (Norway rat)
C: Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999

C:Accession: S62788; S51203; A55304; S49257
 R:Robbi, M.; van Schaftingen, E.; Beaufay, H.
 B:Biochem. J. 313, 821-826, 1996
 A:Title: Cloning and sequencing of rat liver carboxylesterase ES-4 (microsomal, palmitoyl-
 A:Reference number: S62788; MUID:96390723; PMID:8611161
 A:Accession: S62788
 A:Molecule type: mRNA
 A:Residues: 1-561 <ROB>
 A:Cross-References: EMBL:X81825; NID:9550417; PIDN:CA57419.1; PID:9550418
 A:Experimental source: liver
 R:Morjan, E.W.; Yan, B.; Greenway, D.; Petersen, D.R.; Parkinson, A.
 Arch Biochem Biophys. 315, 495-512, 1994
 A:Title: Purification and characterization of two rat liver microsomal carboxylesterases
 A:Reference number: S51203; MUID:95077430; PMID:7986098
 A:Accession: S51203
 A:Molecule type: protein
 A:Residues: 19-48 <MOB>
 A:Experimental source: liver
 R:Yan, B.; Yang, D.; Brady, M.; Parkinson, A.
 J. Biol. Chem. 269, 29688-29696, 1994
 A:Title: Rat kidney carboxylesterase. Cloning, sequencing, cellular localization, and re
 A:Reference number: A55304; MUID:95050819; PMID:7961958
 A:Accession: A55304
 A:Molecule type: mRNA
 A:Residues: 1-6, 'F', 8-59, 'P', 61-212, 'A', 214-252, 'T', 254-309, 'T', 312-341, 'N', 343-424, 'F'
 A:Cross-References: GB:U0697; NID:9562007
 A:Note: the sequence in GenBank entry RNU0697, release 107, (PID:9562008) has the codon
 R:Robbi, M.; Beaufay, H.
 submitted to the EMBL Data Library, September 1994
 A:Reference number: S49257
 A:Accession: S49257
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-561 <RO2>
 A:Cross-References: EMBL:X81825; NID:9550417; PIDN:CA57419.1; PID:9550418
 A:Function:
 A:Description: catalyzes conversion of carboxylic ester to alcohol and carboxylic anion
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; liver
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-561/Product: carboxylesterase ES-4 #status experimental <MAT>
 F:50-551/Domain: cholinesterase homology <CHE>
 F:221-466/Active site: Ser, His #status predicted
 F:301/Binding site: carboxylate (asn) (covalent) #status predicted
 Query Match 1.1%; Score 9; DB 2; Length 561;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 125 EDCLYLNLY 133
 Db 114 EDCLYLNLY 122
 RESULT 18
 S71597
 Carboxylesterase (EC 3.1.1.1) precursor, liver - rat
 N:Alternate names: hydrolase C
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 13-Sep-1998
 C:Accession: S71597
 R:Yan, B.; Yang, D.; Parkinson, A.
 Arch. Biochem. Biophys. 317, 222-234, 1995
 A:Title: Cloning and expression of hydrolase C, a member of the rat carboxylesterase fam
 A:Reference number: S71597; MUID:95177656; PMID:7872788
 A:Accession: S71597
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-561 <YAN>
 A:Experimental source: liver; endoplasmic reticulum
 A:Function:
 A:Description: catalyzes conversion of carboxylic ester to alcohol and carboxylic anion
 C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; liver
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-561/Product: carboxylesterase #status predicted <MAT>
 F:50-551/Domain: cholinesterase homology <CHE>
 F:558-561/Region: endoplasmic reticulum retention signal
 F:79,301/Binding site: carboxylate (asn) (covalent) #status predicted
 F:221,466/Active site: Ser, His #status predicted
 Query Match 1.1%; Score 9; DB 2; Length 561;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 125 EDCLYLNLY 133
 Db 114 EDCLYLNLY 122
 RESULT 19
 JC2447
 Carboxylesterase (EC 3.1.1.1) ES-3 precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 29-Mar-1995 #sequence_revision 26-May-1995 #text_change 18-Jun-1995
 C:Accession: JC2447; S23462
 R:Robbi, M.; Beaufay, H.
 Biochem. Biophys. Res. Commun. 203, 1404-1411, 1994
 A:Title: Cloning and sequencing of rat liver carboxylesterase ES-3 (ECASYN).
 A:Reference number: JC2447; MUID:95032008; PMID:7945287
 A:Accession: JC2447
 A:Molecule type: mRNA
 A:Residues: 1-561 <ROB>
 A:Cross-References: GB:X81995; NID:9550146; PIDN:CA57158.1; PID:9550147
 A:Experimental source: liver
 R:Wedda, S.; Proia, R.L.
 Eur. J. Biochem. 206, 801-806, 1992
 A:Title: The carboxylesterase family exhibits C-terminal sequence diversity reflecting
 A:Reference number: S23460; MUID:92299009; PMID:1606962
 A:Accession: S23462
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 503-554, 'R', 556-561 <MED>
 A:Cross-References: EMBL:X65295; NID:957557; PIDN:CA446390.1; PID:957558
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase; glycoprotein
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-561/Product: carboxylesterase ES-3 #status predicted <MAT>
 F:50-551/Domain: cholinesterase homology <CHE>
 F:79,107,489/Binding site: carboxylate (asn) (covalent) #status predicted
 F:221,466/Active site: Ser, His #status predicted
 Query Match 1.1%; Score 9; DB 2; Length 561;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 125 EDCLYLNLY 133
 Db 114 EDCLYLNLY 122
 RESULT 20
 S47655
 Carboxylesterase (EC 3.1.1.1) precursor - golden hamster
 C:Species: Mesocricetus auratus (golden hamster)
 C:Date: 26-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 20-Jun-2000
 C:Accession: S47655
 R:Score, T.; Isobe, M.; Takabatake, E.; Wang, C.Y.
 Biochem. Biophys. Acta 1207, 138-142, 1994
 A:Title: Cloning and sequence analysis of a hamster liver cDNA encoding a novel putat
 A:Reference number: S47655; MUID:94318665; PMID:8043605
 A:Accession: S47655
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-561 <SON>
 A:Cross-References: EMBL:D85866; NID:9531238; PIDN:BA05913.1; PID:9531239

C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase
F:58-546/Domain: cholinesterase homology <CH2>
F:227,459/Active site: Ser, His #status predicted

Query Match 1.1%; Score 9; DB 2; Length 561;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 EDCLYLNTY 133
Db 120 EDCLYLNTY 128

RESULT 21

A:Accession: A55281
A:Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-562 <OVN>
A:Cross-references: GB:S80191; NID:9244727; PIDN:AB2135.1; PID:9244728
A:Note: sequence extracted from NCBI backbone (NCBI:80191, NCBI:80194)
C:Superfamily: Cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum
F:51-552/Domain: cholinesterase homology <CH5>
F:222,467/Active site: Ser, His #status predicted

Query Match 1.1%; Score 9; DB 2; Length 562;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 EDCLYLNTY 133
Db 115 EDCLYLNTY 123

RESULT 22

A:Accession: S27782
A:Status: precursor - Caenorhabditis briggsae
C:Species: Caenorhabditis briggsae
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Jun-1993
A:Accession: S27782
R:Kennedy, B.P.; Aamodt, E.O.; Allen, F.L.; Chung, M.A.; Heschi, M.F.; McGhee, J.D.
submitted to the EMBL Data Library, June 1992
A:Description: The gut esterase gene (ges-1) from the nematode *Caenorhabditis elegans*
A:Reference number: S27782
A:Accession: S27782
A:Molecule type: DNA
A:Residues: 1-562 <KEN>
A:Cross-references: EMBL:M96144; NID:9156311; PIDN:AA28056.1; PID:9156312
C:Genetics:
A:Gene: ges-1
A:Introns: 54/3; 154/1; 325/-; 403/3; 448/1; 492/2
C:Superfamily: cholinesterase; cholinesterase homology
F:1-16/Domain: signal sequence #status predicted <ST3>
F:17-562/Product: elastase #status predicted <MA>
F:38-540/Domain: cholinesterase homology <CH5>

Query Match 1.1%; Score 9; DB 2; Length 562;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 PVVNTNYGK 35
|||||

Db 18 PVVNTNYGK 26

RESULT 23

T29718
hypothetical protein K11G9.1 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
A:Accession: T29718
R:Greco, T.; Bradshaw, H.
submitted to the EMBL Data Library, July 1996
A:Description: The sequence of *C. elegans* cosmid K11G9.
A:Reference number: Z20672
A:Accession: T29718
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-565 <GRE>
A:Cross-references: EMBL:U64953; PIDN:AB04976.1; GSPDB:GN00023; CESP:K11G9.1
A:Experimental source: strain Bristol N2; clone K11G9
C:Genetics:
A:Gene: CESP:K11G9.1
A:Map position: 5
A:Introns: 31/3; 114/3; 144/2; 282/1; 352/1; 460/1
C:Superfamily: cholinesterase; cholinesterase homology

Query Match 1.1%; Score 9; DB 2; Length 565;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 203 NVRLGILGF 211
Db 157 NVRLGILGF 165

RESULT 24

S19307
carboxylesterase (EC 3.1.1.1) precursor - pig
N:Alternate names: proline-beta-naphthylamidase
C:Species: *Sus scrofa domestica* (domestic pig)
C>Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 18-Jun-1999
A:Accession: S19307; S23607
R:Matsumura, M.; Inoue, H.; Ichinose, M.; Tsukada, S.; Miya, K.; Kurokawa, K.; Takah
FEBS Lett. 293, 37-41, 1991
A:Title: The nucleotide and deduced amino acid sequences of porcine liver proline-bet
A:Reference number: S19307; MUID:92070571; PMID:1959668
A:Accession: S19307
A:Molecule type: mRNA
A:Residues: 1-566 <MAT1>
A:Cross-references: EMBL:X63323; NID:91930; PIDN:CAA44929.1; PID:91931
A:Accession: S23607
A:Molecule type: protein
A:Residues: 19-40 <MAT2>
A:Note: 28-194 and 33-194 were also found
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; homocitri
F:1-18/Domain: signal sequence #status predicted <ST3>
F:19-566/Product: carboxylesterase #status experimental <MA>
F:51-552/Domain: cholinesterase homology <CH5>
F:83/Binding site: carboxylate (Asn) (covalent) #status predicted
F:222,467/Active site: Ser, His #status predicted

Query Match 1.1%; Score 9; DB 2; Length 566;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 EDCLYLNTY 133
Db 115 EDCLYLNTY 123

RESULT 25

A41010
carboxylesterase (EC 3.1.1.1) precursor, monocyte/macrophage [validated] - human


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Query Match          1.1%; Score 9; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      529 NFAKTADPN 537
      |||||
      504 NFAKTADPN 512

RESULT 28
A:Accession: A56920
A:Species: Drosophila melanogaster
C:Date: 11-Aug-1995 #sequence_revision: 11-Aug-1995 #text_change 21-Jul-2000
C:Accession: A56920
A:Accession: A56920
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-956 <AUL>
A:Cross-references: GB:L39083; NID:9899061; PIDN:AA041579.1; PID:G899062
C:Genetics:
A:Gene: FlyBase:G1
A:Cross-references: FlyBase:FBgn0001987
C:Superfamily: Cholinesterase homology
C:Keywords: Transmembrane protein
F:178-701/Domain: cholinesterase homology <CHE>

Query Match          1.1%; Score 9; DB 2; Length 356;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      168 PVMVYIHG 176
      |||||
      253 PVMVYIHG 261

RESULT 29
A:Accession: T19267
A:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T19267
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Accession: T19267
A:Molecule type: DNA
A:Residues: 1-231 <WIL>
A:Cross-references: EMBL:Z37139; PIDN:CAA85488.1; GSPDB:GN00022; CESP:C14B1.8
A:Experimental source: clone C14B1
C:Genetics:
A:Gene: CESP:C14B1.8
A:Map position: 3
A:Introns: 25/1; 58/1; 117/2; 146/2; 181/2

Query Match          1.0%; Score 8; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      320 RNKRYKEU 327
      |||||
      176 RNKRYKEU 183

RESULT 30
A:Accession: T26999
A:Species: Caenorhabditis elegans

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C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
A:Accession: T26999
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Accession: T26999
A:Accession: T26999
A:Molecule type: DNA
A:Residues: 1-281 <WIL>
A:Cross-references: EMBL:AL110490; NID:e1542263; PIDN:CA854443.1; CESP:Y48B6A.15
A:Experimental source: clone Y48B6A
C:Genetics:
A:Gene: CESP:Y48B6A.15
A:Introns: 29/3; 65/2; 139/2; 165/3

Query Match          1.0%; Score 8; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      125 EDCLYLNI 132
      |||||
      125 EDCLYLNI 132

RESULT 31
A:Accession: B75591
A:Species: Deinococcus radiodurans (strain R1)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 15-Sep-2000
C:Accession: B75591
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-289 <WHL>
A:Cross-references: GB:AE001863; GB:AE001825; NID:96460670; PIDN:AA112504.1; PID:96460670
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRA0359
A:Map position: 2
C:Superfamily: Deinococcus radiodurans hypothetical protein DRA0359

Query Match          1.0%; Score 8; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      37 RGLRTPRP 44
      |||||
      78 RGLRTPRP 85

RESULT 32
A:Accession: T40851
A:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
C:Accession: T40851
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-380 <RAN>
A:Cross-references: EMBL:AL121783; PIDN:CA857844.1; GSPDB:GN00068; SPDB:SPCC11E10.02
A:Experimental source: strain 972h-; cosmid c1E10
C:Genetics:

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A:Gene: SPDB:SPCCL1E13.02C
 A:Map position: 3
 C:Keywords: cysteine proteinase; hydrolase

Query Match
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 764 LRSPDDI 771
 |||||
 Db 273 LRSPDDI 280

RESULT 33

D30047
 Hypothetical protein SA2240 (imported) - *Staphylococcus aureus* (strain N315)
 C:Species: *Staphylococcus aureus*
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C:Accession: D90047
 R:Kurda, M.; Chla, T.; Uchiyama, T.; Baba, T.; Yuzawa, H.; Kobayashi, T.; Cui, L.; Oguma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shibata, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hitamatsu, K.
 Lancet 357, 1225-1240, 2001
 A>Title: Whole genome sequencing of *refic111*-resistant *Staphylococcus aureus*.
 A:Reference number: A89758; X013:2311952; PMID:11418146
 A:Accession: D90047
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-450 <R>

A:Cross-references: GB:BA000018; PID:g13702401; F:DN:BA843542.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: SA2240

Query Match
 Best Local Similarity 100.0%; Score 8; DB 2; Length 450;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 ECCLYINI 132
 |||||
 Db 80 ECCLYINI 87

RESULT 34

S32561
 cysteine proteinase - *Plasmodium vinckei*
 C:Species: *Plasmodium vinckei*
 C:Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 13-Sep-1995

C:Accession: S32561
 R:Roenthal, P.U.
 Biochim. Biophys. Acta 1173, 91-93, 1993
 A>Title: A *Plasmodium vinckei* cysteine proteinase shares unique features with its plasmodium reference number: S32561; PMID:8485161
 A:Accession: S32561
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-506 <R>
 A:Cross-references: GB:L08500
 C:Superfamily: trophozoite cysteine proteinase

Query Match
 Best Local Similarity 100.0%; Score 8; DB 2; Length 506;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 677 VTAVGAS 684
 |||||
 Db 391 VTAVGAS 398

RESULT 35

G69804
 multidrug-efflux transporter homolog yfiU - *Bacillus subtilis*
 C:Species: *Bacillus subtilis*

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
 C:Accession: G69804
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berch, C.; Brost, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.Y.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabbre, C.; Ferrari, Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gal, lech, C.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holappell, S.; Hosono, S.; Hullo, M.; Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau, Y.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Poterete, Rieger, M.; Rivoita, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scan, A.; Authors: Schleif, S.; Schriener, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Sekeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A.; Authors: Yoshikawa, H.F.; Zunshtein, E.; Yoshikawa, H.; Danchin, A.

A>Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*
 A:Reference number: A69580; PMID:9804033; PMID:9384377
 A:Accession: G69804
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-518 <R>
 A:Cross-references: GB:299108; GB:AL009126; NID:g2633055; PIDN:CAB12669.1; PID:g263311
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yfiU
 C:Superfamily: multidrug-efflux transporter
 C:Keywords: antibiotic resistance; transmembrane protein

Query Match
 Best Local Similarity 100.0%; Score 8; DB 1; Length 518;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 VEQYGVV 58
 |||||
 Db 300 VEQYGVV 307

RESULT 36

T3252
 Hypothetical protein T28C12.5 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000

C:Accession: T32052
 R:Leewitch, C.; Wohldmann, P.; Graves, T.; Bradshaw, H.
 submitted to the EMBL Data Library, July 1997
 A:Description: The sequence of *C. elegans* csmid T28C12.
 A:Reference number: Z21117
 A:Accession: T32052

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-339 <LED>
 A:Cross-references: EMBL:AF016679; PIDN:AA66162.1; GSPDB:GN00023; CESP:T28C12.5
 A:Experimental source: strain Bristol N2; clone T28C12
 C:Genetics:
 A:Gene: CESP:T28C12.5
 A:Map position: 5
 A:Introns: 16/3; 57/3; 112/3; 262/2; 316/1; 373/3; 466/2
 C:Superfamily: cholinesterase; cholinesterase homology

Query Match
 Best Local Similarity 100.0%; Score 8; DB 2; Length 539;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 LGFSGTGD 216
 |||||
 Db 135 LGFSGTGD 142

RESULT 37

SS1043
 carboxylesterase (EC 3.1.1.1) precursor - Atlantic salmon (fragment)
 N:Alternate names: carboxylester 1lipase

C:Species: *Salmo salar* (Atlantic salmon)
 C:Date: 01-Aug-1995 #sequence_revision 23-Feb-1996 #text_change 18-Jun-1999
 C:Accession: S51043; S37074
 R:Gjellervik, D.R.; Lorens, J.B.; Male, R.
 Eur. J. Biochem. 226, 603-612, 1994
 A:Title: Pancreatic carboxylester lipase from Atlantic salmon (*Salmo salar*): cDNA sequence
 A:Reference number: S51043; MIM:950848.9; PMID:8601575
 A:Accession: S51043
 A:Molecule type: mRNA
 A:Residues: 1-540 <GDE>
 A:Cross-references: EMBL:Z25867; NID:9397952; PIDN:CAA81087.1; PID:9397953
 C:Superfamily: Cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase
 F:1-13/Domain: signal sequence (fragment) #status predicted <SIG>
 F:14-540/Product: carboxylesterase #status predicted <NMT>
 F:43-538/Domain: cholinesterase homology <CHE>

Query Match 1.0%; Score 8; DB 2; Length 544;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 NEDCLYN 132
 DB 91 EDCLYNI 98

RESULT 38
 S41090
 triacylglycerol lipase (EC 3.1.1.3) I precursor - yeast (*Geotrichum candidum*) (strain ATCC 34614
 C:Species: *Geotrichum candidum*
 A:Variety: ATCC 34614
 C:Date: 19-Mar-1997 #sequence_revision 05-Feb-1999 #text_change 18-Jun-1999
 C:Accession: S41090
 R:Bertolini, M.C.; Laramee, L.; Thomas, D.Y.; Cygler, M.; Schrag, J.D.; Vernet, T.
 Eur. J. Biochem. 219, 119-125, 1994
 A:Title: Polymorphism in the lipase genes of *Geotrichum candidum* strains.
 A:Reference number: S41090; MIM:94139683; PMID:8306978
 A:Accession: S41090
 A:Molecule type: DNA
 A:Residues: 1-544 <BER>
 A:Cross-references: GB:U02622; NID:9409275; PIDN:AAA03435.1; PID:9409276
 A:Experimental source: ATCC 34614
 A:Note: only the translation of the mature protein is shown
 C:Genetics:
 A:Gene: lip1
 C:Function:
 A:Description: hydrolyzes triacylglycerols into fatty acids and glycerol
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase; glycoprotein; lipid hydrolysis; pyroglyutamic acid
 F:24-541/Domain: cholinesterase homology <CHE>
 F:215-219/Region: interfacial lipid recognition (GXSGX) motif
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
 F:61-105-276-288/Disulfide bonds: #status predicted
 F:217/Active site: Ser #status predicted
 F:283,364/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 1.0%; Score 8; DB 2; Length 544;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 NEDCLYN 131
 DB 102 NEDCLYN 109

RESULT 39
 S41090
 triacylglycerol lipase (EC 3.1.1.3) I precursor - yeast (*Geotrichum candidum*) (strain NR
 C:Species: *Geotrichum candidum*
 A:Variety: NRCC 205002
 C:Date: 19-Mar-1997 #sequence_revision 05-Feb-1999 #text_change 18-Jun-1999
 C:Accession: S41091

R:Bertolini, M.C.; Laramee, L.; Thomas, D.Y.; Cygler, M.; Schrag, J.D.; Vernet, T.
 Eur. J. Biochem. 219, 119-125, 1994
 A:Title: Polymorphism in the lipase genes of *Geotrichum candidum* strains.
 A:Reference number: S41090; MIM:94139683; PMID:8306978
 A:Accession: S41091
 A:Molecule type: DNA
 A:Residues: 1-544 <BER>
 A:Cross-references: GB:U02525; NID:9408460; PIDN:AAA03429.1; PID:9408461
 A:Experimental source: NRCC 205002
 A:Note: only the translation of the mature protein is shown
 C:Genetics:
 A:Gene: lip1
 C:Function:
 A:Description: hydrolyzes triacylglycerols into fatty acids and glycerol
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase; glycoprotein; lipid hydrolysis; pyroglyutamic acid
 F:24-541/Domain: cholinesterase homology <CHE>
 F:215-219/Region: interfacial lipid recognition (GXSGX) motif
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
 F:61-105-276-288/Disulfide bonds: #status predicted
 F:217/Active site: Ser #status predicted
 F:283,364/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 1.0%; Score 8; DB 2; Length 544;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 NEDCLYN 131
 DB 102 NEDCLYN 109

RESULT 40
 S41092
 triacylglycerol lipase (EC 3.1.1.3) I precursor - yeast (*Geotrichum candidum*) (strain ATCC 34614
 C:Species: *Geotrichum candidum*
 A:Variety: NRRL Y-552
 C:Date: 19-Mar-1997 #sequence_revision 05-Feb-1999 #text_change 18-Jun-1999
 C:Accession: S41092
 R:Bertolini, M.C.; Laramee, L.; Thomas, D.Y.; Cygler, M.; Schrag, J.D.; Vernet, T.
 Eur. J. Biochem. 219, 119-125, 1994
 A:Title: Polymorphism in the lipase genes of *Geotrichum candidum* strains.
 A:Reference number: S41090; MIM:94139683; PMID:8306978
 A:Accession: S41092
 A:Molecule type: DNA
 A:Residues: 1-544 <BER>
 A:Cross-references: GB:U02524; NID:9408459; PIDN:AAA03428.1; PID:9408459
 A:Experimental source: NRRL Y-552
 A:Note: only the translation of the mature protein is shown
 C:Genetics:
 A:Gene: lip1
 C:Function:
 A:Description: hydrolyzes triacylglycerols into fatty acids and glycerol
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase; glycoprotein; lipid hydrolysis; pyroglyutamic acid
 F:24-541/Domain: cholinesterase homology <CHE>
 F:215-219/Region: interfacial lipid recognition (GXSGX) motif
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
 F:61-105-276-288/Disulfide bonds: #status predicted
 F:217/Active site: Ser #status predicted
 F:283,364/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 1.0%; Score 8; DB 2; Length 544;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 NEDCLYN 131
 DB 102 NEDCLYN 109

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RESULT 41
S41093
C:Species: Geotrichum candidum
C:Accession: S41093
C:Date: 19-Mar-1997 #sequence_revision 05-Feb-1999 #text_change 18-Jun-1999
R:Bertolini, M.C.; Laramee, L.; Thomas, D.Y.; Cygler, M.; Schrag, J.D.; Vernet, T.
E:J. Biochem. 219, 119-125, 1994
A:Title: Polymorphism in the lipase genes of Geotrichum candidum strains.
A:Reference number: S41090; MUID:94139683; PMID:8306978
A:Accession: S41093
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-544 <BER>
A:Cross-references: GB:U02387; NID:g406507; PIDN:AAA03425.1; PID:g406508
A:Experimental source: NRRU Y-553
A>Note: only the translation of the mature protein is shown
C:Genetics:
A:Gene: lrp1
A:Function:
A:Description: hydrolyzes triacylglycerols into fatty acids and glycerol
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein; lipid hydrolysis; pyroglutamic acid
F:24-541/Domain: cholinesterase homology <CHE>
F:215-219/Region: interfacial lipid recognition (GXSG) motif
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F:61-105,276-288/Disulfide bonds: #status predicted
F:217/Active site: Ser #status predicted
F:283,364/binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1.0%; Score 8; DB 2; Length 544;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 124 NEDCLYN 131
Db 102 NEDCLYN 109

RESULT 42
S41094
C:Species: Geotrichum candidum
C:Accession: S41094
C:Date: 19-Mar-1997 #sequence_revision 05-Feb-1999 #text_change 18-Jun-1999
R:Bertolini, M.C.; Laramee, L.; Thomas, D.Y.; Cygler, M.; Schrag, J.D.; Vernet, T.
E:J. Biochem. 219, 119-125, 1994
A:Title: Polymorphism in the lipase genes of Geotrichum candidum strains.
A:Reference number: S41090; MUID:94139683; PMID:8306978
A:Accession: S41094
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-544 <BER>
A:Cross-references: GB:U02541; NID:g408466; PIDN:AAA03430.1; PID:g408469
A:Experimental source: NRRU 205002
A>Note: only the translation of the mature protein is shown
C:Genetics:
A:Gene: lrp1
A:Function:
A:Description: hydrolyzes triacylglycerols into fatty acids and glycerol
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein; lipid hydrolysis; pyroglutamic acid
F:24-541/Domain: cholinesterase homology <CHE>
F:215-219/Region: interfacial lipid recognition (GXSG) motif
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F:61-105,276-288/Disulfide bonds: #status predicted
F:217/Active site: Ser #status predicted
F:283,364/binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1.0%; Score 8; DB 2; Length 544;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 124 NEDCLYN 131
Db 102 NEDCLYN 109

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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 124 NEDCLYN 131
Db 102 NEDCLYN 109

RESULT 43
S41095
C:Species: Geotrichum candidum
C:Accession: S41095
C:Date: 19-Mar-1997 #sequence_revision 05-Feb-1999 #text_change 18-Jun-1999
R:Bertolini, M.C.; Laramee, L.; Thomas, D.Y.; Cygler, M.; Schrag, J.D.; Vernet, T.
E:J. Biochem. 219, 119-125, 1994
A:Title: Polymorphism in the lipase genes of Geotrichum candidum strains.
A:Reference number: S41090; MUID:94139683; PMID:8306978
A:Accession: S41095
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-544 <BER>
A:Cross-references: GB:U02623; NID:g409277; PIDN:AAA03436.1; PID:g409278
A:Experimental source: NRRU Y-552
A>Note: only the translation of the mature protein is shown
C:Genetics:
A:Gene: lrp11
A:Function:
A:Description: hydrolyzes triacylglycerols into fatty acids and glycerol
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein; lipid hydrolysis; pyroglutamic acid
F:24-541/Domain: cholinesterase homology <CHE>
F:215-219/Region: interfacial lipid recognition (GXSG) motif
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F:61-105,276-288/Disulfide bonds: #status predicted
F:217/Active site: Ser #status predicted
F:283,364/binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1.0%; Score 8; DB 2; Length 544;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 124 NEDCLYN 131
Db 102 NEDCLYN 109

RESULT 44
S41096
C:Species: Geotrichum candidum
C:Accession: S41096
C:Date: 19-Mar-1997 #sequence_revision 05-Feb-1999 #text_change 18-Jun-1999
R:Bertolini, M.C.; Laramee, L.; Thomas, D.Y.; Cygler, M.; Schrag, J.D.; Vernet, T.
E:J. Biochem. 219, 119-125, 1994
A:Title: Polymorphism in the lipase genes of Geotrichum candidum strains.
A:Reference number: S41090; MUID:94139683; PMID:8306978
A:Accession: S41096
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-544 <BER>
A:Cross-references: GB:U02625; NID:g409279; PIDN:AAA03437.1; PID:g409280
A:Experimental source: NRRU Y-553
A>Note: only the translation of the mature protein is shown
C:Genetics:
A:Gene: lrp11
A:Function:
A:Description: hydrolyzes triacylglycerols into fatty acids and glycerol
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein; lipid hydrolysis; pyroglutamic acid
F:24-541/Domain: cholinesterase homology <CHE>
F:215-219/Region: interfacial lipid recognition (GXSG) motif

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F1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
 F1/1-105,276-288/Disulfide bonds: #status predicted
 F1/17/Active site: Ser #status predicted
 F1/293,364/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 1.0%; Score 8; DB 2; Length 544;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 NEDCLYLN 131
 DB 102 NEDCLYLN 109

RESULT 45
 ACCUGC
 C:tracylglycerol lipase (EC 3.1.1.3) I precursor - yeast (Geotrichum candidum)
 N:Alternate names: lipase
 C:Species: Geotrichum candidum
 C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 31-Mar-2000
 C:Accession: P04992; J00022
 R:Naqao, T.; Shimada, Y.; Sugihara, A.; Tomioka, Y.
 J. Biochem. 113, 776-780, 1993
 A>Title: Cloning and sequencing of two chromosomal lipase genes from Geotrichum candidum
 F1/236/Active site: Ser #status predicted
 F1/302,393/Binding site: carboxylate (Asn) (covalent) #status predicted

A:Accession: P04992; X01D:93380967; PMID:8376874
 A:Molecule type: DNA
 A:Residues: 1-563 <NAG>
 A>Note: the translation of residues 31-550 and the corresponding nucleotide sequence are
 R:Shimada, Y.; Sugihara, A.; Tomioka, Y.; Iizumi, T.; Tsunashima, S.
 J. Biochem. 106, 383-388, 1989
 A>Title: cDNA molecular cloning of Geotrichum candidum lipase.
 A:Reference number: J00022; M01D:90110016; PMID:2481674
 A:Accession: J00022
 A:Molecule type: mRNA
 A:Residues: 1-563 <SH1>
 A:Experimental source: strain ATCC 34614
 A>Note: sequences of several small peptides were also determined
 C:Comment: The extracellular lipase produced by Geotrichum candidum hydrolyzes all ester
 C:Genetics:
 A:Gene: lip1
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase; glycoprotein; pyroglutamic acid
 F1/19/Domain: signal sequence #status predicted <SIG>
 F1/3-563/Product: tracylglycerol lipase #status experimental <MAT>
 F1/3-563/Domain: cholinesterase homology <CHE>
 F1/234-238/Region: interfacial lipid recognition (GXSG) motif
 F1/20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
 F1/80-124,295-307/Disulfide bonds: #status predicted
 F1/236/Active site: Ser #status predicted
 F1/302,393/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 1.0%; Score 8; DB 1; Length 563;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 NEDCLYLN 131
 DB 121 NEDCLYLN 129

RESULT 46
 P04993
 C:tracylglycerol lipase (EC 3.1.1.3) II precursor - yeast (Geotrichum candidum)
 C:Species: Geotrichum candidum
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000
 C:Accession: P04993; A46760
 R:Naqao, T.; Shimada, Y.; Sugihara, A.; Tomioka, Y.
 J. Biochem. 113, 776-780, 1993
 A>Title: Cloning and sequencing of two chromosomal lipase genes from Geotrichum candidum
 A:Reference number: P04992; M01D:93380967; PMID:8376874
 A:Accession: P04993
 A:Molecule type: DNA

A:Residues: 1-563 <NAG>
 A>Note: the translation of residues 31-550 and the corresponding nucleotide sequence
 R:Shimada, Y.; Sugihara, A.; Iizumi, T.; Tomioka, Y.
 J. Biochem. 107, 703-707, 1990
 A>Title: cDNA cloning and characterization of Geotrichum candidum lipase II.
 A:Reference number: A46760; M01D:90375435; PMID:2398037
 A:Accession: A46760
 A:Molecule type: mRNA
 A:Residues: 1-563 <SH1>
 A:Cross-references: GB:D00697; NID:g217926; PID:BA00603.1; PID:g217927
 C:Comment: The extracellular lipase produced by Geotrichum candidum hydrolyzes all es
 C:Genetics:
 A:Gene: lip1
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase; glycoprotein; pyroglutamic acid
 F1/1-19/Domain: signal sequence #status predicted <SIG>
 F1/2-563/Product: tracylglycerol lipase II #status predicted <MAT>
 F1/3-563/Domain: cholinesterase homology <CHE>
 F1/234-238/Region: interfacial lipid recognition (GXSG) motif
 F1/20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
 F1/80-124,295-307/Disulfide bonds: #status predicted
 F1/236/Active site: Ser #status predicted
 F1/302,393/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 1.0%; Score 8; DB 1; Length 563;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 NEDCLYLN 131
 DB 121 NEDCLYLN 128

RESULT 47
 P89068
 C:protein T26C12.4b (imported) - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
 C:Accession: P89068
 R:Anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A>Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
 A:Reference number: A75000; M01D:99069613; PMID:9851916
 A>Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C
 A:Accession: P89068
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-578 <STO>
 A:Cross-references: GB:chr_V; PID:AB66160.1; PID:g215714; GSPDB:GN00023; CESP:T280
 C:Genetics:
 A:Gene: T26C12.4b
 A:Map position: 5
 C:Superfamily: cholinesterase; cholinesterase homology

Query Match 1.0%; Score 8; DB 2; Length 578;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 UGFLSTGD 216
 DB 159 UGFLSTGD 166

RESULT 48
 S25062
 C:tracylglycerol lipase (EC 3.1.1.3) precursor - rabbit
 N:Alternate names: cholesteryl esterase
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S25062; S29847
 R:Collwell, N.; Aleman-Gomez, G.; Kumar, V.B.
 submitted to the EMBL Data Library, May 1992

A:Description: Molecular cloning and expression of rabbit cholesterol esterase reveals
 A:Reference number: S25062
 A:Accession: S25062
 A:Molecule type: mRNA
 A:Residues: 1-593 <COL>
 A:Cross-references: EMBL:X65944
 R:Colwell, N.S.; Aleman-Gomez, J.A.; Vijaya Kumar, S.
 Biochim. Biophys. Acta 1172, 175-183, 1993
 A:Title: Molecular cloning and expression of rabbit pancreatic cholesterol esterase.
 A:Reference number: S29847; MUID:93176805; PMID:8433557
 A:Accession: S29847
 A:Molecule type: mRNA
 A:Residues: 1-44, 'A', 47-416, 'W', 418-457, 'Q', 460-485, 'W', 487-499, 'GSAKRWHPETLENQSYLEEN'
 A:Cross-references: EMBL:X65944
 A:Note: the difference near the carboxyl end is due to a frameshift error
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase; glycoprotein
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-593/Product: triacylglycerol lipase #status predicted <MAT>
 F:51-543/Domain: cholinesterase homology <CHE>
 F:207/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:214,453/Active site: Ser, His #status predicted

Query Match 1.0% Score 8; DB 1; Length 593;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 209 LGFLSTCD 216
 |||||
 168 LGFLSTCD 175

RESULT 49
 ACRYE
 N:Alternate names: acetylcholinesterase, asymmetric form
 C:Species: Torpedo californica (Pacific electric ray)
 C:Date: 17-Mar-1987 #sequence revision 38-Nov-1996 #text change 15-Sep-2003
 C:Accession: A00773; A60820; A1962; A23902; B4117; S15677
 R:Schumacher, M.; Camp, S.; Maule, Y.; Newton, M.; Macphee-Quigley, K.; Taylor, S.S.; F
 Nature 319, 407-409, 1986
 A:Title: Primary structure of Torpedo californica acetylcholinesterase deduced from its
 A:Reference number: A00773; MUID:86118676; PMID:3753747
 A:Accession: A00773
 A:Molecule type: mRNA
 A:Residues: 'NS', 11-596 <SCH>
 A:Cross-references: GB:X03439; NID:964389
 A:Experimental source: electric organ
 A:Note: parts of this sequence, including the amino and carboxyl ends of the mature prot
 R:Schumacher, M.; Camp, S.; Maule, Y.; Newton, M.; Macphee-Quigley, K.; Taylor, S.S.; F
 Fed. Proc. 45, 2976-2981, 1986
 A:Title: Primary structure of acetylcholinesterase: implications for regulation and fund
 A:Reference number: A60820; MUID:87054662; PMID:3536598
 A:Accession: A60820
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 22-596 <SC2>
 R:Schumacher, M.; Maule, Y.; Camp, S.; Taylor, P.
 J. Biol. Chem. 263, 18979-18987, 1988
 A:Title: Multiple messenger RNA species give rise to the structural diversity in acetylch
 A:Reference number: A92701; MUID:89066695; PMID:3198606
 A:Accession: A31962
 A:Molecule type: mRNA
 A:Residues: 1-23 <SC3>
 A:Cross-references: EMBL:X03439; NID:964389
 A:Experimental source: clones AChE-11 and AChE-18
 A:Note: revision to sequence A00773
 A:Accession: B31962
 A:Molecule type: DNA, mRNA
 A:Residues: 499-565 <SC4>
 A:Cross-references: GB:X03439; NID:964389
 A:Experimental source: clone AChE-1
 R:Macphee-Quigley, K.; Taylor, P.; Taylor, S.

J. Biol. Chem. 263, 12185-12189, 1988
 A:Title: Primary structures of the catalytic subunits from two molecular forms of acetylcholinesterase
 A:Reference number: A23902; MUID:86008285; PMID:3900071
 A:Accession: A23902
 A:Molecule type: protein
 A:Residues: 22, 'B', 24-45, 214-237 <MAC>
 A:Note: active site Ser identification
 R:Kreienkamp, H.C.; Weise, C.; Raba, R.; Aaviksaar, A.; Huch, F.
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991
 A:Title: Amino acid residues of the catalytic center of acetylcholinesterase from Torpedo
 A:Accession: B41117; MUID:91296772; PMID:2068091
 A:Cross-references: EMBL:X6516
 A:Molecule type: protein
 A:Residues: 130-108 <RE3>
 A:Note: substrate binding site
 R:Maule, Y.; Camp, S.; Gibney, G.; Rachinsky, T.L.; Ekstrom, T.J.; Taylor, P.
 Nature 4, 289-301, 1990
 A:Title: Single gene encodes glycoprophospholipid-anchored and asymmetric acetylcholine
 A:Reference number: F50113; MUID:90166618; PMID:2306366
 A:Accession: S15677
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 557-596 <XAU>
 A:Cross-references: EMBL:X6516
 R:Macphee-Quigley, K.; Vedvick, T.S.; Taylor, P.; Taylor, S.S.
 J. Biol. Chem. 261, 13565-13570, 1986
 A:Title: Profile of the disulfide bonds in acetylcholinesterase.
 A:Reference number: A43099; MUID:87008586; PMID:3759980
 A:Contents: annotation: disulfide bonds
 R:Sussman, J.L.; Harel, M.; Silman, I.
 Submitted to the Brookhaven Protein Data Bank, October 1991
 A:Reference number: A50061; PDB:1ACE
 A:Contents: annotation: X-ray crystallography, 2.8 angstroms, residues 26-481, 511-55
 R:Sussman, J.L.; Harel, M.; Frolow, F.; Oefner, C.; Goldman, A.; Tokur, L.; Silman, I.
 Science 253, 872-879, 1991
 A:Title: Atomic structure of acetylcholinesterase from Torpedo californica: a prototyp
 A:Reference number: A43098; MUID:91343928; PMID:1678899
 A:Contents: annotation: X-ray crystallography, 2.8 angstroms, residues 26-481, 511-55
 C:Comment: Synapses usually contain this 11S (asymmetric) form of cholinesterase with
 cholinesterase occurs on the outer surfaces of cell membranes, including those of erythro
 C:Complex: 11S form is disulfide linked homodimer; 18S form is homotetramer, a dimer
 C:Function:
 A:Description: hydrolyzes acetylcholine to choline and acetate
 A:Pathway: neurotransmitter degradation
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; membrane
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-596/Product: acetylcholinesterase, 11S form #status experimental <MAT>
 F:51-551/Domain: cholinesterase homology <CHE>
 F:180,478,554/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:188-115,275-286,423-542/Disulfide bonds: #status experimental
 F:105/Binding site: substrate (Tyr) #status experimental
 F:121/Active site: Ser #status experimental
 F:348,461/Active site: Glu, His #status predicted
 F:437/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:593/Disulfide bonds: interchain #status experimental

Query Match 1.0% Score 8; DB 1; Length 596;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 125 EDCYLTNI 132
 |||||
 113 EDCYLTNI 120

RESULT 50
 A38868
 acetylcholinesterase (EC 3.1.1.7) precursor - marbled electric ray
 C:Species: Torpedo marmorata (marbled electric ray)
 C:Date: 23-Apr-1993 #sequence revision 15-Nov-1996 #text change 11-Jun-1999
 C:Accession: A38868; A29682; S15696; A25650
 R:Massoulié, C.; Bon, S.

submitted to the EMBL Data Library, June 1992

A:Reference number: A38868

A:Accession: A38868

A:Molecule type: mRNA

A:Residues: 1-599 <MAC>

A:Cross-references: EMBL:X65497; NID:g64414; PIDD:CAA29347.1; FID:g64415

R:Stokrov, J.L.; Krejci, E.; Massoulié, J.

EMBO J. 6, 1865-1873, 1987

A:Title: cDNA sequences of Torpedo marmorata acetylcholinesterase: primary structure of

A:Reference number: A29682; MUID:88004392; PMID:2820703

A:Accession: A29682

A:Molecule type: mRNA

A:Residues: 1-40, 'G', 42-226, 'G', 228-272, 'G', 274-284, 'E', 286-420, 'N', 422-599 <STK>

A:Cross-references: EMBL:X65497

R:Stokrov, J.L.; Duval, N.; Anselmetti, A.; Bon, S.; Krejci, E.; Legay, C.; Osterlund, M.

EMBO J. 7, 2983-2993, 1988

A:Title: Complex alternative splicing of acetylcholinesterase transcripts in Torpedo e

A:Reference number: S01293; MUID:89050550; PMID:3181125

A:Accession: S15656

A:Molecule type: mRNA

A:Residues: 526-599 <S12>

A:Cross-references: EMBL:X13172; NID:g64416; PIDD:CAA31570.1; PID:g64417

A:Experimental source: clone PAC22

R:Bon, S.; Chang, J.Y.; Strosberg, A.D.

FEBS Lett. 289, 206-212, 1986

A:Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-sol

A:Reference number: A91370; MUID:87380761; PMID:3792544

A:Accession: A25653

A:Molecule type: protein

A:Residues: 25-40, 'G', 42-47 <RON>

C:Genetics:

A:Gene: AChE

C:Function:

A:Description: hydrolyzes acetylcholine to choline and acetate

A:Pathway: neurotransmitter degradation

C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; neurotransm

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-599/Product: acetylcholinesterase #status predicted <MNT>

F:54-554/Domain: acetylcholinesterase homology <CHE>

F:81,440,481,557/Binding site: carbonyl site: #status predicted

F:91-118,278-289,426-545/D:disulfide bonds: #status predicted

F:224,351,464/Active site: Ser, Glu, His #status predicted

F:596/Disulfide bonds: interchain #status predicted

Query Match 1.0%; Score 8; DB 1; Length 599;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLN1 132

DB 116 EDCLYLN1 123

RESULT 51:

A57701

sterol esterase (EC 3.1.1.13) precursor - mouse

N:Alternate names: bile salt-stimulated lipase; carboxy ester lipase; cholesterol ester

C:Species: Mus musculus (house mouse)

C:Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 21-Jan-2000

C:Accession: A57701; J04384

R:Edmeyer, A.S.; Kamnitz, K.; Jundberg, L.; Bjursell, G.; Nilsson, G.

Genomics 29, 115-122, 1995

A:Title: Molecular cloning and characterization of the mouse carboxyl ester lipase gene

A:Reference number: A57701; MUID:96079098; PMID:8530650

A:Accession: A57701

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-599 <LID>

A:Cross-references: GB:U37396; NID:g1049321; PIDD:AA625279.1; FID:g1049322

R:Mackay, K.; Lawn, R.M.

Gene 165, 255-259, 1995

A:Title: Characterization of the mouse pancreatic/mammary gland cholesterol esterase

A:Reference number: J04384; MUID:96096531; PMID:8522186

A:Accession: J04384

A:Molecule type: mRNA

A:Residues: 1-599 <MAC>

A:Cross-references: GB:U33169; NID:g1046362; PIDD:AAA20086.1; PID:g1046363

A:Experimental source: mammary gland

C:Comment: This enzyme is synthesized in the pancreas and is transported to the intest

cholesterol esters and fat-soluble vitamin esters, and acts synergistically with pan

ins.

C:Genetics:

A:Gene: CEase

C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase; cholesterol; heparin binding; mammary gland;

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-599/Product: sterol esterase #status predicted <MNT>

F:51-585/Domain: cholinesterase homology <CHE>

F:81,86/Region: heparin binding #status predicted

F:214,340,455/Active site: Ser, Asp, His #status predicted

Query Match 1.0%; Score 8; DB 2; Length 599;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLN1 132

DB 98 EDCLYLN1 105

RESULT 52

T37254

acetylcholinesterase (EC 3.1.1.7) 4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000

C:Accession: T37254

R:Grasso, M.; Culetto, E.; Combes, D.; Fedon, Y.; Touant, J.P.; Arpagaus, M.

FEBS Lett. 424, 279-284, 1998

A:Title: Existence of four acetylcholinesterase genes in the nematodes Caenorhabdit

A:Reference number: Z21648; MUID:98198570; PMID:9539167

A:Accession: T37254

A:Status: preliminary; translated from GB/EMBL/DDJ

A:Molecule type: mRNA

A:Residues: 1-602 <GRA>

A:Cross-references: EMBL:AF025379; NID:g5091493; PIDD:AA014017.1; PID:g507126

A:Experimental source: strain N2

C:Genetics:

A:Gene: ace-4

C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase

Query Match 1.0%; Score 8; DB 2; Length 602;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLN1 132

DB 113 EDCLYLN1 120

RESULT 53

A34967

sterol esterase (EC 3.1.1.13) precursor - rat

N:Alternate names: bile salt-stimulated lipase; carboxy ester lipase; cholesterol e

C:Species: Rattus norvegicus (Norway rat)

C:Date: 29-Mar-1991 #sequence_revision 22-Apr-1995 #text_change 13-Aug-1999

C:Accession: A34967; A26603; A39595; S33476

R:Kissel, J.A.; Fontaine, R.N.; Turk, C.W.; Brockman, H.L.; Hu, D.Y.

Biochim. Biophys. Acta 1006, 227-236, 1989

A:Title: Molecular cloning and expression of cDNA for rat pancreatic cholesterol est

A:Reference number: A34967; MUID:90089378; PMID:2688744

A:Accession: A34967

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-512, 'T', 514-612 <KIS>
 A:Cross-references: GB:X16054; NID:G955942; PIDN:CAA34169.1; PID:G955943
 R:Han, J.H.; Stratowa, C.; Rulter, W.J.
 C:Species: Aedes aegypti (yellow fever mosquito)
 C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
 C:Accession: S66236
 R:Anthony, N.; Rocheleau, T.; Mocelin, G.; See, H.C.; ffrench-Constant, R.
 FEBS Lett. 366, 461-465, 1995
 A:Title: Cloning, sequencing and functional expression of an acetylcholinesterase gene
 A:Reference number: S66236; MUID:95361924; FXID:7655199
 A:Accession: S66236
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-637 <ANT>
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-637/Product: acetylcholinesterase #status predicted <MAT>
 F:57-594/Domain: cholinesterase homology <CHS>

Query Match 1.0%; Score 8; DB 2; Length 612;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCJYINI 132
 Db 98 EDCJYINI 105

RESULT 54
 S66236
 acetylcholinesterase (EC 3.1.1.7) precursor - yellow fever mosquito
 C:Species: Aedes aegypti (yellow fever mosquito)
 C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
 C:Accession: S66236
 R:Anthony, N.; Rocheleau, T.; Mocelin, G.; See, H.C.; ffrench-Constant, R.
 FEBS Lett. 366, 461-465, 1995
 A:Title: Cloning, sequencing and functional expression of an acetylcholinesterase gene
 A:Reference number: S66236; MUID:95361924; FXID:7655199
 A:Accession: S66236
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-637 <ANT>
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-637/Product: acetylcholinesterase #status predicted <MAT>
 F:57-594/Domain: cholinesterase homology <CHS>

hypothetical protein T02B5.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
 C:Accession: T24344
 R:McMurtry, A.
 submitted to the EMBL Data Library, October 1996
 A:Reference number: 219878
 A:Accession: T24344
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-656 <WIL>
 A:Cross-references: EMBL:T81112; PIDN:CA903273.1; GSPDB:GN00023; CESP:T02B5.3
 A:Experimental source: clone T02B5
 A:Gene: CESP:T02B5.3
 A:Map position: 5
 A:Introns: 24/2; 90/2; 120/3; 188/1; 224/3; 283/3; 332/2; 412/2; 517/2; 622/1
 C:Superfamily: cholinesterase; cholinesterase homology

Query Match 1.0%; Score 8; DB 2; Length 656;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 TNYRIGI 208
 Db 162 TNYRIGI 169

RESULT 56
 T32053
 hypothetical protein T28C12.4a - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 01-Dec-2000
 C:Accession: T32053; T32054
 R:Edwith, J.; Wohldmann, P.; Graves, T.; Bradshaw, H.
 submitted to the EMBL Data Library, Jun. 1997
 A:Description: The sequence of C. elegans coemid T28C12.
 A:Reference number: Z21117
 A:Accession: T32053
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-658 <LED>
 A:Cross-references: EMBL:AF016679; PIDN:AA66159.1; GSPDB:GN00023; CESP:T28C12.4a
 A:Experimental source: strain Bristol N2; clone T28C12
 A:Accession: T32054
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 81-658 <LED>
 A:Cross-references: EMBL:AF016679; PIDN:AA66159.1; GSPDB:GN00023; CESP:T28C12.4b
 A:Experimental source: strain Bristol N2; clone T28C12
 C:Accession: T32053
 A:Gene: CESP:T28C12.4a; CESP:T28C12.4b
 A:Map position: 5
 A:Introns: 70/1; 96/3; 137/3; 192/3; 366/2; 423/1; 480/3; 573/2
 C:Superfamily: cholinesterase; cholinesterase homology

Query Match 1.0%; Score 8; DB 2; Length 658;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 LGFLSTGD 216
 Db 239 LGFLSTGD 246

RESULT 57
 T27394
 hypothetical protein Y75B8A.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T27394
 R:Barlow, K.
 submitted to the EMBL Data Library, November 1998

A:Reference number: Z20361
A:Accession: T77394
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Moecule type: DNA
A:Residues: 1-672 <WIL>
A:Cross-references: EMBL:AL033514; NID:el343351; PDB:QMA2054.1; CESP:Y7538A.3
A:Experimental source: clone Y75B8A
C:Genetics:
A:Gene: CESP:Y75B8A.3
A:Introns: 52/1; 126/3; 243/1; 475/3; 525/1; 615/3

Query Match 1.0%; Score 8; DB 2; Length 672;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 NEDCLYN 121
Db 114 NEDCLYN 121

RESULT 58
T16455
hypothetical protein F5SD10.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16455
R:Leimbach, D.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid F5SD10.
A:Reference number: Z18516
A:Accession: T16455
A:Status: preliminary; translated from GE/EMBL/DBJ
A:Moecule type: DNA
A:Residues: 1-730 <LEI>
A:Cross-references: EMBL:U40948; NID:91072223; PID:91072224; PDB:AAA6127.1; CESP:F5SD10.3
C:Genetics:
A:Gene: CESP:F5SD10.3
A:Introns: 48/3; 125/3; 181/3

Query Match 1.0%; Score 8; DB 2; Length 730;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 EDCLYLN 132
Db 170 EDCLYLN 177

RESULT 59
G64157
probable organic solvent tolerance protein precursor H10730 - Haemophilus influenzae 'set'
C:Species: Haemophilus influenzae
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2000
C:Accession: G64157
R:Flatschmann, R.O.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kestlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M.; Science 269, 486-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.W.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: M64000; MUID:95350630; PMID:7542800
A:Accession: G64157
A:Status: nucleic acid sequence not shown; translation not shown
A:Moecule type: DNA
A:Residues: 1-782 <TICR>
A:Cross-references: GB:U3756; GB:42023; NID:51573729; PDB:AAQ2389.1; PID:G1573734;
C:Superfamily: organic solvent tolerance protein
C:Keywords: periplasmic space
F:1-73/Domain: signal sequence #status predicted <SIG>
F:24-782/Product: organic solvent tolerance protein #status predicted <MA>

Query Match 1.0%; Score 8; DB 1; Length 782;
Best Local Similarity 100.0%; Pred. No. 22;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 PVEQYGV 57
Db 705 PVEQYGV 712

RESULT 60
A42112
mucin-like peptide MLP 2677 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 10-Oct-1997
C:Accession: A42112
R:Xu, G.; Han, L.; Khatri, I.A.; Wang, D.; Bennick, A.; Fahim, R.E.; Forstner, G.; Biol. Chem. 267, 5401-5407, 1992
A:Title: cDNA for the carboxyl-terminal region of a rat intestinal mucin-like peptide
A:Reference number: A42112; MUID:92184794; PMID:13371999
A:Accession: A42112
A:Status: preliminary
A:Moecule type: nucleic acid; protein
A:Residues: 1-837 <XU>
A:Experimental source: intestine
A:Note: sequence inconsistent with the nucleotide translation
C:Superfamily: von Willebrand factor type C repeat homology
F:582-650/Domain: von Willebrand factor type C repeat homology <VWC>

Query Match 1.0%; Score 8; DB 2; Length 937;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 635 TTKRPAIT 642
Db 329 TTKRPAIT 336

RESULT 61
A53215
protein kinase C (EC 2.7.1.1-) mu precursor - human
N:Alternate names: protein kinase D
C:Species: Homo sapiens (man)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jun-1999
C:Accession: A53215; S40279
R:Johannes, F.J.; Prestle, J.; Eis, S.; Oberhagenann, P.; Pfleiderer, K.; J. Biol. Chem. 269, 6140-6146, 1994
A:Title: PKCmu is a novel, atypical member of the protein kinase C family.
A:Reference number: A53215; MUID:94164979; PMID:8119958
A:Accession: A53215
A:Moecule type: mRNA
A:Residues: 1-912 <JOH>
A:Cross-references: EMBL:X75756; NID:9438372; PDB:QMA53384.1; PID:9438373
C:Genetics:
A:Gene: GDB:FRKCM; HS:2891; PKCM
A:Cross-references: GDB:310794
A:Map position: 21pter-21qter
C:Function:
A:Description: catalyzes the formation of peptideL-serine-phosphate or peptideL-thre
A:Note: expressed at low levels in a variety of tissues; phosphorylates a 30k protei
C:Superfamily: protein kinase C mu; protein kinase C zinc-binding repeat homology; F
C:Keywords: ATP; autophosphorylation; duplication; phospholipid binding; phosphoran
F:1-25/Domain: signal sequence #status predicted <SIG>
F:126-912/Product: protein kinase mu #status predicted <MAT>
F:147-196/Domain: protein kinase C zinc-binding repeat homology <K21>
F:171-320/Domain: protein kinase C zinc-binding repeat homology <K22>
F:581-839/Domain: protein kinase homology <K1N>
F:589-597/Region: protein kinase ATP-binding motif
F:612,630,706,708/Active site: Lys, Glu, Asp, Tyr #status predicted

Query Match 1.0%; Score 8; DB 1; Length 912;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 EDEDIDHQ 153
 D3 795 EDEDIDHQ 792

RESULT 62

148719 protein kinase C (EC 2.7.1.1) mu precursor - mouse
 N/Alternate names: protein kinase D
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jun-1995
 C/Accession: 148719
 R/Valverde, A.M.; Siment-Smith, J.; Van Lint, C.; Rozengurt, E.
 Proc. Natl. Acad. Sci. U.S.A. 91, 8572-8576, 1994
 A/Title: Molecular cloning and characterization of protein kinase D: a target for diacyl
 A/Reference number: 148719; MIM:34359973; PMID:8078925
 A/Accession: 148719
 A/Status: translated from GE/EMBL/DCBU
 A/Molecule type: mRNA
 A/Residues: 1-918 <RES>
 A/Cross-references: EMBL:Z34524; NID:9520877; PIDN:CAA84283.1; PID:9520878
 C/Function:

A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
 sely related human enzyme, this protein is reported to bind photol esters
 C/Superfamily: protein kinase C mu; protein kinase C zinc-binding repeat homology; prote
 C/Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipid
 F.1-25/Domain: signal sequence #status predicted <SIG>
 F.126-918/Product: protein kinase mu #status predicted <MAT>
 F.145-194/Domain: protein kinase C zinc-binding repeat homology <K21>
 F.127-326/Domain: protein kinase C zinc-binding repeat homology <K22>
 F.187-845/Domain: protein kinase homology <K1N>
 F.1595-603/Region: protein kinase ATP-binding motif
 F.618,636,712,714/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 1.0%; Score 6; DB 1; Length 918;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 EDEDIDHQ 163
 D3 791 EDEDIDHQ 798

RESULT 63

Se1041

glutamate synthase (NADH2) (EC 1.4.1.14) glt1 precursor [similarity] - yeast (Saccharomy
 N/Alternate names: protein D1448; protein YD1.71c
 C/Species: Saccharomyces cerevisiae
 C/Date: 15-Feb-1995 #sequence_revision 01-Mar-1996 #text_change 03-Jun-2002
 C/Accession: S61041; S67723
 R/Pohl, T.M.
 submitted to the EMBL Data Library, November 1995
 A/Reference number: S61041
 A/Accession: S61041
 A/Molecule type: DNA
 A/Residues: 1-2145 <POH>
 A/Cross-references: EMBL:Z67750; NID:9161256; PIDN:CAA91574.1; PID:9161267
 R/Pohl, T.M.
 submitted to the Protein Sequence Database, July 1996
 A/Reference number: S67708
 A/Accession: S67723
 A/Molecule type: DNA
 A/Residues: 1-2145 <POW>
 A/Cross-references: EMBL:Z74429; NID:91431273; PIDN:CAA98745.1; PID:91431274; MIPS:YDL17
 A/Experimental source: strain S289C
 C/Genetics:
 A/Gene: SGD:GLT1
 A/Cross-references: SGD:S0002330; MIPS:YDL171c
 A/Map position: 4L
 C/Superfamily: glutamate synthase (NADH)
 C/Keywords: 3Fe-4S; metalloprotein; oxidoreductase; transmembrane protein
 F.1-53/Domain: propeptide #status predicted <PRO>

F.54-2145/Product: glutamate synthase #status predicted <YLT>
 F.1077-1093/Domain: transmembrane #status predicted <TM1>
 F.1172-1188/Domain: transmembrane #status predicted <TM2>
 F.54/Active site: Cys #status predicted
 F.1185,1191,1196/Binding site: 3Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 1.0%; Score 8; DB 2; Length 2145;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 702 KRREHTR 709
 D3 1648 KRREHTR 1655

RESULT 64

334739 trans-cinnamate 4-monooxygenase (EC 1.14.13.11) - kidney bean (fragment)
 N/Alternate names: trans-cinnamic acid hydroxylase
 C/Species: Phaseolus vulgaris (kidney bean)
 C/Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 05-Mar-1999
 C/Accession: S34739
 R/Rodgers, M.W.; Zimmerlin, A.; Merck-Reichhart, D.; Bolwell, G.P.
 Arch. Biochem. Biophys. 304, 74-80, 1993
 A/Title: Microsomal associated heme proteins from French bean: characterization of
 A/Reference number: S34739; MIM:93312024; PMID:8323300
 A/Accession: S34739
 A/Molecule type: protein
 A/Residues: 1-23 <ROD>
 C/Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
 C/Keywords: heme; oxidoreductase

Query Match 0.9%; Score 7; DB 2; Length 23;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 439 KTLVALF 445
 D3 8 KTLVALF 14

RESULT 65

A38196 sterol esterase (EC 3.1.1.13) - pig (fragment)
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 14-Nov-1997
 C/Accession: A38196
 R/D.Persio, L.P.; Fontaine, R.N.; Hui, D.Y.
 J. Biol. Chem. 265, 16801-16806, 1990
 A/Title: Identification of the active site serine in pancreatic cholesteryl esterase
 A/Reference number: A38196; MIM:91009095; PMID:2211595
 A/Accession: A38196
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-29 <DIP>
 C/Superfamily: cholinesterase; cholinesterase homology
 C/Keywords: carboxylic ester hydrolase; glycoprotein

Query Match 0.9%; Score 7; DB 2; Length 29;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 AFGGDPK 247
 D3 11 AFGGDPK 17

RESULT 66

742967 hypothetical protein 53 - ateline herpesvirus 3 (strain 73)
 C/Species: ateline herpesvirus 3
 A/Variety: strain 73
 C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 19-May-2000

C/Accession: T42967
R:Albrecht, C.C.; Fleckenstein, B.
Submitted to the EMBL Data Library, August 1998
A:Description: Primary structure of the herpesvirus acies genome.
A:Reference number: 222274
A:Accession: T42967
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-89 <ALB>
A:Cross-references: EMBL:AF063424; PIDN:AAC95579.1
A:Experimental source: strain 73
C:Superfamily: cytomagalovirus UL73 protein

Query Match 0.3%; Score 7; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 682 GASLFL 689
|||||
DB 69 CASLFL 75

RESULT 67
F70511
Probable PE protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 03-Nov-2000
A:Accession: F70511
R:Cole, S.T.; Broese, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandram, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: F70511
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-98 <COL>
A:Cross-references: GB:Z97559; GB:AL123456; NID:G3361820; PIDN:GAB10700.1; PID:ej29638;
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: PE
C:Superfamily: Mycobacterium leprae hypochetrical protein B1620_C2_218

Query Match 0.9%; Score 7; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 610 TTKVPP 616
|||||
DB 36 TTKVPP 42

RESULT 66
A73155
Hypochetrical protein PAB2083 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
A:Accession: A73155
R:Anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A73001
A:Accession: A73155
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-103 <KAM>
A:Cross-references: GB:AJ248284; GB:AJ096836; NID:95457730; PIDN:GAB49320.1; PID:e51522
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB2083

Query Match 0.9%; Score 7; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 623 YGRRSP 629
|||||
DB 74 YGRRSP 80

RESULT 69
AG1814
Ribosome binding factor A (imported) - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
A:Accession: AG1814
R:Karako, T.; Nakamura, Y.; WolK, C.P.; Kurita, T.; Sasamoto, S.; Watanabe, A.; Iriig
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG1814
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-113 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA877587.1; PID:G17135041; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: rbfA
C:Superfamily: Escherichia coli protein P15B

Query Match 0.9%; Score 7; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 766 RSPDIP 772
|||||
DB 118 RSPDIP 124

RESULT 70
G39768
Cholinesterase (EC 3.1.1.8) - rhesus macaque (fragment)
C:Species: Macaca mulatta (rhesus macaque)
C>Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 18-Jun-1999
A:Accession: G39768
R:Apparatus, M.; Chaconnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.;
A:Biochem. 266, 6966-6974, 1991
A:Title: Use of the polymerase chain reaction for homology probing of butyrylcholin
A:Reference number: A39768; MUID:91201348; PMID:2016308
A:Accession: G39768
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-141 <ARP>
A:Cross-references: GB:M62777; NID:9342078; PIDN:AAA36836.1; PID:G342079
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein
F:1-141/Domain: cholinesterase homology (fragment) <CHE>

Query Match 0.9%; Score 7; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 125 EDCLYN 131
|||||
DB 23 EDCLYN 29

RESULT 71
B39768
Cholinesterase (EC 3.1.1.8) - sheep (fragment)
C:Species: Ovis orientalis aries; Ovis ammon aries (domestic sheep)
C>Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 18-Jun-1999

```

C:Accession: E39768
R:Arpagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Nog
U: Biol. Chem. 266, 6966-6974, 1991
A:Title: Use of the polymerase chain reaction for homology probing of butyrylcholinester
A:Reference number: A39768; MUID:91201348; PMID:2016306
A:Accession: E39768
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-141 <ARP>
A:Cross-references: GB:M62780; NID:G165830; PIDN:AAA1509.1; PID:G165831
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein
F:1-141/Domain: cholinesterase homology (fragment) <CHE>

Query Match          0.9%; Score 7; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

125 EDCLYLN 131
Db          23 EDCLYLN 29

RESULT 72
E39768
Cholinesterase (EC 3.1.1.8) - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 18-Jun-1999
C:Accession: E39768
R:Arpagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Nog
U: Biol. Chem. 266, 6966-6974, 1991
A:Title: Use of the polymerase chain reaction for homology probing of butyrylcholinester
A:Reference number: A39768; MUID:91201348; PMID:2016306
A:Accession: E39768
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-141 <ARP>
A:Cross-references: GB:M62410; NID:G162738; PIDN:AAA51412.1; PID:G162739
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein
F:1-141/Domain: cholinesterase homology (fragment) <CHE>

Query Match          0.9%; Score 7; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

125 EDCLYLN 131
Db          23 EDCLYLN 29

RESULT 73
E39768
Cholinesterase (EC 3.1.1.8) - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 16-Jun-1999
C:Accession: E39768
R:Arpagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Nog
U: Biol. Chem. 266, 6966-6974, 1991
A:Title: Use of the polymerase chain reaction for homology probing of butyrylcholinester
A:Reference number: A39768; MUID:91201348; PMID:2016306
A:Accession: E39768
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-141 <ARP>
A:Cross-references: GB:M62778; NID:G164387; PIDN:AAA31005.1; PID:G164388
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein
F:1-141/Domain: cholinesterase homology (fragment) <CHE>

Query Match          0.9%; Score 7; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY          125 EDCLYLN 131
Db          23 EDCLYLN 29

RESULT 74
E39768
Cholinesterase (EC 3.1.1.8) - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C>Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 18-Jun-1999
C:Accession: E39768
R:Arpagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.;
U: Biol. Chem. 266, 6966-6974, 1991
A:Title: Use of the polymerase chain reaction for homology probing of butyrylcholine
A:Reference number: A39768; MUID:91201348; PMID:2016306
A:Accession: E39768
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-141 <ARP>
A:Cross-references: GB:M62411; NID:G163910; PIDN:AAA51451.1; PID:G163911
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein
F:1-141/Domain: cholinesterase homology (fragment) <CHE>

Query Match          0.9%; Score 7; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

125 EDCLYLN 131
Db          23 EDCLYLN 29

RESULT 75
A41503
AF/R1 pilus chain A precursor - Escherichia coli (strain RDEC-1)
C:Species: Escherichia coli
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Oct-1999
C:Accession: A41503
R:Wolfe, M.K.; Boedeker, E.C.
U: Infect. Immun. 58, 1124-1128, 1990
A:Title: Cloning of the genes for AF/R1 pilus from rabbit enteroadherent Escherichia
A:Reference number: A41503; MUID:90202141; PMID:2969392
A:Accession: A41503
A:Molecule type: DNA
A:Residues: 1-162 <MOJ>
A:Cross-references: GB:M32083; NID:G145209; PIDN:AAA23422.1; PID:G145210
C:Comment: An 86-megadalton plasmid mediates production of the AF/R1 pilus for attac
the AF/R1 pilus.
C:Genetics:
A:Gene: atpA
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-162/Product: AF/R1 pilus A chain #status predicted <XAT>

Query Match          0.9%; Score 7; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          127 VIVITIN 203
Db          9 VIVITIN 15

Search completed: November 5, 2003, 15:26:16
Job time : 24 secs

```


GenCore Version 5.1.6
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OM protein - protein search, using SW model

Run on: November 5, 2003, 15:25:49 ; Search time 35 Seconds

(without alignments)
4004.212 Million cell updates/sec

Title: US-09-978-423A-375

Perfect score: 816

Sequence: 1 WNSNVLMKTALAIKFTLL.....TFSGGCGNTLPHGHSTTRY 816

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 644079 seqs, 171749292 residues

Word size: 0

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database: Published Applications AA:
1: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubppa/PTC_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubppa/PTCUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubppa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep.*
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14: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep.*
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Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	816	100.0	816	10	US-09-978-295A-375 Sequence 375, App
2	816	100.0	816	10	US-09-978-697-375 Sequence 375, App
3	816	100.0	816	10	US-09-978-192A-375 Sequence 375, App
4	816	100.0	816	10	US-09-999-812A-375 Sequence 375, App
5	816	100.0	816	10	US-09-978-89-375 Sequence 375, App
6	816	100.0	816	11	US-09-978-608A-375 Sequence 375, App
7	816	100.0	816	11	US-09-978-585A-375 Sequence 375, App
8	816	100.0	816	11	US-09-978-91A-375 Sequence 375, App
9	816	100.0	816	11	US-09-978-403A-375 Sequence 375, App
10	816	100.0	816	11	US-09-978-564A-375 Sequence 375, App
11	816	100.0	816	11	US-09-999-832A-375 Sequence 375, App
12	816	100.0	816	11	US-09-961-815A-375 Sequence 375, App
13	816	100.0	816	11	US-09-978-824-375 Sequence 375, App
14	816	100.0	816	11	US-09-918-585A-375 Sequence 375, App
15	816	100.0	816	11	US-09-978-423A-375 Sequence 375, App

16	816	100.0	816	11	US-09-978-193A-375 Sequence 375, App
17	816	100.0	816	11	US-09-999-830A-375 Sequence 375, App
18	816	100.0	816	11	US-09-978-757A-375 Sequence 375, App
19	816	100.0	816	11	US-09-978-187B-375 Sequence 375, App
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56	816	100.0	816	12	US-10-017-081A-375 Sequence 375, App
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59	816	100.0	816	15	US-10-013-929A-375 Sequence 375, App
60	816	100.0	816	15	US-10-018-117A-375 Sequence 375, App
61	816	100.0	816	15	US-10-166-709A-375 Sequence 375, App
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63	48	5.9	801	12	US-09-924-323-6 Sequence 12, Appl1
64	48	5.9	801	12	US-10-274-694-12 Sequence 12, Appl1
65	48	5.9	835	10	US-09-934-323-2 Sequence 2, Appl1
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67	46	5.6	49	9	US-09-864-761-46697 Sequence 46697, A
68	32	3.9	848	12	US-09-875-353-5 Sequence 5, Appl1
69	28	3.4	157	12	US-10-029-386-31666 Sequence 31666, A
70	24	2.9	61	12	US-10-029-386-30476 Sequence 30476, A
71	12	1.5	359	9	US-09-925-297-778 Sequence 718, Appl1
72	12	1.5	568	11	US-09-418-176-4 Sequence 4, Appl1
73	12	1.5	612	15	US-10-156-932-7 Sequence 7, Appl1
74	12	1.5	722	11	US-09-418-176-3 Sequence 3, Appl1
75	12	1.5	745	11	US-09-418-176-2 Sequence 2, Appl1
76	9	1.1	581	14	US-10-023-515-2 Sequence 1177, Ap
77	9	1.1	583	9	US-09-925-301-1177 Sequence 1177, Ap
78	9	1.1	875	12	US-09-949-029-122 Sequence 122, App
79	8	1.0	65	12	US-10-022-386-11861 Sequence 11861, A
80	8	1.0	144	9	US-09-925-297-844 Sequence 844, App
81	8	1.0	178	10	US-09-747-835A-31 Sequence 551, App
82	8	1.0	210	15	US-10-222-516-551 Sequence 551, App
83	8	1.0	334	10	US-09-747-835A-32 Sequence 32, Appl1
84	8	1.0	396	10	US-09-949-025-2-2 Sequence 2, Appl1
85	8	1.0	574	14	US-10-023-515-4 Sequence 4, Appl1
86	8	1.0	585	10	US-09-934-333-4 Sequence 4, Appl1
87	8	1.0	612	10	US-09-875-353-4 Sequence 4, Appl1
88	8	1.0	894	14	US-10-066-332-4 Sequence 4, Appl1

92	5	1.0	894	16	US-10-339-657-4	Sequence 4, Appl:
93	8	1.0	1314	10	US-09-747-835A-29	Sequence 29, App:
91	7	0.9	76	9	US-09-764-869-347	Sequence 947, App
92	7	0.9	76	5	US-10-091-504-947	Sequence 547, App
93	7	0.9	85	9	US-09-867-550-878	Sequence 878, App
94	7	0.9	94	12	US-10-029-586-30361	Sequence 30361, A
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96	7	0.9	109	15	US-10-083-357-775	Sequence 775, App
97	7	0.9	117	8	US-08-976-063C-12	Sequence 12, Appl
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ALIGNMENTS

RESULT 1
US-09-978-295A-375Sequence 375, Application US/09978295A
Patent No. US20020156006A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

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APPLICANT: Grimaldi, C. Christopher

APPLICANT: Gurev, Asit L.

APPLICANT: Hillan, Kenneth J

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APPLICANT: Kuo, Sophia S.

APPLICANT: Kuper, Mary A.

APPLICANT: Par, James

APPLICANT: Paoni, Nicholas P.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane polypeptides and Nucleic

FILE REFERENCE: P26302C11

CURRENT APPLICATION NUMBER: US/09/978, 295A

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

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APPLICANT: Filvaroff, Ellen
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
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US-09-999-832A-375
Sequence 375, Application US/09999832A
Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnecy, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
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APPLICANT: Goddard, Audrey
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC3
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PRIOR FILING DATE: 1998-05-13
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PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0% Score 816; DB 10; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 3;

Cy 1 MNSVLLWLTALAIKFTLIDSOAYPVVNTVYKIRGIRFLPNEILGPEVGYGVYA 60
Db 1 MNSVLLWLTALAIKFTLIDSOAYPVVNTVYKIRGIRFLPNEILGPEVGYGVYA 60
Cy 61 SPTGRRRPPRPPSSWTKIRNTTQFAVCPGHLDESLIHDMLPIWFTNLCTLMYV 120

Db 61 SPTGERRFPPEPSSMTGIRNTGFANVCQHLDERSLHEKYLWITFANLDTMTV 120
Qy 121 QDQNEDELNTIYVPTEDGANTKKNADJITSNDRGEDEDIHQNSKKPVMVYIHGSGYME 180
Db 122 QDQNEDELNTIYVPTEDGANTKKNADJITSNDRGEDEDIHQNSKKPVMVYIHGSGYME 180
Qy 181 GTGNMIGSILASTGNNVITITINRGLIGLPSTGDOAKANGNLDDOIALMWEENWG 240
Db 181 GTGNMIGSILASTGNNVITITINRGLIGLPSTGDOAKANGNLDDOIALMWEENWG 240
Qy 241 AFGDPRKVTIFSGAGASCVSLLTSHSEGLFOKATIGSGTALSMAKVPKATYR 300
Db 241 AFGDPRKVTIFSGAGASCVSLLTSHSEGLFOKATIGSGTALSMAKVPKATYR 300
Qy 301 LADKVGCMNDITDMVECELRKRYKELIQOTITPATYHAFGPVIGDVPIDPQJLMEQ 360
Db 301 LADKVGCMNDITDMVECELRKRYKELIQOTITPATYHAFGPVIGDVPIDPQJLMEQ 360
Qy 361 GEFILNDIMGNVQGBELKFEVQGVNEDGVITNEDGFSVSNVCLNKGFBKCTLRET 420
Db 361 GEFILNDIMGNVQGBELKFEVQGVNEDGVITNEDGFSVSNVCLNKGFBKCTLRET 420
Qy 421 IKFMYTCMAKXENETPRKCTVALFTCHQVAFVAVADHAQYSPTYEAFYHGOSEM 480
Db 421 IKFMYTCMAKXENETPRKCTVALFTCHQVAFVAVADHAQYSPTYEAFYHGOSEM 480
Qy 481 KPSWADSHGDEVPYVFGIPMIGPTELFSCNFSKNDVYSAVYVYTWTFKAGDPKQYV 540
Db 481 KPSWADSHGDEVPYVFGIPMIGPTELFSCNFSKNDVYSAVYVYTWTFKAGDPKQYV 540
Qy 541 POCFKFHTKPNRFEVAMSKYKPKQJLYHIGKPRVPRHYNATYAAFLVEYELNHL 600
Db 541 POCFKFHTKPNRFEVAMSKYKPKQJLYHIGKPRVPRHYNATYAAFLVEYELNHL 600
Qy 601 NEFOYSTTTKVPPTMTSEFYCTRSPAKTPTTRSPAITPANNPKSHKCKHKTGPE 660
Db 601 NEFOYSTTTKVPPTMTSEFYCTRSPAKTPTTRSPAITPANNPKSHKCKHKTGPE 660
Qy 661 TTVLETKRDYSELSTVIAVGASJLFLLNLAFAPALYKCKRRHETHRRSPQRNTND 720
Db 661 TTVLETKRDYSELSTVIAVGASJLFLLNLAFAPALYKCKRRHETHRRSPQRNTND 720
Qy 721 IAHQNEIMSLQKQLEHDBECSCAHQZCLPTGPDVTLTLRSPDIPXTNNTT 780
Db 721 IAHQNEIMSLQKQLEHDBECSCAHQZCLPTGPDVTLTLRSPDIPXTNNTT 780
Qy 781 MIPNLTGMQPLHTFNTFSGQNSTNLPKHSSTRV 816
Db 781 MIPNLTGMQPLHTFNTFSGQNSTNLPKHSSTRV 816

RESULT 5
US-09-978-189-375
Sequence 375, Application US/C0978189
Publication No. US20030004102A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul C.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavrin, Ivar C.

APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumes, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William J.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/066250
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PRIOR APPLICATION NUMBER: 60/085697

Query Match: 100.0%; Score 816; DB 1; Length 816;
Best Local Similarity: 100.0%; Pred. No. 0;
Matches 916; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MNSVLLMLTALAIKFTLDSQAVPVNTNGKIRGLRPLNEILGPECYLGPPYA 60
1 MNSVLLMLTALAIKFTLDSQAVPVNTNGKIRGLRPLNEILGPECYLGPPYA 60
61 SEPTGERPQPEPSSWGTGRNTTQFNAVCPQHLDBSLHMLPIWFTNLDTMTYV 120
61 SEPTGERPQPEPSSWGTGRNTTQFNAVCPQHLDBSLHMLPIWFTNLDTMTYV 120
61 SEPTGERPQPEPSSWGTGRNTTQFNAVCPQHLDBSLHMLPIWFTNLDTMTYV 120
121 QDNEDCLYNIYVEEGANTKRAODITSDNGEDCDHDKSKKPVWY:HGGSYNE 180
121 QDNEDCLYNIYVEEGANTKRAODITSDNGEDCDHDKSKKPVWY:HGGSYNE 180
181 GTGNMIDSLASYNVIVITINRAGLGFSTGQAKKNYGLLDQALRWIEENVG 240
181 GTGNMIDSLASYNVIVITINRAGLGFSTGQAKKNYGLLDQALRWIEENVG 240
181 GTGNMIDSLASYNVIVITINRAGLGFSTGQAKKNYGLLDQALRWIEENVG 240
241 AFGSPKAVTIFGSGAGASCVSLLTSHYSSGLCKALIOGCTALSSAANVCPAKYRI 300
241 AFGSPKAVTIFGSGAGASCVSLLTSHYSSGLCKALIOGCTALSSAANVCPAKYRI 300
301 LADKXGCMMLDTTDWVECLRNKNYKE:ICQITTPATYHAFGPVIDGV:DDPOLLKEQ 360
301 LADKXGCMMLDTTDWVECLRNKNYKE:ICQITTPATYHAFGPVIDGV:DDPOLLKEQ 360
361 GFLNYDMLGVNQGEGKPFVDGIVDNEDGVTDPNDFSVSNFVNDLGYEGKDTLRET 420
361 GFLNYDMLGVNQGEGKPFVDGIVDNEDGVTDPNDFSVSNFVNDLGYEGKDTLRET 420
421 IKFMYTDADKENPEPTRKKTVALFTTEQWMAAPAAADLHNOYGSPTFFYAFYHHCQSEM 480
421 IKFMYTDADKENPEPTRKKTVALFTTEQWMAAPAAADLHNOYGSPTFFYAFYHHCQSEM 480
481 KPSWADSAHGDEVVPFGIPMIGTEPLSCNFSKNDVLAHVMTYKTNFAKTGDPNPV 540
481 KPSWADSAHGDEVVPFGIPMIGTEPLSCNFSKNDVLAHVMTYKTNFAKTGDPNPV 540

Db 491 KPSWADSHAGCEVPYVVGICIMIGSTELFSCNFSKNDVMSAVMTYTNPAKTGDENGPY 540
Qy 541 POCSTFIHKPRNEEEVAVMSKYNPKDQLYHIGLKRVRDHYRATKVAFWLELVPHLNL 600
Db 541 PODTKFIHKPRNEEEVAVMSKYNPKDQLYHIGLKRVRDHYRATKVAFWLELVPHLNL 600
Qy 601 NEIFQVSTTTKVPPEPMTSPFYGRSPAKIWPTRKPAITPANNPKSKDHPKGTGED 660
Db 601 NEIFQVSTTTKVPPEPMTSPFYGRSPAKIWPTRKPAITPANNPKSKDHPKGTGED 660
Qy 661 TTVLIEFRDSTELSTIIVAGASLFLNLIAPALYKKKXPHETRRSPQRTTND 720
Db 661 TTVLIEFRDSTELSTIIVAGASLFLNLIAPALYKKKXPHETRRSPQRTTND 720
Qy 721 IAHQNEIWSLQMKQLEHDEHCESLQAHDTLRITCPDYLTLRRSFDIPLMTPTIT 780
Db 721 IAHQNEIWSLQMKQLEHDEHCESLQAHDTLRITCPDYLTLRRSFDIPLMTPTIT 780
Qy 781 MIPNTLTGMQPLHTFNFTSGGQNSTNLPHGSTRV 816
Db 781 MIPNTLTGMQPLHTFNFTSGGQNSTNLPHGSTRV 816

RESULT 6

US-09-978-608A-375
; Sequence 375, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijaviri, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Acids Encoding and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P26302P22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 375
; LENGTH: 816
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-375

Query Match: 100.0%; Score 816; DB 11; Length 816;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 XNSNVLLMTALAIKFTLLDSQAQYFVNTWYQKIRGLRPLFNEILGPVEQYLVGPVA 60

Db 1 MINSNVLLMTALAIKFTLLDSQAQYFVNTWYQKIRGLRPLFNEILGPVEQYLVGPVA 60
Qy 61 SPTGERFRFPPEPSSWTGIRNTOTFAAVCFQHLDEBSLHDMPLMTFTANLDTLMTYV 120
Db 61 SPTGERFRFPPEPSSWTGIRNTOTFAAVCFQHLDEBSLHDMPLMTFTANLDTLMTYV 120
Qy 121 QDQNEDCLYINIYVTEDEGANTKKXADDITSNDRGEDEHDQNSKKPVWVYIHGGSYME 180
Db 121 QDQNEDCLYINIYVTEDEGANTKKXADDITSNDRGEDEHDQNSKKPVWVYIHGGSYME 180
Qy 181 GTGNMIDGSIILASGNVITITINRGLIGLSLSTGQDAKKNVGLLOIQALRMIEENVG 240
Db 181 GTGNMIDGSIILASGNVITITINRGLIGLSLSTGQDAKKNVGLLOIQALRMIEENVG 240
Qy 241 AFQGPDKRVTIFGSGAGASCVSLLTSISYSGLQKAIQSGTILSSAAVYQPAKYTRI 300
Db 241 AFQGPDKRVTIFGSGAGASCVSLLTSISYSGLQKAIQSGTILSSAAVYQPAKYTRI 300
Qy 301 LADKVGCMMDTTDMVECLRNKXKELIQOTTTPATYHIAFGPVLDGVIPODDQILMEQ 360
Db 301 LADKVGCMMDTTDMVECLRNKXKELIQOTTTPATYHIAFGPVLDGVIPODDQILMEQ 360
Qy 361 GEFLNYDMLGNVCGEGLKFPVDSIVDNEDGVTPNDFPSVSNFYDNLGYREGKDTRET 420
Db 361 GEFLNYDMLGNVCGEGLKFPVDSIVDNEDGVTPNDFPSVSNFYDNLGYREGKDTRET 420
Qy 421 IKFMYTDADKENPETRRKTILVALFTDQWAPAQAADLHAQYGSPTYFYAFHHCQSEM 480
Db 421 IKFMYTDADKENPETRRKTILVALFTDQWAPAQAADLHAQYGSPTYFYAFHHCQSEM 480
Qy 481 KPSWADSHAGCEVPYVVGICIMIGSTELFSCNFSKNDVMSAVMTYTNPAKTGDENGPY 540
Db 481 KPSWADSHAGCEVPYVVGICIMIGSTELFSCNFSKNDVMSAVMTYTNPAKTGDENGPY 540
Qy 541 PODTKFIHKPRNEEEVAVMSKYNPKDQLYHIGLKRVRDHYRATKVAFWLELVPHLNL 600
Db 541 PODTKFIHKPRNEEEVAVMSKYNPKDQLYHIGLKRVRDHYRATKVAFWLELVPHLNL 600
Qy 601 NEIFQVSTTTKVPPEPMTSPFYGRSPAKIWPTRKPAITPANNPKSKDHPKGTGED 660
Db 601 NEIFQVSTTTKVPPEPMTSPFYGRSPAKIWPTRKPAITPANNPKSKDHPKGTGED 660
Qy 661 TTVLIEFRDSTELSTIIVAGASLFLNLIAPALYKKKXPHETRRSPQRTTND 720
Db 661 TTVLIEFRDSTELSTIIVAGASLFLNLIAPALYKKKXPHETRRSPQRTTND 720
Qy 721 IAHQNEIWSLQMKQLEHDEHCESLQAHDTLRITCPDYLTLRRSFDIPLMTPTIT 780
Db 721 IAHQNEIWSLQMKQLEHDEHCESLQAHDTLRITCPDYLTLRRSFDIPLMTPTIT 780
Qy 781 MIPNTLTGMQPLHTFNFTSGGQNSTNLPHGSTRV 816
Db 781 MIPNTLTGMQPLHTFNFTSGGQNSTNLPHGSTRV 816

RESULT 7

US-09-978-585A-375
; Sequence 375, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey

```

/ Appl::CANT: Godowski, Paul J.
/ Applicant: Grimaldi, J. Christopher
/ Applicant: Gurney, Austin L.
/ Applicant: Hillan, Kenneth J.
/ Applicant: Kijavina, Ivar J.
/ Applicant: Kuo, Sophia S.
/ Applicant: Napier, Mary A.
/ Applicant: Pan, James.
/ Applicant: Paoni, Nicholas F.
/ Applicant: Roy, Margaret Ann
/ Applicant: Shelton, David L.
/ Applicant: Stewart, Timothy A.
/ Applicant: Tumas, Daniel
/ Applicant: Williams, P. Mickey
/ Applicant: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ TITLE OF INVENTION: Acids Encoding the Same
/ FILE REFERENCE: P2630P-C15
/ CURRENT APPLICATION NUMBER: US/09/978,385A
/ CURRENT FILING DATE: 2001-10-16
/ NUMBER OF SEQ ID NOS: 624
/ Prior Application removed - See File Wrapper or Palm
/ SEQ ID NO 375
/ LENGTH: 816
/ TYPE: PR
/ ORGANISM: Homo sapiens
/ US-09-978-585A-375

Query Match      100.0% Score 816; DB 11; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Cy 131 GTCNMIDGSLASGVYVITITNFGSLIGFSTDDQAKNGYGLDQICLRITSENVG 240
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Db 241 AFGSDPKRYTTFSGAGAGCSVLLTSHYSEGLFQKALIQSGTALSSAAVYCPAKYTRI 300
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Db 241 AFGSDPKRYTTFSGAGAGCSVLLTSHYSEGLFQKALIQSGTALSSAAVYCPAKYTRI 300
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Cy 301 LADKVGCMLOTTDMVECLRNKNYKELLQOTTTPATYHIAFGPVIGCVTFEDQITLMEQ 360
Db 301 LADKVGCMLOTTDMVECLRNKNYKELLQOTTTPATYHIAFGPVIGCVTFEDQITLMEQ 360
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Db 781 MIPNTLMQPLHTFNTFSGGQNSTLPHGSTRV 816

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US-09-978-192A-375
/ Sequence 375, Application US/09978191A
/ Publication No. US20030050239A1
/ GENERAL INFORMATION:
/ Applicant: Ashkenazi, Avi
/ Applicant: Baker Kevin P.
/ Applicant: Botstein, David
/ Applicant: Desnoyers, Luc
/ Applicant: Eaton, Dan
/ Applicant: Ferrara, Napoleon
/ Applicant: Flivaroff, Ellen
/ Applicant: Fong, Sherman
/ Applicant: Gao, Wei-Qiang
/ Applicant: Geider, Hanspeter
/ Applicant: Gerltzen, Mary E.
/ Applicant: Goddard, Audrey
/ Applicant: Godowski, Paul J.
/ Applicant: Grimaldi, J. Christopher
/ Applicant: Gurney, Austin L.
/ Applicant: Hillan, Kenneth J.
/ Applicant: Kijavina, Ivar J.
/ Applicant: Kuo, Sophia S.
/ Applicant: Napier, Mary A.
/ Applicant: Pan, James.
/ Applicant: Paoni, Nicholas F.
/ Applicant: Roy, Margaret Ann
/ Applicant: Shelton, David L.
/ Applicant: Stewart, Timothy A.
/ Applicant: Tumas, Daniel
/ Applicant: Williams, P. Mickey
/ Applicant: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2630P-C15
/ CURRENT APPLICATION NUMBER: US/09/978,191A
/ CURRENT FILING DATE: 2001-10-15
/ PRIOR APPLICATION NUMBER: 09/918565
/ PRIOR FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: 60/06225C
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/ PRIOR FILING DATE: 1998-03-11
/ PRIOR APPLICATION NUMBER: 60/077791
/ PRIOR FILING DATE: 1998-03-12
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3	PRIOR FILING DATE: 1998-03-20	3	PRIOR APPLICATION NUMBER: 60/078936	3	PRIOR FILING DATE: 1998-04-22	3	PRIOR APPLICATION NUMBER: 60/082796
4	PRIOR FILING DATE: 1998-03-20	4	PRIOR APPLICATION NUMBER: 60/078910	4	PRIOR FILING DATE: 1998-04-23	4	PRIOR APPLICATION NUMBER: 60/083336
5	PRIOR APPLICATION NUMBER: 60/078939	5	PRIOR FILING DATE: 1998-03-20	5	PRIOR FILING DATE: 1998-04-27	5	PRIOR APPLICATION NUMBER: 60/083322
6	PRIOR FILING DATE: 1998-03-23	6	PRIOR APPLICATION NUMBER: 60/079294	6	PRIOR FILING DATE: 1998-04-28	6	PRIOR APPLICATION NUMBER: 60/083392
7	PRIOR FILING DATE: 1998-03-25	7	PRIOR APPLICATION NUMBER: 60/079556	7	PRIOR FILING DATE: 1998-04-29	7	PRIOR APPLICATION NUMBER: 60/083495
8	PRIOR FILING DATE: 1998-03-26	8	PRIOR APPLICATION NUMBER: 60/079664	8	PRIOR FILING DATE: 1998-04-29	8	PRIOR APPLICATION NUMBER: 60/083496
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10	PRIOR FILING DATE: 1998-03-27	10	PRIOR APPLICATION NUMBER: 60/079663	10	PRIOR APPLICATION NUMBER: 60/083545	10	PRIOR APPLICATION NUMBER: 60/083550
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12	PRIOR APPLICATION NUMBER: 60/079766	12	PRIOR FILING DATE: 1998-03-27	12	PRIOR APPLICATION NUMBER: 60/083558	12	PRIOR APPLICATION NUMBER: 60/083555
13	PRIOR FILING DATE: 1998-03-27	13	PRIOR APPLICATION NUMBER: 60/079920	13	PRIOR FILING DATE: 1998-04-25	13	PRIOR APPLICATION NUMBER: 60/083500
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17	PRIOR APPLICATION NUMBER: 60/080165	17	PRIOR FILING DATE: 1998-03-31	17	PRIOR APPLICATION NUMBER: 60/084639	17	PRIOR APPLICATION NUMBER: 60/084640
18	PRIOR FILING DATE: 1998-03-31	18	PRIOR APPLICATION NUMBER: 60/080194	18	PRIOR FILING DATE: 1998-05-07	18	PRIOR APPLICATION NUMBER: 60/084640
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21	PRIOR FILING DATE: 1998-04-01	21	PRIOR APPLICATION NUMBER: 60/080333	21	PRIOR FILING DATE: 1998-05-07	21	PRIOR APPLICATION NUMBER: 60/084639
22	PRIOR APPLICATION NUMBER: 60/080334	22	PRIOR FILING DATE: 1998-04-01	22	PRIOR APPLICATION NUMBER: 60/084598	22	PRIOR APPLICATION NUMBER: 60/084598
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24	PRIOR FILING DATE: 1998-04-08	24	PRIOR APPLICATION NUMBER: 60/081049	24	PRIOR FILING DATE: 1998-05-07	24	PRIOR APPLICATION NUMBER: 60/084627
25	PRIOR FILING DATE: 1998-04-08	25	PRIOR APPLICATION NUMBER: 60/081071	25	PRIOR FILING DATE: 1998-05-07	25	PRIOR APPLICATION NUMBER: 60/084633
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30	PRIOR FILING DATE: 1998-04-15	30	PRIOR APPLICATION NUMBER: 60/082568	30	PRIOR FILING DATE: 1998-05-15	30	PRIOR FILING DATE: 1998-05-15
31	PRIOR FILING DATE: 1998-04-21	31	PRIOR APPLICATION NUMBER: 60/082569	31	PRIOR APPLICATION NUMBER: 60/085704	31	PRIOR APPLICATION NUMBER: 60/085697
32	PRIOR FILING DATE: 1998-04-22	32	PRIOR APPLICATION NUMBER: 60/082804	32	PRIOR APPLICATION NUMBER: 60/085697	32	PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 816; DB 11; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 SPTGERRFPPEPSSWTGIRNTTQFAVCPOLPERSLHDMCLPWFAN:PLTMATV 120
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DB 121 QDQNECLYINIVPTBEDGANTKXADITSNDRGEDEDHDCNSKKPVVYHGGSYNE 180
CY 181 GTGNMIDGSLIASGNVITVITNRLGLFLSGDQMAKNGCLDQIALPMIENNG 240
DB 181 GTGNMIDGSLIASGNVITVITNRLGLFLSGDQMAKNGCLDQIALPMIENNG 240
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DB 241 AFGDPRKVTIFSGAGASCVALTSLSHVSEGLFQKA:IGSGTALSSMANVYPAKYFI 300
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DB 361 GEFILNYDMLGVNGEGLEKVDGIVDNEEDGVPDPEFSNSVDNLYGPESKDTLPET 420
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DB 541 FQTKYFHTKFNREEEVAMSKYKPKDLYLHIGKPRVCHYATKAYFMLEVPLAHN 600
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DB 761 MIPNTLIGMCP:HTFNTPSGGQNSCNLPHGSHSTRV 816

RESULT 3
US-09-978-403A-375
Sequence 375, Application US/0978403A
Publication No. US200305024CA1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurey, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kirsav, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Acids and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC7
CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 816; DB 11; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MNSVTLMTALAKFTLLDSOAVPVVNTYNGKIRGRTPLPNEILGVEOYGVPA 60
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121 CGONEPCLYNIYVPTDGNATCKKADDITSDRGDEDDHDSKRPVYIHGSSYVE 180
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181 GTGNMIDGSLASGVNIYVITINRGLIGFJSTGQAAKNGVGLDQIALRWIEENVG 240
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241 AFGGDPKRVITIFSGGACASVSLITSHVSEGLFOKAITIOSGTAASSMAVNOAPAYTRI 300
241 AFGGDPKRVITIFSGGACASVSLITSHVSEGLFOKAITIOSGTAASSMAVNOAPAYTRI 300
301 LADYVGCNMLDTTDMVECLRNKXYKELICQITITPATYHIAFGVYIGDVIYIPDDPQILMEQ 360
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QY	361	GEFANYIMGVNGDEGLKFLVDGIVJNEDDVTENDEPVSNSVNDLVNGVPEKCDLART	420
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Db	421	IKFWYTMADKENEETRRKTLVA-LFTDHQWAPAAVADLPAQVGSPTVFYAFYHCCGSM	480
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Db	481	KPSWADSAHGEVYVFGIEMIGTELFSCNFSKNDYMLSAVVMYTWYPAKTGDNPQV	540
QY	541	PCGKFLHTEKNEFEVYVFGIEMIGTELFSCNFSKNDYMLSAVVMYTWYPAKTGDNPQV	600
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Db	601	NEIFQVYSTTKVPPDMTSPFYQTRSPAKIMPTTSEPAITANNPKSKDHPKTKGPD	660
QY	661	TTVLEFKRQVSTSLSTITAVGASLFLNLALFAALYKKQCKRRHSTHRSPSCNTND	720
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QY	721	IAHIONEIMSLQKQKQEHDEHCESLQAHDTLRITCQPEYTLIRSPDIPMTNNTIT	780
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US-09-978-564A-375			
Sequence 375, Application US/09978564A			
Publication No. US2003005024A1			
GENERAL INFORMATION:			
APPLICANT: Ashkenazi, Avi			
APPLICANT: Baker, Kevin P.			
APPLICANT: Bolstein, David			
APPLICANT: Desnoyers, Luc			
APPLICANT: Eacott, Dan			
APPLICANT: Ferrara, Napoleon			
APPLICANT: Filvaroff, Sliem			
APPLICANT: Fong, Sherman			
APPLICANT: Gao, Wei-Giang			
APPLICANT: Gerber, Hanspeter			
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APPLICANT: Goddard, Audrey			
APPLICANT: Godowski, Paul C.			
APPLICANT: Grimaldi, C. Christopher			
APPLICANT: Gurney, Austin L.			
APPLICANT: Hillan, Kenneth J.			
APPLICANT: Kijavitt, Ivar C.			
APPLICANT: Kuo, Sophia S.			
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APPLICANT: Pan, James			
APPLICANT: Paoni, Nicholas F.			
APPLICANT: Roy, Margaret Ann			
APPLICANT: Shelton, David L.			
APPLICANT: Stewart, Timothy A.			
APPLICANT: Tumas, Daniel			
APPLICANT: Williams, P. Mickey			
APPLICANT: Wood, William J.			
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
FILE REFERENCE: P2630PIC25			
CURRENT APPLICATION NUMBER: US/09/978,564A			
CURRENT FILING DATE: 2001-10-16			
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Query Match 100.0% Score 816, DB 11, Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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121 GQONEDCYLNIYVPTGANTKXKADITSDNGEDSDIDQSKKPVVYIHGSGYME 183
121 GQONEDCYLNIYVPTGANTKXKADITSDNGEDSDIDQSKKPVVYIHGSGYME 180
181 GTGNMIDGSLASVGNV:VITINVRGLIGF:LTGDOAKKNYGL:QOIQALRWIENVG 240
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241 AFGDPRKVTTFGSGAGSCVSL:TLHSYSGLFQKAI:CGSTLSSNANVYQPAKTRI 300
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301 LADKVCNMLDITTDVNECLRNKNYKE:TCQTTTATYHIAFGPVIDGVI:PDDEQIMEQ 360
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361 GEFVNYDMLGVOGEGK:FDVGDIVNEDGVTPNDPFSV:NFDN:YGVPEGKOTLRET 420
361 GEFVNYDMLGVOGEGK:FDVGDIVNEDGVTPNDPFSV:NFDN:YGVPEGKOTLRET 420
421 IKFVTTDADKENPETRKTLYAL:FTDQWVAPVAAADLHAQVGSPTYFAFYHCOSEM 480
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481 KPSMADSAHGDVEPVFG:IPMIGTELFSCNFSXNDVLA:VWV:YWTNPAKTGDPQPV 540
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721 IAHIONEFMSLOXQLEHDEHCESLQADTL:RLTQCPDYLLT:RRSPDOJ:PLMTPTIT 780
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761 MENTIGMOPLHNTFFSGGONSLPHGHSTRV 816
DB [|||||]|||||
761 MENTIGMOPLHNTFFSGGONSLPHGHSTRV 816

RESULT 11
US-99-999-833a-375
Sequence 375, Application US/09999833a
Publication No. US20030054405a1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desrochers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Flivauff, Ellen
APPLICANT: Ford, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James J.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C65
CURRENT APPLICATION NUMBER: US/09/999.833a
CURRENT FILING DATE: 200-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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Query Match      100.0%; Score 816; DB 11; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Cy      61  SPTGGRFOPPEPSSWTGIRNTTCFAAGCGCHLDRSLHKLPLKFWANLDTLNTY 120
Db      61  SPTGGRFOPPEPSSWTGIRNTTCFAAGCGCHLDRSLHKLPLKFWANLDTLNTY 120
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Cy      121  QONEDCLYNTIYVPTEDGANTKKNADITSNRGEDEDIHDQNSKXPVWVYIHGGSYME 180
Db      121  QONEDCLYNTIYVPTEDGANTKKNADITSNRGEDEDIHDQNSKXPVWVYIHGGSYME 180
Cy      181  GTGNMIDGSIILASGVNVIITINYPJGILGFLSTGDAKAGNYGLDQICALFIEENVG 240
Db      181  GTGNMIDGSIILASGVNVIITINYPJGILGFLSTGDAKAGNYGLDQICALFIEENVG 240
Cy      241  AFGDDPKRVTFSSGAGASCVSLLTSHVSEGGFKKJIOSGALSSMAVNOYPAKXTRI 300
Db      241  AFGDDPKRVTFSSGAGASCVSLLTSHVSEGGFKKJIOSGALSSMAVNOYPAKXTRI 300
Cy      361  LADYVGCMLDITDMVECELRKNKXKELIQOTITPATYHIAFGVIDGDIIPDDPOLIMEQ 360
Db      361  LADYVGCMLDITDMVECELRKNKXKELIQOTITPATYHIAFGVIDGDIIPDDPOLIMEQ 360
Cy      421  IKFWYTDWADKENETRRKTLVALFTDHCWAPAAADLHAQVGSPTYFYAFYHCOSEY 480
Db      421  IKFWYTDWADKENETRRKTLVALFTDHCWAPAAADLHAQVGSPTYFYAFYHCOSEY 480
Cy      481  KPSMADSAGDEVEYVVGIGIMIGTELFSQNFSSNDVMJSAVMTTYTNTNPAKIGDPQPV 540
Db      481  KPSMADSAGDEVEYVVGIGIMIGTELFSQNFSSNDVMJSAVMTTYTNTNPAKIGDPQPV 540
Cy      541  PDKTFHTKPNRFEEDVAMSKYNKCDLYLHIGLXPRVHYATKAFLMELVPHLNL 600
Db      541  PDKTFHTKPNRFEEDVAMSKYNKCDLYLHIGLXPRVHYATKAFLMELVPHLNL 600
Cy      601  NEIFQVSTTKVPBPMTSPFYGTTRSPAKIWTETKRPATPANNPKSKDPKATGPEP 660
Db      601  NEIFQVSTTKVPBPMTSPFYGTTRSPAKIWTETKRPATPANNPKSKDPKATGPEP 660
Cy      661  TVLIERKRDYSTLSTIANGASLELNTLAFALYXDKPRHETRRPSPORNTND 720
Db      661  TVLIERKRDYSTLSTIANGASLELNTLAFALYXDKPRHETRRPSPORNTND 720
Cy      721  IAHIONEEIMSLQKQLEHDECELSQAHOTLRITCPDDYTLTLRRSPDIPJMTPTIT 780
Db      721  IAHIONEEIMSLQKQLEHDECELSQAHOTLRITCPDDYTLTLRRSPDIPJMTPTIT 780
Cy      781  MIPNLTGMOPLTPTNPNFSSGQNSTNPHGASTTRV 816
Db      781  MIPNLTGMOPLTPTNPNFSSGQNSTNPHGASTTRV 816

RESULT 12
US-09-981-915A-375
/ Sequence 375, Application US/09981915A
/ Publication No. US20030054986A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Boeststein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Geisler, Hanspeter
/ APPLICANT: Gerritsen, Mary B.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul C.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kijavira, Ivar J.
/ APPLICANT: Kuo, Sophia S.
```

APPLICANT: Kapler, Mary A.
APPLICANT: Pat, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David J.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secured and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C12
CURRENT APPLICATION NUMBER: US/09/981.915A
PRIOR FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/0662250
PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/085573
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PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 816; DB 11; Length 216;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MANSVLLMLTALAIAKTLDSCQYVNTNNGKRGRLTPJNELLGPEYOLGVERA 60
CY 61 SPPTGERRFPQPPPPSSKWTGIRNTQCPAAVCPOGLPERSJCHMLTINFANLCTNTEV 120
DB 61 SPPTGERRFPQPPPPSSKWTGIRNTQCPAAVCPOGLPERSJCHMLTINFANLCTNTEV 120
CY 121 ODQNECLYNTIVVPEEDGANTKKNADITSNRGEDEIDHONSKKPVVYIHGGSYME 190
DB 121 ODQNECLYNTIVVPEEDGANTKKNADITSNRGEDEIDHONSKKPVVYIHGGSYME 190
CY 121 ODQNECLYNTIVVPEEDGANTKKNADITSNRGEDEIDHONSKKPVVYIHGGSYME 190
DB 121 ODQNECLYNTIVVPEEDGANTKKNADITSNRGEDEIDHONSKKPVVYIHGGSYME 190
CY 191 GTGMWDSILASGVNIVITNIRGLGLSTGQAAGNVGLDQICARMEENVG 240
DB 191 GTGMWDSILASGVNIVITNIRGLGLSTGQAAGNVGLDQICARMEENVG 240
CY 181 GTGMWDSILASGVNIVITNIRGLGLSTGQAAGNVGLDQICARMEENVG 240
DB 181 GTGMWDSILASGVNIVITNIRGLGLSTGQAAGNVGLDQICARMEENVG 240
CY 241 AFGDPRKVTIFSGAGASCVSLLTSHYSEGLFOKAIIOGSLALSSMANVQPAKYT31 300
DB 241 AFGDPRKVTIFSGAGASCVSLLTSHYSEGLFOKAIIOGSLALSSMANVQPAKYT31 300
CY 301 LACKVGNXLLDTTNYECLANKYKELQCTITPATYHIAFGVINGDVIPDDPOLMEQ 360
DB 301 LACKVGNXLLDTTNYECLANKYKELQCTITPATYHIAFGVINGDVIPDDPOLMEQ 360
CY 301 LACKVGNXLLDTTNYECLANKYKELQCTITPATYHIAFGVINGDVIPDDPOLMEQ 360
DB 301 LACKVGNXLLDTTNYECLANKYKELQCTITPATYHIAFGVINGDVIPDDPOLMEQ 360
CY 361 GEFANDIMLVNNGEGCKFEVDGIVNEDGVTFRDFFSVSNVZKLYGPECKTLRET 420
DB 361 GEFANDIMLVNNGEGCKFEVDGIVNEDGVTFRDFFSVSNVZKLYGPECKTLRET 420
CY 361 GEFANDIMLVNNGEGCKFEVDGIVNEDGVTFRDFFSVSNVZKLYGPECKTLRET 420
DB 361 GEFANDIMLVNNGEGCKFEVDGIVNEDGVTFRDFFSVSNVZKLYGPECKTLRET 420
CY 421 IKFMYTMAKKNENETRRKTLVALFTDHQVAVAAADLAQYGSFTYVAYVHRCQSM 480
DB 421 IKFMYTMAKKNENETRRKTLVALFTDHQVAVAAADLAQYGSFTYVAYVHRCQSM 480
CY 481 KPSVADSAGGEVYVVGIPMIGTELFSCNFSKNVMSAVMTVTPAKTGDDNOV 540
DB 481 KPSVADSAGGEVYVVGIPMIGTELFSCNFSKNVMSAVMTVTPAKTGDDNOV 540

CY 541 POSTKFIHCKPNFEEVANSKYKPKDLYLHGLXZRVBDHYRATVAFMLEVPHLNT 600
DB 541 POSTKFIHCKPNFEEVANSKYKPKDLYLHGLXZRVBDHYRATVAFMLEVPHLNT 600
CY 601 NEIFQVSTTTKVPDPMTSPFYGRSPAKIWPTRKPAITPANNPKSKDPKTKGED 660
DB 601 NEIFQVSTTTKVPDPMTSPFYGRSPAKIWPTRKPAITPANNPKSKDPKTKGED 660
CY 661 TTVLIEFKRXYSTELSVTLAVGASLLFNLILAPALYYKKDKRRHETRRSPQRXTND 720
DB 661 TTVLIEFKRXYSTELSVTLAVGASLLFNLILAPALYYKKDKRRHETRRSPQRXTND 720
CY 721 IAHQNEIWSLQKLEHDECESLQADTLRLTCCPPDYTLIRSPDDIPLMPTNTT 780
DB 721 IAHQNEIWSLQKLEHDECESLQADTLRLTCCPPDYTLIRSPDDIPLMPTNTT 780
CY 781 MIPNTLTGMQPLHTFNTFSGQNSTVLPHGSHSTRV 816
DB 781 MIPNTLTGMQPLHTFNTFSGQNSTVLPHGSHSTRV 816

RESULT 13
US-09-978-824-375
Sequence 375, Application: US/09978824
Publication No. US20030055216A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bostein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Mei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grima-di, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavrin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Peptideptides and Nucleic
FILE REFERENCE: P2630P1C14
CURRENT APPLICATION NUMBER: US/09/978, 824
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/385573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 816; DB 1; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MUNSVM:MTALAIKFTLLDSQAQYPVNTNNGKTRGKTRPLNPIILQVQYGVYPA 63
DB 1 MUNSVM:MTALAIKFTLLDSQAQYPVNTNNGKTRGKTRPLNPIILQVQYGVYPA 60
QY 61 SPTGERRFPQPPSPSSMTGIRNTQPAVCPQHLDERSCLDNM:PIWFTALMOTLMYV 120
DB 61 SPTGERRFPQPPSPSSMTGIRNTQPAVCPQHLDERSCLDNM:PIWFTALMOTLMYV 120
QY 122 QDQNEDECLYNIYVFTEDGANTKKADITSNRGEDEDIHQNSKKPVMYTHQGSYVE 180
DB 122 QDQNEDECLYNIYVFTEDGANTKKADITSNRGEDEDIHQNSKKPVMYTHQGSYVE 180
QY 121 QDQNEDECLYNIYVFTEDGANTKKADITSNRGEDEDIHQNSKKPVMYTHQGSYVE 180
DB 121 QDQNEDECLYNIYVFTEDGANTKKADITSNRGEDEDIHQNSKKPVMYTHQGSYVE 180
QY 181 GTGNMIDGSLASAGNVYVTTINRGLIAGFLSTQDAKXGVGLDQIQLRMEYNG 240
DB 181 GTGNMIDGSLASAGNVYVTTINRGLIAGFLSTQDAKXGVGLDQIQLRMEYNG 240
QY 241 AFGQDPKRVVTFSSGAGASVSLTLSSVSEGLFQKALIQSGTASNNANXQPKYTR 300
DB 241 AFGQDPKRVVTFSSGAGASVSLTLSSVSEGLFQKALIQSGTASNNANXQPKYTR 300
QY 301 LARXGCMJDTTDMVECLANKYKE:CGTITRATY:AFQVADGQVFPDQCLMEQ 350
DB 301 LARXGCMJDTTDMVECLANKYKE:CGTITRATY:AFQVADGQVFPDQCLMEQ 350
QY 361 GEFUNDMGVNQEGQLKXVDGIVNEDGVYVNDPFCFSVSNFVDMVXVPEKCLTET 420
DB 361 GEFUNDMGVNQEGQLKXVDGIVNEDGVYVNDPFCFSVSNFVDMVXVPEKCLTET 420
QY 421 IKRNYTMKRNKRNKTRKTLVAFTHQVAVAVADLAQVGSFTYVAYVHHCQSEM 480
DB 421 IKRNYTMKRNKRNKTRKTLVAFTHQVAVAVADLAQVGSFTYVAYVHHCQSEM 480
QY 481 KPSWADSAHGDEVYVYVGIPIMISPTLFCNSKNDVYLSAVYVYVWVAFKGGPNCV 540
DB 481 KPSWADSAHGDEVYVYVGIPIMISPTLFCNSKNDVYLSAVYVYVWVAFKGGPNCV 540
QY 541 PCKTK:HTKPNRFEVYVAMSKNPKDOLYHILAKRYVDH:RATKAAWELVYH:NL 600
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QY 601 NEIFQVYSTTKVPPDNTSFPYGRSPAKIWPTRKPAITFPAKPKSKDPKGTGPD 660
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QY 661 TVVLETRDYSTEJLSTVAVGASLLFLNLAPALYKDKRKHETRRSPQNTTND 720
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QY 721 IAHQNEIMSLCKQLEHDECS:QAHNT:ALTCPPYVTLTIRSPDIDLMKNTIT 780
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QY 781 MIPVLTGQOPLTFTNTFFSGQNSTNLPHQSTTRV 816
DB 781 MIPVLTGQOPLTFTNTFFSGQNSTNLPHQSTTRV 816

RESULT 14
US-09-978-585A-375
Sequence 375, Application US/09918585A
Publication No. US2003060406A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Destrofers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Oiang
APPLICANT: Gerber, Hanspeter
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APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, V. Christopher
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APPLICANT: Pan, James J.
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APPLICANT: Roy, Margaret Ann
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumes, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C1
CURRENT APPLICATION NUMBER: US/09/918,585A
PRIOR APPLICATION NUMBER: 2001-07-30
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Prior	FILING DATE: 1998-05-15
Prior	APPLICATION NUMBER: 60/086623

Query Match: 100.0%; Score 816; DB 11; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy	1	MUNSWLWLTALAIKFTLLDSOQAPVNTNYGIRGRFLPBEILIGPVCEYGVYA	60
Cb	1	MUNSWLWLTALAIKFTLLDSOQAPVNTNYGIRGRFLPBEILIGPVCEYGVYA	60
Cy	61	SPTGRRFQPPEPPSSWTGITINTTQAFAVCPQSJDEBSLHCDMIPMTANLDITMYV	120
Cb	61	SPTGRRFQPPEPPSSWTGITINTTQAFAVCPQHLSRSLHDMIPMTANLDITMYV	120
Cy	121	QONNEGLYINIVYPEDDANKKKACADJTSNDREGEPIHQNSKKPKPMYYIHGSVYE	180
Cb	121	QONNEGLYINIVYPEDDANKKKACADJTSNDREGEPIHQNSKKPKPMYYIHGSVYE	180
Cy	181	GTONMDGSLASGVAVIITINYR-GILGFUSTCDAQAKNGVGLDQIALRWIEENVG	240
Cb	181	GTONMDGSLASGVAVIITINYR-GILGFUSTCDAQAKNGVGLDQIALRWIEENVG	240
Cy	241		

Db 241 AFGGDPKRVITIFSGGAGACVSLLLISHSEJ:FQAIITQSGTASSMWVNYQPKYTRI 300
Qy 301 LADKVGCMMLDTDMWECLEKRNKYKEJICQITIPATYHAFGPVTDGVPFPDQPOLHEQ 360
Db 301 LADKVGCMMLDTDMWECLEKRNKYKEJICQITIPATYHAFGPVTDGVPFPDQPOLHEQ 360
Qy 361 GEFNLNDIMGVNQGGLKRFVDSIVNEDGVTPNDFSVSNFVNLXGYPGKQJLEET 420
Db 361 GEFNLNDIMGVNQGGLKRFVDSIVNEDGVTPNDFSVSNFVNLXGYPGKQJLEET 420
Qy 421 IKFNTDMADKEMPEFRKKTVAJFTDQWVAFAVAALDADYGSTFYATYHHCQSEM 480
Db 421 IKFNTDMADKEMPEFRKKTVAJFTDQWVAFAVAALDADYGSTFYATYHHCQSEM 480
Qy 481 KPSMADSACDEVPYFPGIPIKIPTECFSCNFSKNDVM:SAVMYTWTFATGPNQPV 540
Db 481 KPSMADSACDEVPYFPGIPIKIPTECFSCNFSKNDVM:SAVMYTWTFATGPNQPV 540
Qy 541 PQTKEIHTKPNRFEVAVSKYVNPQDLYLHIGLKPRVDHYRATKVAFWLELVHLNR 600
Db 541 PQTKEIHTKPNRFEVAVSKYVNPQDLYLHIGLKPRVDHYRATKVAFWLELVHLNR 600
Qy 601 NEFOYVSTTKVPPEDMTSPYGTGRSPAKIMPTTKRPAFPANPKSKPKKTSQED 660
Db 601 NEFOYVSTTKVPPEDMTSPYGTGRSPAKIMPTTKRPAFPANPKSKPKKTSQED 660
Qy 661 TTVLETKRQYS:ELSVITVAAGASJLFNLLAFVAVYKQKRRHSHRRPSPQNTND 720
Db 661 TTVLETKRQYS:ELSVITVAAGASJLFNLLAFVAVYKQKRRHSHRRPSPQNTND 720
Qy 721 IAHQNEELMSLQKLEHDEHES:QAHCTLRCTPPRYTITLRSPQCLPLN:FNIT 780
Db 721 IAHQNEELMSLQKLEHDEHES:QAHCTLRCTPPRYTITLRSPQCLPLN:FNIT 780
Qy 781 MENTLTCNPLHTFNTFSGGQRTYLPCHSTTRV 846
Db 781 MENTLTCNPLHTFNTFSGGQRTYLPCHSTTRV 846

RESULT 15
US-09-978-423a-375
Sequence 375, Application JS/03978423A
Publication No. US20030369176A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Flaxman, Ellen
APPLICANT: Gong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerbert, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, V. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: K-Javin, Ivar J.
APPLICANT: Kuc, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paout, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David J.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P26301C21
CURRENT APPLICATION NUMBER: US/09/978,423A
CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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Query Match 100.0% Score 816, DB 11, Length 816;
 Best Local Similarity 100.0% Pred. No. 0;
 Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MUNSVM:MTLTAIKFTLIDSOAQPVTNTYKIRGLRTPLNEILGPVEQYAGPVA 60
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 61 SPTGERFOPPEPSSWTGIRNTTQPAVCPQALDRSLHDMPTMTANLDTLMTYV 120
 61 SPTGERFOPPEPSSWTGIRNTTQPAVCPQALDRSLHDMPTMTANLDTLMTYV 120
 121 QONEDCYLNIYVTEGANTKKNADITSDNGEDSDHDCSKKPVWYIHGGSYME 180
 121 QONEDCYLNIYVTEGANTKKNADITSDNGEDSDHDCSKKPVWYIHGGSYME 180
 181 GTGNMIDGSIASGVNVTINNYRLGILGSLTGDQAKKNYGLDQIALRMTEENVG 240
 181 GTGNMIDGSIASGVNVTINNYRLGILGSLTGDQAKKNYGLDQIALRMTEENVG 240
 181 GTGNMIDGSIASGVNVTINNYRLGILGSLTGDQAKKNYGLDQIALRMTEENVG 240
 241 AFGDPKXVTIFGSGAGACVSLTSLYSGLFOKALOGCTALSSAANYOPAKTRI 300
 241 AFGDPKXVTIFGSGAGACVSLTSLYSGLFOKALOGCTALSSAANYOPAKTRI 300
 301 LADKVCNMULTTDEVECLRNKNYKELQOTITPATYHIAAGPVIJGCVIPDDPOLMEQ 360
 301 LADKVCNMULTTDEVECLRNKNYKELQOTITPATYHIAAGPVIJGCVIPDDPOLMEQ 360
 361 GEFLLNYDMLGVNOGEGKPYDGVNEDGVTPTDFDSVSNFYDNLVGYEGKQZLRET 420
 361 GEFLLNYDMLGVNOGEGKPYDGVNEDGVTPTDFDSVSNFYDNLVGYEGKQZLRET 420
 421 IKEMYTADKDNENPTRRKTLVALFTHQWAPAAALHAYOSPTTFYAFYHCOSEX 480
 421 IKEMYTADKDNENPTRRKTLVALFTHQWAPAAALHAYOSPTTFYAFYHCOSEX 480
 481 KPMASDAHGDGEVYFVGIPMIGPTELSFCSXNDVLSAVVYTWMTNFAKTDPOPV 540
 481 KPMASDAHGDGEVYFVGIPMIGPTELSFCSXNDVLSAVVYTWMTNFAKTDPOPV 540
 541 PCOTKFITKPRFEVAVMSKYNPDQLYLHGLKPRRDRHYRATKAVFELVPLHLNL 600
 541 PCOTKFITKPRFEVAVMSKYNPDQLYLHGLKPRRDRHYRATKAVFELVPLHLNL 600
 601 NEIFQVSTTFVPPEDKTSFPYGRSRPAKIMPTTKAPATIPANNPGHSCDPRKTCGED 660
 601 NEIFQVSTTFVPPEDKTSFPYGRSRPAKIMPTTKAPATIPANNPGHSCDPRKTCGED 660
 661 ITVLLETADYSTELSVTIAVAGALLFNILAFALVYKKDKRREHTRRPSFORNTTND 720
 661 ITVLLETADYSTELSVTIAVAGALLFNILAFALVYKKDKRREHTRRPSFORNTTND 720

Db 661 TTUJIEFKDYSTLSVTIAVGSLEJLNIAPALYYKKDKRHEHRRSPQKNTND 723
Qy 721 IAHIQNEIMSLQKQLEHDECELSQAHDLRLTCCPDYTLIRSPDDIPMTENTIT 790
Db 721 IAHIQNEIMSLQKQLEHDECELSQAHDLRLTCCPDYTLIRSPDDIPMTENTIT 793
Qy 791 MIPMTLTGMOPLHTFNTFSSGQNSTNLPHGSTRV 816
Db 781 MIPMTLTGMOPLHTFNTFSSGQNSTNLPHGSTRV 816
RESULT 16
US-09-978-193A-375
Sequence 375, Application US/09978193A
Publication No. US20030073624A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertelsen, Vary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavrin, Ivar O.
APPLICANT: Kuo, Sophia S.
APPLICANT: Mader, Mary A.
APPLICANT: Mac, James;
APPLICANT: Paori, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William T.
TITLE OF INVENTION: Selected and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Agc5 Encoding the Same
FILE REFERENCE: P2630P1C6
CURRENT APPLICATION NUMBER: US/099781, 193A
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/062253
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/064249
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 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0% Score 816 DB 1: Length 816;
 Best Local Similarity 100.0% Pred. No. 0;
 Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MNSNVLLMTALAIKFTLIDSOAQYPTWNTYKIRGLRTPFLPRETLGPVECYLGVYA 60

DB 1 MNSNVLLMTALAIKFTLIDSOAQYPTWNTYKIRGLRTPFLPRETLGPVECYLGVYA 60
 61 SEPTGERFOPPEPSSWTG:RNTTQFAAVCPGLJESRLHMLPIMFTANLCTMTYV 120
 61 SPTEERFPPEPSSWTG:RNTTQFAAVCPGLJESRLHMLPIMFTANLCTMTYV 120
 121 ODONEDCLYNIYVTEDEGANTKKNADITNSDGEDEHDQSKKRVWYIIGGSYME 180
 121 ODONEDCLYNIYVTEDEGANTKKNADITNSDGEDEHDQSKKRVWYIIGGSYME 180
 121 ODONEDCLYNIYVTEDEGANTKKNADITNSDGEDEHDQSKKRVWYIIGGSYME 180
 181 GTGNMIDSGIILASVNVVITINRGLGLSLSTGCOAKKNYGLDIOALRMIEENVG 240
 181 GTGNMIDSGIILASVNVVITINRGLGLSLSTGCOAKKNYGLDIOALRMIEENVG 240
 241 AFGSDPKAVTIFGSGAGASCYSLTLTSHYSEGLTCKAIQSGTALSSAAVYQPAKYRI 300
 241 AFGSDPKAVTIFGSGAGASCYSLTLTSHYSEGLTCKAIQSGTALSSAAVYQPAKYRI 300
 301 LADKVCNNLETTIDWVECLRNKRYELCCQITTPATYHAFGPVIGDVIEDDQIIMEQ 360
 301 LADKVCNNLETTIDWVECLRNKRYELCCQITTPATYHAFGPVIGDVIEDDQIIMEQ 360
 361 GEFINVDMLGVNCGESLKFVDGIVJNEDGTPNDPDSVSNFYDNLGYEGEGLTRET 420
 361 GEFINVDMLGVNCGESLKFVDGIVJNEDGTPNDPDSVSNFYDNLGYEGEGLTRET 420
 421 IKFYTDMAKXENPETRRKTLVALFTCHQWAPAVAADJHAQYSGPTFYAFYHCOSEM 480
 421 IKFYTDMAKXENPETRRKTLVALFTCHQWAPAVAADJHAQYSGPTFYAFYHCOSEM 480
 481 KPSWADSAHGDVVPVFGIEMIGPELESCNPKQDVNLSAVMTYKTNFAKTGPNOPV 540
 481 KPSWADSAHGDVVPVFGIEMIGPELESCNPKQDVNLSAVMTYKTNFAKTGPNOPV 540
 541 POCSTKFIHKPRFEVWASKYNPNDOYLHIGLKRPRRDHYRAIKVAFMLELVPHLNL 600
 541 POCSTKFIHKPRFEVWASKYNPNDOYLHIGLKRPRRDHYRAIKVAFMLELVPHLNL 600
 601 NEIFOYVSTTKVPPDMTSPFYGTRSPAKIMPTKRPATTPANNPHSKDPKHTGED 660
 601 NEIFOYVSTTKVPPDMTSPFYGTRSPAKIMPTKRPATTPANNPHSKDPKHTGED 660
 661 TVVLETRKDYSTEISVITAVGASLLPLNLAFAALYKKRKHETRRSPORNTND 720
 661 TVVLETRKDYSTEISVITAVGASLLPLNLAFAALYKKRKHETRRSPORNTND 720
 721 IAHIONBEIWSLOKQLEHCHCESLOAHDTLRLTCCPDYTLTJRRSPDDIPLMTPTIT 780
 721 IAHIONBEIWSLOKQLEHCHCESLOAHDTLRLTCCPDYTLTJRRSPDDIPLMTPTIT 780
 781 MIPNLTGQPLHTNTTSGGNSNLPHGSHSTRV 816
 781 MIPNLTGQPLHTNTTSGGNSNLPHGSHSTRV 816

US-09-999-830A-375

Sequence 375, Application US/09999830A

Publication No. US2003007700A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Juc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleo

APPLICANT: Filvaroff, Ellen

APPLICANT: Forg, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaidi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavira, Ivar U.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ACIDS
FILE REFERENCE: P2630P-C70
CURRENT APPLICATION NUMBER: US/09/999,83CA
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/918565
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064245
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05

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? PRIOR APPLICATION NUMBER: 60/084644
? PRIOR FILING DATE: 1998-05-06
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? PRIOR FILING DATE: 1998-05-15
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? PRIOR FILING DATE: 1998-05-15
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? PRIOR FILING DATE: 1998-05-15
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? PRIOR FILING DATE: 1998-05-15
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? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085704
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085697

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Query Match :00.04; Score 816; DB 11; Length 816;

Best Local Similarity :00.04; Pred. No. 0;

Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MNSVILMLTALA:KFTLIDSOQYVNVNTNKG:IGLS:TPLEK:ELGVEGYLQVPA 60
DB 1 MNSVILMLTALA:KFTLIDSOQYVNVNTNKG:IGLS:TPLEK:ELGVEGYLQVPA 60
QY 61 SPTGERFPPEPPSSWTGIRNTTOFAVCPCHLDEPSILHMLPMTFAN:DTJXTY 120
DB 61 SPTGERFPPEPPSSWTGIRNTTOFAVCPCHLDEPSILHMLPMTFAN:DTJXTY 120
QY 121 QONEDCLYLYVPTEDGANTKQADDI:SNDRGEED:HDONSKKPYVYIHGGSYE 180
DB 121 QONEDCLYLYVPTEDGANTKQADDI:SNDRGEED:HDONSKKPYVYIHGGSYE 180
QY 121 QONEDCLYLYVPTEDGANTKQADDI:SNDRGEED:HDONSKKPYVYIHGGSYE 180
DB 121 QONEDCLYLYVPTEDGANTKQADDI:SNDRGEED:HDONSKKPYVYIHGGSYE 180
QY 181 GTGNMIDGSLIAGSNVYITINRLGLISL:STRPAAAGNIGLL:QIOLAK:TEENWG 240
DB 181 GTGNMIDGSLIAGSNVYITINRLGLISL:STRPAAAGNIGLL:QIOLAK:TEENWG 240
QY 241 AFGGPKRVTIFGSGAGASCVSLTTL:SHYSG:LFQKX:IGSTAL:SEMANVCPAYAT 300
DB 241 AFGGPKRVTIFGSGAGASCVSLTTL:SHYSG:LFQKX:IGSTAL:SEMANVCPAYAT 300
QY 301 LADKVGCMLEDTTMEVELKRNK:KEJ:QCTITATYH:AFGPAV:ISGCV:PDGQILMEQ 360
DB 301 LADKVGCMLEDTTMEVELKRNK:KEJ:QCTITATYH:AFGPAV:ISGCV:PDGQILMEQ 360
QY 361 GEFANVJML:GVNCGEG:KFDVG:VDNEDG:STPRCEP:PSV:FNQNYG:YGEK:FTL:EE 420
DB 361 GEFANVJML:GVNCGEG:KFDVG:VDNEDG:STPRCEP:PSV:FNQNYG:YGEK:FTL:EE 420
QY 421 IKFWITMAOKENETRTKTLVALFTDQWVAAPVAAADLFAQYSGSPTYFAFHHGQSEM 480
DB 421 IKFWITMAOKENETRTKTLVALFTDQWVAAPVAAADLFAQYSGSPTYFAFHHGQSEM 480

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DB 421 IKFWITMAOKENETRTKTLVALFTDQWVAAPVAAADLFAQYSGSPTYFAFHHGQSEM 480
QY 481 KPSWADSAHGEVYVYEGIPMIGTELFSQNFSGKNVMSAVVYTYWTFPAKTGDPNOZY 540
DB 481 KPSWADSAHGEVYVYEGIPMIGTELFSQNFSGKNVMSAVVYTYWTFPAKTGDPNOZY 540
QY 541 PODKFLHTKRNREEVYAKSKYNKPDOLYHIGLKPRVRYHYATKAFLELVPH:HLN 600
DB 541 PODKFLHTKRNREEVYAKSKYNKPDOLYHIGLKPRVRYHYATKAFLELVPH:HLN 600
QY 601 NEIFOVYSTKVPPEPMTSFPYOTRSPAKIMPTTRPAITFANPKSKDCHK:GPD 660
DB 601 NEIFOVYSTKVPPEPMTSFPYOTRSPAKIMPTTRPAITFANPKSKDCHK:GPD 660
QY 661 TVULFETKDYSTLSVTIAGASLFL:NLAFAPALYKKOKKREH:THRRPSQORNTND 720
DB 661 TVULFETKDYSTLSVTIAGASLFL:NLAFAPALYKKOKKREH:THRRPSQORNTND 720
QY 721 IAH:QNEEIMSLQKOLEHDECESLQAHDTL:CTCPDYT:TLRSPPD:PLMTPTT 780
DB 721 IAH:QNEEIMSLQKOLEHDECESLQAHDTL:CTCPDYT:TLRSPPD:PLMTPTT 780
QY 781 MPTLTOMQPLHTFNTFSGGQNSTLPHCHSTTRV 816
DB 781 MPTLTOMQPLHTFNTFSGGQNSTLPHCHSTTRV 816

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RESULT 18

US-09-978-757A-375

Sequence 375, Application US/09978757A

Publication No. US20030083248A1

GENERAL INFORMATION:

```

? APPLICANT: Ashkenazi, Avi
? APPLICANT: Baker Kevin P.
? APPLICANT: Botstein, David
? APPLICANT: Deenoyers, Luc
? APPLICANT: Eaton, Dan
? APPLICANT: Ferrara, Napoleon
? APPLICANT: Filvaroff, Ellen
? APPLICANT: Fong, Sherman
? APPLICANT: Gao, Wei-Qiang
? APPLICANT: Gerber, Hanspeter
? APPLICANT: Gerritsen, Maty E.
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Grimaldi, J. Christopher
? APPLICANT: Gurney, Austin L.
? APPLICANT: Hillan, Kenneth J.
? APPLICANT: Kijavira, Ivar J.
? APPLICANT: Kuo, Sophia S.
? APPLICANT: Nader, Maty A.
? APPLICANT: Pan, James
? APPLICANT: Paoni, Nicholas F.
? APPLICANT: Roy, Margaret Ann
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tumaas, Daniel
? APPLICANT: Williams, P. Mickey
? APPLICANT: Wood, William J.
? TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
? FILE REFERENCE: P2630P1C26
? CURRENT FILING DATE: US/09/978, 757A
? PRIOR APPLICATION NUMBER: 2002-03-19
? PRIOR FILING DATE: 2001-07-30
? PRIOR APPLICATION NUMBER: 39/918585
? PRIOR FILING DATE: 2001-07-30
? PRIOR APPLICATION NUMBER: 60/062250
? PRIOR FILING DATE: 1997-10-17
? PRIOR APPLICATION NUMBER: 60/064249
? PRIOR FILING DATE: 1997-11-03
? PRIOR APPLICATION NUMBER: 60/065311
? PRIOR FILING DATE: 1997-11-13

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PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081952
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081838
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/082568
PRIOR FILING DATE:	1998-04-21
PRIOR APPLICATION NUMBER:	60/062565
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PRIOR APPLICATION NUMBER:	60/082704
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Query Match 100.0%; Score 816; DB 11; Length 816;
 Best Local Similarity 100.0%; Pred No. 3;
 Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MUNSVMMLTALAIKFTJDSQAQYPPVNTYNGKRGJRTPLPNEILGQYGVPA 60
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 DB 61 SPTGERRFPPEPSSWTGIRNTTQFAVCPHLDERSLHMLPIMFTALMTYV 120
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 DB 121 QDQNECCYLNIVYPTEDGANTKKNADITSDRGEDCDHONSKKPYVYIHGSSVME 180
 QY 181 GTGNMIDGSLASGNVYTTINRGLGLFTSTGDAAGNGLDQIOALWIEENNG 240
 DB 181 GTGNMIDGSLASGNVYTTINRGLGLFTSTGDAAGNGLDQIOALWIEENNG 240
 QY 241 AFGSDPKRTIFSGAGACVSLTSHYSESFOKXJSSSTALSMANVPAYTETI 300
 DB 241 AFGSDPKRTIFSGAGACVSLTSHYSESFOKXJSSSTALSMANVPAYTETI 300
 QY 301 LADRVGCMMLDTTDMVECLRNKNKELIQTTTPATYHAFGPVIGDVPDQECILMEQ 360
 DB 301 LADRVGCMMLDTTDMVECLRNKNKELIQTTTPATYHAFGPVIGDVPDQECILMEQ 360
 QY 361 GEFLNYDMLGVNGBELKFDVGVNEDCGVTENDPEFSNPNVNLXGPEKCTLRET 420
 DB 361 GEFLNYDMLGVNGBELKFDVGVNEDCGVTENDPEFSNPNVNLXGPEKCTLRET 420
 QY 421 IKFMYTDMADKENETRRKTLVALFTDHQWAPAVADLHMQGSPTYFAFYHHCQSEK 480
 DB 421 IKFMYTDMADKENETRRKTLVALFTDHQWAPAVADLHMQGSPTYFAFYHHCQSEK 480
 QY 481 KPSWADSHGDEVYVVGIPYIGTELFSCNFSKNDVLSAVVMTVTNPAKGDPRQPV 540
 DB 481 KPSWADSHGDEVYVVGIPYIGTELFSCNFSKNDVLSAVVMTVTNPAKGDPRQPV 540
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 DB 541 PODKFIHTKPREEEVWMSKYNPKDCYLIHJLKPAPRPHYATKAFMLEVPHLHNL 600
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 DB 601 NEIFQYVSTTKVPPDVTSPFYGTSSPAKIMPTTSPATTPANPKSKPHKGPED 660
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 DB 661 TTVLIETKPDVSTSVTIAGASLLENTLAFALAYKKQKREHHRSPSQKNTNG 720
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 DB 721 IAHQNEEINSLQKQLEHCEHCESLQAHDTLRJCTEDVTTLTRSPDIPVXTPTT 780
 QY 781 MIPNTLTGMPLEHTNTSSGQNSNLPHGSTRV 816
 DB 781 MIPNTLTGMPLEHTNTSSGQNSNLPHGSTRV 816

RESULT 19

us-09-978-187b-375

Sequence 375, Application US/09978187b
 Publication No. US20030096744A1

GENERAL INFORMATION:

APPLICANT: Askenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Flivaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gertelsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillar, Kenneth J.
 APPLICANT: K.Javan, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630PICS
 CURRENT APPLICATION NUMBER: US/09/978,187b
 PRIOR FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/077450
 PRIOR FILING DATE: 1998-03-10
 PRIOR APPLICATION NUMBER: 60/077632
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 PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/379689
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PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085597

Query Match 100.0%; Score 816; DB 1; Length 866;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MNSNVLMWLTALAKFTLIDSOAYVWNTNGKIRGJRTPLNNEILGVEQYLGVPYA 60
1 MNSNVLMWLTALAKFTLIDSOAYVWNTNGKIRGJRTPLNNEILGVEQYLGVPYA 60
61 SPPTGERRFOPEPESSWTGIRNTTOPAAVCPQHLDRSLJLHMLPMTFANLDTLMTYV 120
61 SPPTGERRFOPEPESSWTGIRNTTOPAAVCPQHLDRSLJLHMLPMTFANLDTLMTYV 120
121 QDQNEDECLYNIYPTEDGANTKXADITSNDGDEDEJHDQNSKXPPWVYIHGGSYME 180
121 QDQNEDECLYNIYPTEDGANTKXADITSNDGDEDEJHDQNSKXPPWVYIHGGSYME 180
DB 121 QDQNEDECLYNIYPTEDGANTKXADITSNDGDEDEJHDQNSKXPPWVYIHGGSYME 180

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QY 161 GTGMMTGGSTLASGNNVVTITNRLGSLGSLSTGCGAANKNVCLLJQICLALMBENNG 240
DB 161 GTGMMTGGSTLASGNNVVTITNRLGSLGSLSTGCGAANKNVCLLJQICLALMBENNG 240
QY 241 AFGGDKPRVTIFGSGAGASCVSLLTSHSEGLFQKAIJOSGTLSSMAVNYCPAKYTRI 300
DB 241 AFGGDKPRVTIFGSGAGASCVSLLTSHSEGLFQKAIJOSGTLSSMAVNYCPAKYTRI 300
QY 301 LADKVGCMMLDTTDMVECLRNKNKYKELIQOTITPATYHIAFGVYDGDVI PDDQILMEQ 360
DB 301 LADKVGCMMLDTTDMVECLRNKNKYKELIQOTITPATYHIAFGVYDGDVI PDDQILMEQ 360
QY 361 GEFNLVDIMLVNQGEGKAFVDSIVNEDGVTPDPCPSNPFMDNYGPECKTLPET 420
DB 361 GEFNLVDIMLVNQGEGKAFVDSIVNEDGVTPDPCPSNPFMDNYGPECKTLPET 420
QY 421 IKFMYTMAADKENPETRRKTLVALFTDHCQWAFVAAADLIAQVGSPTFYFAFYHHCQSEM 480
DB 421 IKFMYTMAADKENPETRRKTLVALFTDHCQWAFVAAADLIAQVGSPTFYFAFYHHCQSEM 480
QY 481 KPSWADSAHGDDEVYVFGIPMIGPTELFSCNFSKNDVMSAVVMTWTNPAKTDGPNQPV 540
DB 481 KPSWADSAHGDDEVYVFGIPMIGPTELFSCNFSKNDVMSAVVMTWTNPAKTDGPNQPV 540
QY 541 PODTKFIHTKPRREPEEVAWSKYNPKDQLYHIGLKPVRDCHVRATKVAFAFCELVPHLHNT 600
DB 541 PODTKFIHTKPRREPEEVAWSKYNPKDQLYHIGLKPVRDCHVRATKVAFAFCELVPHLHNT 600
QY 601 NEIFQVSTTTKVPVPPDMSFPYGRSRSPAKIWTTRKPAITPANPKHCKDHKTGPEP 660
DB 601 NEIFQVSTTTKVPVPPDMSFPYGRSRSPAKIWTTRKPAITPANPKHCKDHKTGPEP 660
QY 661 TTVLIETKRDYSTSLSTIIVAGASLFLNLIAPALYKXKRRHETRRSPQPTTNE 720
DB 661 TTVLIETKRDYSTSLSTIIVAGASLFLNLIAPALYKXKRRHETRRSPQPTTNE 720
QY 721 IAHQNEEIMSLQKQLEHDEHCESLQAHDTLRLTCPPDYTLTLRRSPDDIPMTNNTIT 780
DB 721 IAHQNEEIMSLQKQLEHDEHCESLQAHDTLRLTCPPDYTLTLRRSPDDIPMTNNTIT 780
QY 781 MIPNTLTGKQPLHTENTPFGGONSNTLPHGSHSTRV 816
DB 781 MIPNTLTGKQPLHTENTPFGGONSNTLPHGSHSTRV 816

RESULT 2C
US-09-978-643a-375
Sequence 375, Application US/0978643a
Publication No. US20030104998A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Borstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geisler, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaud, J. Christopher
APPLICANT: Garney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavita, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Panni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
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Qy 781 MIPNLTGQPCUHTFNTFSGGGNSINLEPHGSTTRV 816
Db 781 MIPNLTGQPCUHTFNTFSGGGNSINLEPHGSTTRV 816

RESULT 21

US-09-978-375a-375
Sequence 375, Application US/09978375A
Publication No. US20030130181A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar C.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James:
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C24
CURRENT APPLICATION NUMBER: US/09/978,375A
CURRENT FILING DATE: 2002-04-19
Prior Application removed - See File Wrapper or Paim
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 375
LENGTH: 816
TYPE: PRT
ORGANISM: Homo sapiens
US-09-978-375A-375

Query Match 100.0% Score 816, DE 12, Length 816;
Best Local Similarity 100.0% Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MINSNVLTWLTALAKFETJCSOACYPVNTYNGKIRGRTPEIIGVPCYGVY 60
Qy 61 SPTGERRPOPEPESSWTGIRNTTQFAAVCPQJDERSLDHMLPIWFTANLDTLMTYV 120
Db 61 SPTGERRPOPEPESSWTGIRNTTQFAAVCPQJDERSLDHMLPIWFTANLDTLMTYV 120
Qy 121 QONNECLYLTNYPPEEDANTRKAAADCTISNDRGEDEIHQNSKKPVMVYIHGGSTWE 180
Db 121 QONNECLYLTNYPPEEDANTRKAAADCTISNDRGEDEIHQNSKKPVMVYIHGGSTWE 180
Qy 181 GTGNMIDGSIASGVAVYTTINVRGLIGFLSTGQAAKGVGLDQIQALRNIEENVG 240
Db 181 GTGNMIDGSIASGVAVYTTINVRGLIGFLSTGQAAKGVGLDQIQALRNIEENVG 240
Qy 241 AFGDPEKRVITFGSGAGACVSLLTLSHVSGLFQKATIQSGTALSNAVNYQPAKYTRI 300
Db 241 AFGDPEKRVITFGSGAGACVSLLTLSHVSGLFQKATIQSGTALSNAVNYQPAKYTRI 300

Qy 301 LADKVGCMMLDTTDVWECGRNKNYKELLIOQTTPATYHIAFGSVIDGVIPDDPQILMEQ 360
Db 301 LADKVGCMMLDTTDVWECGRNKNYKELLIOQTTPATYHIAFGSVIDGVIPDDPQILMEQ 360
Qy 361 GEFLLNDIMLGVNQSGGLKAFVDQIVNEDGVTPNDPDFSVSNVNDLXGYPSEKOTLRST 420
Db 361 GEFLLNDIMLGVNQSGGLKAFVDQIVNEDGVTPNDPDFSVSNVNDLXGYPSEKOTLRST 420
Qy 421 IKFMYTDMADKENPERRKTVALFTDQWAVAPVADJLAQYGSPTYPYAFYHGCSEK 480
Db 421 IKFMYTDMADKENPERRKTVALFTDQWAVAPVADJLAQYGSPTYPYAFYHGCSEK 480
Qy 481 KPSWADSAGDEVYVFGIPIMGPTLEFSCNFSKNDVMSAVVMYTWTFEAKTGDPNQPV 540
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RESULT 22

US-09-978-188A-375
Sequence 375, Application US/09978188A
Publication No. US20030139328A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar C.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James:
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C8

[illegible]

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? PRIOR APPLICATION NUMBER: 60/065339
? PRIOR FILING DATE: 1998-05-13
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? PRIOR FILING DATE: 1998-05-13
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? PRIOR FILING DATE: 1998-05-15
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? PRIOR APPLICATION NUMBER: 60/065697
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Query Match 100.0% Score 816; DB 12; Length 816;

Best Local Similarity 100.0%; Pred No. 0; Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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? 121 QONEDGCLYNIYVPEEDGATCKNADCTSDNREGEDRCHONSKRPVYIHGSGTYE 180
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? 301 LADKVCNMLDTTDEYECRLRNKYKELICQITTPATYHAFSPVTDGVIPOPPQILNEQ 360
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? 361 SEFLNDYKVGVOGSGGLKRVGVDNENGVPRNCDSEVSNFVNLGYPERKTLSET 420
? 361 SEFLNDYKVGVOGSGGLKRVGVDNENGVPRNCDSEVSNFVNLGYPERKTLSET 420
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? 421 IKEMYTEADKREPERRRTLVLEFCDHONVAPAVACDHAAYGSETVYAVYHHCSEN 480
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? 721 IAHONEEIMSLQKLEHDECESQAADTURLTCCPPDYTLTJRRSPDIPLXTPNTIT 780
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? 721 IAHONEEIMSLQKLEHDECESQAADTURLTCCPPDYTLTJRRSPDIPLXTPNTIT 780
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? 781 MIPNTLTGMQPLHTENTFSGGQNSTLPHGSHSTRV 816
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RESULT 23

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US-09-978-298A-375
? Sequence 375, Application US/09978298A
? Publication No. US20030134785A1
? GENERAL INFORMATION:
? APPLICANT: Ashkenazi, Avi
? APPLICANT: Baker Kevin P.
? APPLICANT: Botstein, David
? APPLICANT: Desnoyers, Luc
? APPLICANT: Eaton, Dan
? APPLICANT: Ferrara, Napoleon
? APPLICANT: Filvaroff, Ellen
? APPLICANT: Fong, Sherman
? APPLICANT: Gao, Wei-Qiang
? APPLICANT: Gerber, Hanspeter
? APPLICANT: Gertlisen, Mary E.
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Grimaldi, J. Christopher
? APPLICANT: Guiney, Austin B.
? APPLICANT: Hillan, Kenneth J.
? APPLICANT: Kijavich, Ivar J.
? APPLICANT: Kuo, Sophia S.
? APPLICANT: Napier, Mary A.
? APPLICANT: Pan, James
? APPLICANT: Paoni, Nicholas F.
? APPLICANT: Roy, Margaret Ann
? APPLICANT: Shelton, David B.
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tamas, Daniel
? APPLICANT: Williams, P. Mickey
? APPLICANT: Wood, William I.
? TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
? TITLE OF INVENTION: Acids Encoding the Same
? FILE REFERENCE: P2630PIC2
? CURRENT APPLICATION NUMBER: US/09/978,298A
? CURRENT FILING DATE: 2001-10-15
? PRIOR APPLICATION NUMBER: 09/918585
? PRIOR FILING DATE: 2001-07-30
? PRIOR APPLICATION NUMBER: 60/062250
? PRIOR FILING DATE: 1997-10-17
? PRIOR APPLICATION NUMBER: 60/064249
? PRIOR FILING DATE: 1997-11-03
? PRIOR APPLICATION NUMBER: 60/065311
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? PRIOR APPLICATION NUMBER: 60/066364
? PRIOR FILING DATE: 1997-11-21
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? PRIOR APPLICATION NUMBER: 60/077632
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? PRIOR FILING DATE: 1998-03-20
? PRIOR APPLICATION NUMBER: 60/078936
? PRIOR FILING DATE: 1998-03-20
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1 PRIOR APPLICATION NUMBER: 60/075910
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3 PRIOR APPLICATION NUMBER: 60/078939
4 PRIOR FILING DATE: 1998-03-20
5 PRIOR APPLICATION NUMBER: 60/079294
6 PRIOR FILING DATE: 1998-03-25
7 PRIOR APPLICATION NUMBER: 60/079656
8 PRIOR FILING DATE: 1998-03-26
9 PRIOR APPLICATION NUMBER: 60/079664
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14 PRIOR FILING DATE: 1998-03-27
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16 PRIOR FILING DATE: 1998-03-27
17 PRIOR APPLICATION NUMBER: 60/079786
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23 PRIOR APPLICATION NUMBER: 60/083105
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73 PRIOR APPLICATION NUMBER: 60/082757
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1 PRIOR FILING DATE: 1998-04-23
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3 PRIOR FILING DATE: 1998-04-27
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5 PRIOR FILING DATE: 1998-04-28
6 PRIOR APPLICATION NUMBER: 60/083392
7 PRIOR FILING DATE: 1998-04-29
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9 PRIOR FILING DATE: 1998-04-29
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11 PRIOR FILING DATE: 1998-04-29
12 PRIOR APPLICATION NUMBER: 60/083499
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17 PRIOR FILING DATE: 1998-04-29
18 PRIOR APPLICATION NUMBER: 60/083558
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42 PRIOR APPLICATION NUMBER: 60/084627
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66 PRIOR APPLICATION NUMBER: 60/085697

Query Watch 100.0%; Score 816; EB 12; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8.6; Conservative 0; Mismatches 0; indels 0; Gaps 0;

0Y 1 XANSVULMFLAKFTLISQCPYVNTNGKIRGRTPLPNEILGPVEQYLGYPYA 60
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Qy      61 SPTGERRFOPPEPPSSMTGIRNTTQFAAVCPQHLDBRSLLHMLPMTFANLDTLMTYV 120
Db      62 SPTGERRFOPPEPPSSMTGIRNTTQFAAVCPQHLDBRSLLHMLPMTFANLDTLMTYV 120
Qy      121 QDQNEDECLYNTIYVPTEDGANTKKNAADITSNDRGEDEDHDCNSKKPVMVYTHGGSYME 180
Db      121 QDQNEDECLYNTIYVPTEDGANTKKNAADITSNDRGEDEDHDCNSKKPVMVYTHGGSYME 180
Qy      161 GTGNMIDGSIILASVGNVIVITINRGLGFLSTGDDAAGNGLDQIALRWIEENVG 240
Db      181 GTGNMIDGSIILASVGNVIVITINRGLGFLSTGDDAAGNGLDQIALRWIEENVG 240
Qy      241 AFGDPRKVTIFSGGAGASCVSLLTSHYSEGLFOKALIOSGTLSSMAVNYCPAKYTRI 300
Db      241 AFGDPRKVTIFSGGAGASCVSLLTSHYSEGLFOKALIOSGTLSSMAVNYCPAKYTRI 300
Qy      301 LADYVGCMALDTTDMVECLRNKYNKELICQTTIPATYHIAFGVIDGVIPDDPQILMEQ 360
Db      301 LADYVGCMALDTTDMVECLRNKYNKELICQTTIPATYHIAFGVIDGVIPDDPQILMEQ 360
Qy      361 GEFPLNDYLVGAVQGBELKFPDGIIVNEDGVTECNCFVSNSVNDMLYGPESKTLRET 420
Db      361 GEFPLNDYLVGAVQGBELKFPDGIIVNEDGVTECNCFVSNSVNDMLYGPESKTLRET 420
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Db      421 IKFMYTDMADKENPETRKTLLVALFTDHCQVAVAAVADLAHQYGSPTFYAFYHQCSEM 480
Qy      481 KPSMADSAHGDDEVYVFGIMIGTFELFSCNFSKNDVMISAVMTYVTFATKGDENOVY 540
Db      481 KPSMADSAHGDDEVYVFGIMIGTFELFSCNFSKNDVMISAVMTYVTFATKGDENOVY 540
Qy      541 PPTKFIHTKPNFEEVYASKNPKDOLYHIGLKRPRDHYATVAFELLEVPHLETL 600
Db      541 PPTKFIHTKPNFEEVYASKNPKDOLYHIGLKRPRDHYATVAFELLEVPHLETL 600
Qy      601 NEIFQYVSTTKYPPPDWTSFPYGTRRSPAKIMPTTKPPIIFANNEFKSKKEFKTGSPD 660
Db      601 NEIFQYVSTTKYPPPDWTSFPYGTRRSPAKIMPTTKPPIIFANNEFKSKKEFKTGSPD 660
Qy      661 TTVLIEFKRQYSTELASTYVAGSLFLNLAFNAYKKCKXRRRSHRRPSQCRNTMD 720
Db      661 TTVLIEFKRQYSTELASTYVAGSLFLNLAFNAYKKCKXRRRSHRRPSQCRNTMD 720
Qy      721 IAHIONEELMSLQKLEHDECESLQAMDTLRLTGPEDYTJTLRSPDIPXTPNIT 780
Db      721 IAHIONEELMSLQKLEHDECESLQAMDTLRLTGPEDYTJTLRSPDIPXTPNIT 780
Qy      781 MIPVLTGQPLHTNTFSGGONSTNLPHGSHSTRY 816
Db      781 MIPVLTGQPLHTNTFSGGONSTNLPHGSHSTRY 816

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RESULT 24
US-10-143-375
Sequence 375, Application US-10-143031A
Publication No. US20030138439A1
GENERAL INFORMATION:

APPLICANT: Askerazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Betstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geisler, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.

```

APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavira, Ivar C.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P26301C39
CURRENT APPLICATION NUMBER: US/10/143,031A
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
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PRIOR APPLICATION NUMBER: 60/077450
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PRIOR APPLICATION NUMBER: 60/077632
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PRIOR APPLICATION NUMBER: 60/077649
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PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 375
LENGTH: 816
TYPE: PRT
ORIGIN: Homo sapiens
US-10-143-375
Query Match :00.0% Score 816; DB 12; Length 816;
Best Local Similarity :00.0% Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 331 LADKVCNMLTDTTDMVECLRNKNYKELIQITTPATYHIAFGV.DGDVA.PDDPQI.MEG 360
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Db 361 GEPLNYD.MLGVNGGEGJ.KFVDSIVENEDGCTPNDPFPSSNFNDNIXSPRGDLRER 420
Prior Filing Date: 1997-11-03
Prior Application Number: 60/065311
Qy 421 IKFMYTMAADKENPETRRKTLVALFTCHQWAPAVAADLHNOVSPTYFAFYHHCSEM 480
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Qy 481 KPSVADSAGSDEVPVFGIPMIGSTELFSNFSNDVMSAVONTWYTNFAKTQDPQPV 540
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Prior Application Number: 60/07649
Qy 541 PODTFHITKPNRFEVAVMSKYNPNPCOYLHIGLKPVRDGRATKVAFWELVYRHL 600
Prior Filing Date: 1998-03-11
Prior Application Number: 60/07791
Db 541 PODTFHITKPNRFEVAVMSKYNPNPCOYLHIGLKPVRDGRATKVAFWELVYRHL 600
Prior Filing Date: 1998-03-12
Prior Application Number: 60/07804
Qy 601 NEIFQVYSTTKVPDPNTSFPYGTIRSGPANIMTTRKPA.TTPANNRQSKDPKKTSED 660
Prior Filing Date: 1998-03-12
Prior Application Number: 60/078910
Db 601 NEIFQVYSTTKVPDPNTSFPYGTIRSGPANIMTTRKPA.TTPANNRQSKDPKKTSED 660
Prior Filing Date: 1998-03-20
Prior Application Number: 60/078936
Qy 661 TTVLETRKRVSTELSTYTAGASJLEMLAFAALYKKDKRHEHREESPQRNTNF 720
Prior Filing Date: 1998-03-20
Prior Application Number: 60/079294
Db 661 TTVLETRKRVSTELSTYTAGASJLEMLAFAALYKKDKRHEHREESPQRNTNF 720
Prior Filing Date: 1998-03-25
Prior Application Number: 60/07956
Qy 721 IAH:ONEEIVSLQWQCEHDECESLQAHDTLRLTCPPDYTLTLRRSPDIPLXTPTT 780
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Prior Application Number: 60/079664
Db 721 IAH:ONEEIVSLQWQCEHDECESLQAHDTLRLTCPPDYTLTLRRSPDIPLXTPTT 780
Prior Filing Date: 1998-03-27
Prior Application Number: 60/079699
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Prior Application Number: 60/079663
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Prior Application Number: 60/081203
Prior Filing Date: 1998-04-09

RESULT 25
US-10-002-967A-375
Sequence 375, Application US/10002967A
Publication No. US20030148373A1
GENERAL INFORMATION:
Applicant: Ashkenazi, Avi
Applicant: Baker Kevin P.
Applicant: Botstein, David
Applicant: Desnovers, Luc
Applicant: Eaton, Dan
Applicant: Ferrara, Napoleone
Applicant: Filvaroff, Ellen
Applicant: Fong, Sherman
Applicant: Gao, Wei-Qiang
Applicant: Geider, Hanspeter
Applicant: Gerltzen, Mary E.
Applicant: Goddard, Audrey
Applicant: Godowski, Paul J.
Applicant: Grimaldi, J. Christopher
Applicant: Gueney, Austin L.
Applicant: Hillan, Kenneth J.
Applicant: Kiliafin, Ivar J.
Applicant: Kuo, Sophia S.
Applicant: Napier, Mary A.
Applicant: Pan, James
Applicant: Pechl, Nicholas F.
Applicant: Roy, Margaret Ann
Applicant: Stetson, David L.
Applicant: Stewart, Timothy A.
Applicant: Tumas, Daniel
Applicant: Williams, P. Mickey
Applicant: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Peptides and Nucleic
FILE REFERENCE: P2630P.C72
CURRENT APPLICATION NUMBER: US/10-002,967A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585

PRIOR APPLICATION NUMBER: 60/081229
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PRIOR APPLICATION NUMBER: 60/081955
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PRIOR APPLICATION NUMBER: 60/085573
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 816; DB 12; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MUNSVMMLTALAKETLDSOAOVRYNTNNGKIRGRTPLPNETIGVEQYLGVPYA 60
1 MUNSVMMLTALAKETLDSOAOVRYNTNNGKIRGRTPLPNETIGVEQYLGVPYA 60
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61 SPPTGERFQPEPPSSMTGIRNTTQPAACPOHLDERSLHMLPIWFTANDLTMTYV 120
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121 QDNEDCLYNTVFTEDGANTKMAADITSNDGEDEDIDONSKKPVMTYHGSSYME 180
121 QDNEDCLYNTVFTEDGANTKMAADITSNDGEDEDIDONSKKPVMTYHGSSYME 180
181 GTGMIDGSLASGNVYITINYPRLIGFLSTGQAAKANYGLDIOIQAARKIEENVG 240
181 GTGMIDGSLASGNVYITINYPRLIGFLSTGQAAKANYGLDIOIQAARKIEENVG 240
181 GTGMIDGSLASGNVYITINYPRLIGFLSTGQAAKANYGLDIOIQAARKIEENVG 240
241 AFGSDPKRVITFGSGAGASCVSJLTLSHYSEGLFQKAIIOGSTALLSSMAVYQPAKYTRI 300
241 AFGSDPKRVITFGSGAGASCVSJLTLSHYSEGLFQKAIIOGSTALLSSMAVYQPAKYTRI 300
301 LADVGGCMMLDITDMECELRKNYKELIOCTIIPATYHRAFGVIGDVIIPDPQILMEQ 360
301 LADVGGCMMLDITDMECELRKNYKELIOCTIIPATYHRAFGVIGDVIIPDPQILMEQ 360
361 GEFNYVDIMGVNQGSEGLKFPVDGIVNEDGVTEPNDPFSVSNFVDNXYGYPSEKTLRAT 420
361 GEFNYVDIMGVNQGSEGLKFPVDGIVNEDGVTEPNDPFSVSNFVDNXYGYPSEKTLRAT 420
421 IKENYTTMACXENPETRRKTUVALFTDHQWVAAYAAJLHAQVGSFTTYRYAFYHRCQSEM 480
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481 KPSWADSAHGCZVPYVVGFPYIGPTELSGNEFKNOVMJSAVYTYWNTPAKCGDNOQY 540
541 PCDTKEFHTRPNREEVAMSKYNPKQULYHIGLKPVRDHYATYVAFWELVPHLNL 600
541 PCDTKEFHTRPNREEVAMSKYNPKQULYHIGLKPVRDHYATYVAFWELVPHLNL 600
601 NEIFOVSTTKVPPPMTSFPYGTGRSPAKIPTTRKPAITANPNKSKDPKXGKPEP 660
601 NEIFOVSTTKVPPPMTSFPYGTGRSPAKIPTTRKPAITANPNKSKDPKXGKPEP 660
661 TTVLETRKDYSTELSTIYVAGASLFLNLLAFYAAALYKXKRRHETHRSPQRTYND 720
661 TTVLETRKDYSTELSTIYVAGASLFLNLLAFYAAALYKXKRRHETHRSPQRTYND 720
721 IAHIONEISLQKOLEHDECESIQADHTLRLCPDPYTLTLRSPDDIPLMTNTYIT 780
721 IAHIONEISLQKOLEHDECESIQADHTLRLCPDPYTLTLRSPDDIPLMTNTYIT 780

Dd 721 IAH1QNEIWSLQWKQLEHCEESLQADHTLRCPDYTLTLRRSPDDIP-MTENTIT 780
Cy 781 MIPTLTGKQPLHTFNTFSGGQSNLPHGHSTTRV 816
Db 781 MIPTLTGKQPLHTFNTFSGGQSNLPHGHSTTRV 816

RESULT 26
US-10-017-083A-375
Sequence 375 Application US/1017083A
Publication No. US2003014876A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bostein, David
APPLICANT: Desroyers, Luc
APPLICANT: Eaton, Dar
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey E.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuc, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pat, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P167
CURRENT APPLICATION NUMBER: US/10/017.083A
CURRENT FILING DATE: 2001-10-24
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 375
LENGTH: 816
TYPE: PRT
ORGANISM: Homo sapiens
US-10-017-083A-375

Query Match 100.0% Score 816, DB 12, Length 816,
Best Local Similarity 100.0% Pred. No. 0,
Matches 816, Conservative 0, Mismatches 0, Indels 0, Gaps 0,
Cy 1 MUNSVMMLTALAKETLISQAOYPVNTNYSKIRGTEPLPNEILSGVEGYLPPYA 60
Db 1 MUNSVMMLTALAKETLISQAOYPVNTNYSKIRGTEPLPNEILSGVEGYLPPYA 60
Cy 61 SPTTGERRFPQEPPESSWTGIRNTTQFAAVCPCHLDERSLHDXLPTMTFANLDTMTYV 120
Db 61 SPTTGERRFPQEPPESSWTGIRNTTQFAAVCPCHLDERSLHDXLPTMTFANLDTMTYV 120
Cy 121 GQNEECLYMNIYVTEGANTKKAADITSDNGCEBD-HDQSKKPKVNYHGGSYVE 180
Db 121 GQNEECLYMNIYVTEGANTKKAADITSDNGCEBD-HDQSKKPKVNYHGGSYVE 180
Cy 181 GTGNVIGDSILASYGNVYVITINRILGLIGFLSTGDAKQNGGLDQIDALAEIENWG 240
Db 181 GTGNVIGDSILASYGNVYVITINRILGLIGFLSTGDAKQNGGLDQIDALAEIENWG 240
Cy 241 AFGGPKRVTIFSGAGASCVSLLTSHYSEGLCKA-IGSGTALSSKAVNYOPAKYTRI 300

Dd 241 AFGGPKRVTIFSGAGASCVSLLTSHYSEGLCKA-IGSGTALSSKAVNYOPAKYTRI 300
Cy 301 LADRVGNNMLDITDMVECLRNKRYKELIQOTITPATYHIAFGVVIDGVIPDDPQILMEQ 360
Db 301 LADRVGNNMLDITDMVECLRNKRYKELIQOTITPATYHIAFGVVIDGVIPDDPQILMEQ 360
Cy 361 GEPINLYDIMGVNGSEGLKFDVGIJUNNEGVTPNDPDFSVNSVNDLYGYPBEKDTLRET 420
Db 361 GEPINLYDIMGVNGSEGLKFDVGIJUNNEGVTPNDPDFSVNSVNDLYGYPBEKDTLRET 420
Cy 421 IKFWYTMADKNEPCTRRKTLVALFTDHCWAPAVADLHAQYGSPTYFYAFYHHCQSEY 480
Db 421 IKFWYTMADKNEPCTRRKTLVALFTDHCWAPAVADLHAQYGSPTYFYAFYHHCQSEY 480
Cy 481 KPSMADSHAGDEVYVYVIGIMIGTFLPSCNFEKNDVMASAVMTWTWTFAKGDENQVY 540
Db 481 KPSMADSHAGDEVYVYVIGIMIGTFLPSCNFEKNDVMASAVMTWTWTFAKGDENQVY 540
Cy 541 PQDTKFIHTKPNRFEVYVAMSKYKPKDLYHIGLKPRVRZHYRATYVAFVCELVPLHLND 600
Db 541 PQDTKFIHTKPNRFEVYVAMSKYKPKDLYHIGLKPRVRZHYRATYVAFVCELVPLHLND 600
Cy 601 NEIFQVSTTTKVPDPYTSPPYGTSSPAKIWPITKRPAITPANPKASKDPTKGPED 660
Db 601 NEIFQVSTTTKVPDPYTSPPYGTSSPAKIWPITKRPAITPANPKASKDPTKGPED 660
Cy 661 TTVALETRKDYSTLSTIIVAGASCLFLNITLAFMAIYKKDKRRHETRRSPQRCTTND 720
Db 661 TTVALETRKDYSTLSTIIVAGASCLFLNITLAFMAIYKKDKRRHETRRSPQRCTTND 720
Cy 721 IAH1QNEIWSLQWKQLEHCEESLQADHTLRCPDYTLTLRRSPDDIP-MTENTIT 780
Db 721 IAH1QNEIWSLQWKQLEHCEESLQADHTLRCPDYTLTLRRSPDDIP-MTENTIT 780
Cy 781 MIPTLTGKQPLHTFNTFSGGQSNLPHGHSTTRV 816
Db 781 MIPTLTGKQPLHTFNTFSGGQSNLPHGHSTTRV 816

RESULT 27
US-10-143-030A-375
Sequence 375 Application US/10143030A
Publication No. US20030147901A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bostein, David
APPLICANT: Desroyers, Luc
APPLICANT: Eaton, Dar
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey E.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuc, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pat, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C33
CURRENT APPLICATION NUMBER: US/10/143,010A
CURRENT FILING DATE: 2002-08-27
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/06364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 375
LENGTH: 816
TYPE: PRT
ORGANISM: Homo sapiens
US-10-143-030A-375
Query Match 100.0%; Score 816; DS 12; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 MUNSVMJWCTALAIKFTLDSQAOYVNTVNGKIRGKRTPLNELLGVEYGVPA 60
DB 1 MUNSVMJWCTALAIKFTLDSQAOYVNTVNGKIRGKRTPLNELLGVEYGVPA 60
CY 61 SPTGERRFQPPPEPSSWTGIRNTTQFAVCPQJLERSLJHMDLZAFYANLDTXVY 120
DB 61 SPTGERRFQPPPEPSSWTGIRNTTQFAVCPQJLERSLJHMDLZAFYANLDTXVY 120
CY 121 QDQRECCLYNIYVPEDEGAKTKKMDLISNDRGCEEDHONSKKPKVYVTHGSSYE 180
DB 121 QDQRECCLYNIYVPEDEGAKTKKMDLISNDRGCEEDHONSKKPKVYVTHGSSYE 180
CY 181 GTNKLIGSILASVGNVYVITINVRLOLIGLSTGDAQAKNGYGLDDQALRWLEENVG 240
DB 181 GTNKLIGSILASVGNVYVITINVRLOLIGLSTGDAQAKNGYGLDDQALRWLEENVG 240
CY 241 AFGGDPKRVITFSGGAGACVSLITLHYSEGLFCFALIIQSGILSSWAVYQFAKTYMI 300
DB 241 AFGGDPKRVITFSGGAGACVSLITLHYSEGLFCFALIIQSGILSSWAVYQFAKTYMI 300
CY 301 LADVGCNMJDTDMVECLRNKYKELIQITTPATYHAFGVLDGVDIPRPPQIMEQ 360
DB 301 LADVGCNMJDTDMVECLRNKYKELIQITTPATYHAFGVLDGVDIPRPPQIMEQ 360
CY 361 GEFANVIMLGVNCGELKFCVGIIVNEEDCVTPNDPDSVSNVDMLVGVPEKQTLRET 420
DB 361 GEFANVIMLGVNCGELKFCVGIIVNEEDCVTPNDPDSVSNVDMLVGVPEKQTLRET 420
CY 421 IKPNVTEMADEXNEPTEPKTLVALFTDHCVAFAVAADLAQVGSPTVYAFHHQOSM 480
DB 421 IKPNVTEMADEXNEPTEPKTLVALFTDHCVAFAVAADLAQVGSPTVYAFHHQOSM 480
CY 481 KPSWASAHGDEVYVFGIPMIGTELLFSCNFSKRDVYMSAVMTMTWTFATGDENGPV 540
DB 481 KPSWASAHGDEVYVFGIPMIGTELLFSCNFSKRDVYMSAVMTMTWTFATGDENGPV 540
CY 541 PQTKEFHTKPNFEEVAVMSKNPKOOLYHIGLKRVRVDRHATKVAALVELVPHLNL 600
DB 541 PQTKEFHTKPNFEEVAVMSKNPKOOLYHIGLKRVRVDRHATKVAALVELVPHLNL 600

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C46
CURRENT APPLICATION NUMBER: US/10/145,128A
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/06364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
RESULT 28
US-10-145-128A-375
Sequence 375, Application US/10145128A
Publication No. US2003015761S1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deeneyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsens, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gutrey, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James J.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Snelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLES OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C46
CURRENT APPLICATION NUMBER: US/10/145,128A
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/06364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
DB 541 PQTKEFHTKPNFEEVAVMSKNPKOOLYHIGLKRVRVDRHATKVAALVELVPHLNL 600
CY 601 NEIFQVSTTKVPPDMTSPYGTSSPAKIMPTKRAIIPANNPKSKDPPKTPED 660
DB 601 NEIFQVSTTKVPPDMTSPYGTSSPAKIMPTKRAIIPANNPKSKDPPKTPED 660
CY 661 TTVLIERKDYSTELSVTAWASLLEFNILAFALYKDKRHEHRRPSPORTTND 720
DB 661 TTVLIERKDYSTELSVTAWASLLEFNILAFALYKDKRHEHRRPSPORTTND 720
CY 721 IAHQNEIWSLQKQLEHDECEISQADHILRLTPEPYTTLRSSPDILUMPTNTT 780
DB 721 IAHQNEIWSLQKQLEHDECEISQADHILRLTPEPYTTLRSSPDILUMPTNTT 780
CY 781 MIRPILTMQPLHTFNTFSGQNSTLPHSHSTRV 816
DB 781 MIRPILTMQPLHTFNTFSGQNSTLPHSHSTRV 816

PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 375
LENGTH: 816
TYPE: PRT
ORGANISM: Homo sapiens
US-13-145-228A-375

Query Match 100.0%; Score 816; DE 12; Length 816;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNSVVLNLTNLAIKFLIDSOQYPRVNTNKGKIGLATTENELGVEEYLNPYA 60
DB 1 MNSVVLNLTNLAIKFLIDSOQYPRVNTNKGKIGLATTENELGVEEYLNPYA 60
QY 61 SPTGERRFPPEPSSWTGIRNTTOFANVCPQHLDEBSLHPMLPIWFTANDTMTYV 120
DB 61 SPTGERRFPPEPSSWTGIRNTTOFANVCPQHLDEBSLHPMLPIWFTANDTMTYV 120
QY 121 QDQNEDCYKLVITYTEEGANTKKACDITSNQGEDETHDQSKKRWVYHSGSYME 180
DB 121 QDQNEDCYKLVITYTEEGANTKKACDITSNQGEDETHDQSKKRWVYHSGSYME 180
QY 181 GTXNYIGSILASQNVYVITINRGLGLGELSTQDAKNGYGLDQIALKEENYK 240
DB 181 GTXNYIGSILASQNVYVITINRGLGLGELSTQDAKNGYGLDQIALKEENYK 240
QY 241 AFGGPKKVVITFGSGAGASCVSLTLSHYSEGFCQKAISSGIALSSWAVNCPAKYTRI 300
DB 241 AFGGPKKVVITFGSGAGASCVSLTLSHYSEGFCQKAISSGIALSSWAVNCPAKYTRI 300
QY 301 LADKVGCMILDTTEMECTRNKQYKELIQOTIPATYHAFGPIVDCVFPDDPOLMEQ 360
DB 301 LADKVGCMILDTTEMECTRNKQYKELIQOTIPATYHAFGPIVDCVFPDDPOLMEQ 360
QY 361 GEFLLYDMLGNQCEGKIFVDGIIVDNEDGVTPLNDFPFSVNFEDNLYGYPECKDLRET 420
DB 361 GEFLLYDMLGNQCEGKIFVDGIIVDNEDGVTPLNDFPFSVNFEDNLYGYPECKDLRET 420
QY 421 IKFVYTDMADEKNEPTEKKTVALFTDHQWAPVADLHAQGSFYFAFHHGQSEM 480
DB 421 IKFVYTDMADEKNEPTEKKTVALFTDHQWAPVADLHAQGSFYFAFHHGQSEM 480
QY 481 KPSWADSAHGDVPPVFGIPMIGPTEJSCNFSKNDVYMLSAVVTYWTNFAKGDPRQPV 540
DB 481 KPSWADSAHGDVPPVFGIPMIGPTEJSCNFSKNDVYMLSAVVTYWTNFAKGDPRQPV 540
QY 541 PODTFFITKRRFEFVWMSKYNPRDQYLHIGKPRVCHYRATKAPFLDLVPHLNU 600
DB 541 PODTFFITKRRFEFVWMSKYNPRDQYLHIGKPRVCHYRATKAPFLDLVPHLNU 600
QY 601 NEIFQVASTTKVPPPEXTSPYGTRRSPAKIMETTRPAITPANNPKSHKDKGPEP 660
DB 601 NEIFQVASTTKVPPPEXTSPYGTRRSPAKIMETTRPAITPANNPKSHKDKGPEP 660
QY 661 TVLLETKADYSTELSVTAVGASLFLNIAFAALVYKKDKRRHHRSPQRNTTND 720
DB 661 TVLLETKADYSTELSVTAVGASLFLNIAFAALVYKKDKRRHHRSPQRNTTND 720
QY 721 IAHICNEISLQMKQLEHDECESLQMDTLRLTCEPDDTILTRSPDDIPMTPTTT 780
DB 721 IAHICNEISLQMKQLEHDECESLQMDTLRLTCEPDDTILTRSPDDIPMTPTTT 780
QY 781 MIPNLTGMOPLHFNNTSSGQNSNLPRCHSTRTV 816
DB 781 MIPNLTGMOPLHFNNTSSGQNSNLPRCHSTRTV 816

RESULT 29
US-10-017-191A-375
Sequence 375, Application US/10017191A
Publication No. US20030170254A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gueney, Austin L.
APPLICANT: Hillan, Kenneth C.
APPLICANT: Kljavan, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pat, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P162
CURRENT APPLICATION NUMBER: US/10/017,191A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/079669
 PRIOR FILING DATE: 1998-03-27
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 PRIOR FILING DATE: 1998-03-27
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 PRIOR FILING DATE: 1998-03-27
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 PRIOR FILING DATE: 1998-03-30
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 PRIOR APPLICATION NUMBER: 60/080165
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080194
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080327
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080328
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 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
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 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083495
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PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083499
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083545
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083554
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083558
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083559
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083500
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083742
 PRIOR FILING DATE: 1998-04-30
 PRIOR APPLICATION NUMBER: 60/084366
 PRIOR FILING DATE: 1998-05-05
 PRIOR APPLICATION NUMBER: 60/084414
 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/084441
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 PRIOR APPLICATION NUMBER: 60/084637
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 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084640
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 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
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 PRIOR APPLICATION NUMBER: 60/084643
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/085339
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 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085323
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 PRIOR APPLICATION NUMBER: 60/085582
 PRIOR FILING DATE: 1998-05-15
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 PRIOR APPLICATION NUMBER: 60/085579
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 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match: 100.0%; Score 816; DB 12; Length 816;
 Best Local Similarity: 100.0%; Pred. No. 0;
 Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSNVJLMLTALIKFTLDSQOQYVNVNTNYGKIRGLTLPJNEILGPVEOYLGPYA 60
 DB 1 MNSNVJLMLTALIKFTLDSQOQYVNVNTNYGKIRGLTLPJNEILGPVEOYLGPYA 60
 QY 61 SPTGERFOPPEPPSSWTG:RNTQFAAVCPQHLDERSLHDYLPWFTANLDTMTYV 120
 DB 61 SPTGERFOPPEPPSSWTG:RNTQFAAVCPQHLDERSLHDYLPWFTANLDTMTYV 120
 QY 121 ODQWEDCXLNYIVPTREGANTKCAADISNDGSDGEDIHDQSKKXWVYIHGSSYME 180
 DB 121 ODQWEDCXLNYIVPTREGANTKCAADISNDGSDGEDIHDQSKKXWVYIHGSSYME 180

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QY 181 GTGMMIDGSIILASGNGVIVITINRGLGLSLSTGDDAAGKNGVLLDQIQALRMIEENVG 240
DB 181 GTGMMIDGSIILASGNGVIVITINRGLGLSLSTGDDAAGKNGVLLDQIQALRMIEENVG 240
QY 241 AFGGDPKRVITIFGSGAGASCVSLLTSHYSGLFOKAIIOGGLSSMANVQPAKTR 300
DB 241 AFGGDPKRVITIFGSGAGASCVSLLTSHYSGLFOKAIIOGGLSSMANVQPAKTR 300
QY 301 LADKVGCMNLDITDMVECLRNKNYKELIQOTITPATYHIAFGPVIDGVIIPDDPQIMXEQ 360
DB 301 LADKVGCMNLDITDMVECLRNKNYKELIQOTITPATYHIAFGPVIDGVIIPDDPQIMXEQ 360
QY 361 GEFUNYDMLGNGOEGSKFVDSGVNNEGVTNDFPVSNSPFYCNLYSPKSCOTRET 420
DB 361 GEFUNYDMLGNGOEGSKFVDSGVNNEGVTNDFPVSNSPFYCNLYSPKSCOTRET 420
QY 421 IKFVYTDWADKENETRRKTLVALFTDQWAPAVAAJLHAQYGSPTFYAFYHHCOSEM 480
DB 421 IKFVYTDWADKENETRRKTLVALFTDQWAPAVAAJLHAQYGSPTFYAFYHHCOSEM 480
QY 481 KPSWADSAHGDEVPYVFGIEMIGPTELFSCNFSKXDVYLSVWTVYTNFAKTODEVQPV 540
DB 481 KPSWADSAHGDEVPYVFGIEMIGPTELFSCNFSKXDVYLSVWTVYTNFAKTODEVQPV 540
QY 541 PDKTFITKXENREPEVAMSKYNPKCOYLHIGSKPRVDPKPTKXAFPLEYVPHLHNI 600
DB 541 PDKTFITKXENREPEVAMSKYNPKCOYLHIGSKPRVDPKPTKXAFPLEYVPHLHNI 600
QY 601 NEIFQVSTTKRVPDPVTSFPGYRASPANIPWTTKSPA-TTPANPQSKDPRKGTGPEP 660
DB 601 NEIFQVSTTKRVPDPVTSFPGYRASPANIPWTTKSPA-TTPANPQSKDPRKGTGPEP 660
QY 661 TTVLIEKRDYSTEISVLIANGASJLFENILAFALYKKDKRHEHTRRSPQGRNTTND 720
DB 661 TTVLIEKRDYSTEISVLIANGASJLFENILAFALYKKDKRHEHTRRSPQGRNTTND 720
QY 721 IAHIONEIYSLOMKOLEHRECECSLOHDTLRLTCPPDYLLLRASDDPLXTANKTIT 780
DB 721 IAHIONEIYSLOMKOLEHRECECSLOHDTLRLTCPPDYLLLRASDDPLXTANKTIT 780
QY 781 MIPNTLTGMQPLHFNTEFGGQNSTNLPHGHSTTRV 816
DB 781 MIPNTLTGMQPLHFNTEFGGQNSTNLPHGHSTTRV 816

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RESULT 30

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US-10-143-028A-375
/ Sequence 375, Application US/10143028A
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Boistein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Geisler, Hanspeter
/ APPLICANT: Geritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin J.
/ APPLICANT: Hillan, Kenneth C.
/ APPLICANT: Kijavits, Ivar J.
/ APPLICANT: Kuc, Sophia S.
/ APPLICANT: Kuper, Mary A.
/ APPLICANT: Pan, James.
/ APPLICANT: Paothi, Nicholas P.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.

```

```

/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2630P1C37
/ CURRENT APPLICATION NUMBER: US/10143-028A
/ PRIOR FILING DATE: 2001-10-19
/ PRIOR APPLICATION NUMBER: 09/918585
/ PRIOR FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: 60/066255
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/064249
/ PRIOR FILING DATE: 1997-11-03
/ PRIOR APPLICATION NUMBER: 60/065311
/ PRIOR FILING DATE: 1997-11-13
/ PRIOR APPLICATION NUMBER: 60/066364
/ PRIOR FILING DATE: 1997-11-27
/ PRIOR APPLICATION NUMBER: 60/077450
/ PRIOR FILING DATE: 1998-03-10
/ PRIOR APPLICATION NUMBER: 62/077632
/ PRIOR FILING DATE: 1998-03-11
/ PRIOR APPLICATION NUMBER: 62/077642
/ PRIOR FILING DATE: 1998-03-11
/ PRIOR APPLICATION NUMBER: 62/077649
/ PRIOR FILING DATE: 1998-03-11
/ PRIOR APPLICATION NUMBER: 60/377791
/ PRIOR FILING DATE: 1998-03-12
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 624
/ SEQ ID NO: 375
/ LENGTH: 816
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-143-028A-375

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Query Match 100.0%; Score 816; DB 12; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MNSNVLLMTALAIKFTLLIDSDQAYPVVNTNYGKIRGLRTPAPENILGVEQYLGVPVA 60
DB 1 MNSNVLLMTALAIKFTLLIDSDQAYPVVNTNYGKIRGLRTPAPENILGVEQYLGVPVA 60
QY 61 SPTGERRFPQPEPPSSWTGIRNTTQPAAVCPQHLDBRSJLHDLPTMFTANLDTMTYV 120
DB 61 SPTGERRFPQPEPPSSWTGIRNTTQPAAVCPQHLDBRSJLHDLPTMFTANLDTMTYV 120
QY 121 QDQNEEDCLYINIVYPTEDGANTKXNADDTISNDRGEDEDIHDQSKKPVWVYIHGGSYME 180
DB 121 QDQNEEDCLYINIVYPTEDGANTKXNADDTISNDRGEDEDIHDQSKKPVWVYIHGGSYME 180
QY 181 GTGMMIDGSIILASGNGVIVITINRGLGLSLSTGDDAAGKNGVLLDQIQALRMIEENVG 240
DB 181 GTGMMIDGSIILASGNGVIVITINRGLGLSLSTGDDAAGKNGVLLDQIQALRMIEENVG 240
QY 241 AFGGDPKRVITIFGSGAGASCVSLLTSHYSGLFOKAIIOGGLSSMANVQPAKTR 300
DB 241 AFGGDPKRVITIFGSGAGASCVSLLTSHYSGLFOKAIIOGGLSSMANVQPAKTR 300
QY 301 LADKVGCMNLDITDMVECLRNKNYKELIQOTITPATYHIAFGPVIDGVIIPDDPQIMXEQ 360
DB 301 LADKVGCMNLDITDMVECLRNKNYKELIQOTITPATYHIAFGPVIDGVIIPDDPQIMXEQ 360
QY 361 GEFUNYDMLGNGOEGSKFVDSGVNNEGVTNDFPVSNSPFYCNLYSPKSCOTRET 420
DB 361 GEFUNYDMLGNGOEGSKFVDSGVNNEGVTNDFPVSNSPFYCNLYSPKSCOTRET 420
QY 421 IKFVYTDWADKENETRRKTLVALFTDQWAPAVAAJLHAQYGSPTFYAFYHHCOSEM 480
DB 421 IKFVYTDWADKENETRRKTLVALFTDQWAPAVAAJLHAQYGSPTFYAFYHHCOSEM 480

```

CY 481 KPSWASAHGDEVPYVVGIGPTELFSCRFKSKNDYKLSAVVYTWLNFANCGDNCPV 540
DB 481 KPSWASAHGDEVPYVVGIGPTELFSCRFKSKNDYKLSAVVYTWLNFANCGDNCPV 540
CY 541 PCDTKFHTKPNRFEENAKSKYKPKDLYHIGIKRVRNHVATVAAWLELVPLHNL 600
DB 541 PCDTKFHTKPNRFEENAKSKYKPKDLYHIGIKRVRNHVATVAAWLELVPLHNL 600
CY 601 NEIFQVSTTKVPPDPTSPFYCTRSPAKIMPTTRPAITFANNPKSKDHRKGPDD 660
DB 601 NEIFQVSTTKVPPDPTSPFYCTRSPAKIMPTTRPAITFANNPKSKDHRKGPDD 660
CY 661 TTULITKRDVSTLSTLAVGASLFLNLILAPALYKCKGRHETRRPSPQRTTND 720
DB 661 TTULITKRDVSTLSTLAVGASLFLNLILAPALYKCKGRHETRRPSPQRTTND 720
CY 721 IAHQNEEISLCKQKEHCECELOAHDTLTLCPDPTLTLRSPDDPLMPTNTIT 780
DB 721 IAHQNEEISLCKQKEHCECELOAHDTLTLCPDPTLTLRSPDDPLMPTNTIT 780
CY 781 MIPNTLTGMOPLMTFNTFSGQNSYMLFCHSTTRV 816
DB 781 MIPNTLTGMOPLMTFNTFSGQNSYMLFCHSTTRV 816

RESULT 31
US-10-143-029A-375
Sequence 375, Application US/10143029A
Publication No. US20030180311A1
GENERAL INFORMATION:
APPLICANT: Asakemazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botschein, David
APPLICANT: Deecoyers, Luc
APPLICANT: Ealon, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul C.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hilan, Kenneth J.
APPLICANT: Kilavan, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Par, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Ray, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Acids Encoding and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 22630PIC4
CURRENT FILING DATE: US/10/143,029A
PRIOR APPLICATION NUMBER: 2001-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
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PRIOR APPLICATION NUMBER: 60/077450

PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
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PRIOR APPLICATION NUMBER: 60/084640
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PRIOR APPLICATION NUMBER: 60/084598
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PRIOR FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579

PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 816; DB 12; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MNSNYLMTALATATLFTLLDSOAPVPMYNGKIRGRTLPMEHLCGPVQYGVYA 63
|||||
1 XLNSKVLMLTALATLFTLLDSOAPVPMYNGKIRGRTLPMEHLCGPVQYGVYA 60
61 SPTGERRFQPEPSSWTGIRNTTQFAVCEQHLDERSLHDMPLMFTALDTMTYV 120
61 SPTGERRFQPEPSSWTGIRNTTQFAVCEQHLDERSLHDMPLMFTALDTMTYV 120
121 QDNEDCLYNIYVPREDGANTKMDTDSNDGDEFCHONSKRPMTYIHGQSYNE 180
|||||
121 QDNEDCLYNIYVPREDGANTKMDTDSNDGDEFCHONSKRPMTYIHGQSYNE 180
181 GTGNMIDGSLASGVNVIYITNYRAGLGFPLSTGDOAKGVGLDQIALRWIEYNG 240
121 GTGNMIDGSLASGVNVIYITNYRAGLGFPLSTGDOAKGVGLDQIALRWIEYNG 240
241 AFGSDPKRVITFSSGAGACSVLITLSHSEGLFOKALICSTALSSNANVCPAKYRI 300
|||||
241 AFGSDPKRVITFSSGAGACSVLITLSHSEGLFOKALICSTALSSNANVCPAKYRI 300
301 LADKVGCMXMDITDMEGCRNKRYKELICOTTPATYHAFQPVJGDVFPDPOILMEC 360
301 LADKVGCMXMDITDMEGCRNKRYKELICOTTPATYHAFQPVJGDVFPDPOILMEC 360
361 GEFNLNDXMGVNGSGKLFVDCIYVNDGVTTPNDFEVSNFYDNLGYPPGKCTLST 420
361 GEFNLNDXMGVNGSGKLFVDCIYVNDGVTTPNDFEVSNFYDNLGYPPGKCTLST 420
421 IKFWYTPMAKXENPEPRKTLVALFTDQOMVAPAAVADJAAQYGSFYFYAYHAGOSEM 480
421 IKFWYTPMAKXENPEPRKTLVALFTDQOMVAPAAVADJAAQYGSFYFYAYHAGOSEM 480
481 KPSWADSAHGDDEVYVFGIPMIGPTEJFSCNFSKNDVMSAVVMYTMNFAKTGDPNOJV 540
481 KPSWADSAHGDDEVYVFGIPMIGPTEJFSCNFSKNDVMSAVVMYTMNFAKTGDPNOJV 540
541 PDKTKFHTKPNRFEVANSKNPKQCLTILGKRRVMDHRAIKVAFKVELVHNLNL 600
541 PDKTKFHTKPNRFEVANSKNPKQCLTILGKRRVMDHRAIKVAFKVELVHNLNL 600
601 NEIFQYVSTTKVPDPDMTSFYGTTRSPAKTIMPTTKRPAITPANNPKSKDPHTGCEB 660
601 NEIFQYVSTTKVPDPDMTSFYGTTRSPAKTIMPTTKRPAITPANNPKSKDPHTGCEB 660
661 TTVLETRDXYSTELSTIAVAGSLFLNLFAALYKXCDRRBHTHRPSPORTNND 720
661 TTVLETRDXYSTELSTIAVAGSLFLNLFAALYKXCDRRBHTHRPSPORTNND 720
721 IAHIONEIWSLOKOLEHDECECSAHDJTLRTPPYTLTLRRSPDCLMTPNIT 780
721 IAHIONEIWSLOKOLEHDECECSAHDJTLRTPPYTLTLRRSPDCLMTPNIT 780
781 MIPNTLTGQPLHTFNTFSGGONSJLDPHSHSTRY 816
781 MIPNTLTGQPLHTFNTFSGGONSJLDPHSHSTRY 816

RESULT 32
US-10-145-069A-375
Sequence 375, Application US/10145089A


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Publication No. US20030180867A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geiber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2630P1C1
CURRENT APPLICATION NUMBER: US/10/145,389A
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062253
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/365311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077645
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 375
LENGTH: 816
TYPE: PRT
ORGANISM: Homo sapiens
US-10-145-089A-375

Query Match          100.0%; Score 816; DB 12; Length 816;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 121 QDQNEDECLYNIYVPTEDGANTKKNADDTISNDGDEDECIHDQNSKKPVWVYTHGGSYME 180
DB 121 CQQNEDECLYNIYVPTEDGANTKKNADDTISNDGDEDECIHDQNSKKPVWVYTHGGSYME 180
QY 181 GTGKVDSSIASGCVNIYVITINRGLIGLPLSTGDDAAGNIGLLDQICAKITEENVG 240
DB 181 GTGKVDSSIASGCVNIYVITINRGLIGLPLSTGDDAAGNIGLLDQICAKITEENVG 240
QY 241 AFGGDPKRVTFSGGAGASCVSLTLTHYSGLFCKAIIOSGTALSSMANVYCPAKYTR 300
DB 241 AFGGDPKRVTFSGGAGASCVSLTLTHYSGLFCKAIIOSGTALSSMANVYCPAKYTR 300
QY 301 LADKVGCMMLDTTMEVCELRNKYKELIQQITTPATYHAFFGPTDGDVLPDDFQILMRQ 360
DB 301 LADKVGCMMLDTTMEVCELRNKYKELIQQITTPATYHAFFGPTDGDVLPDDFQILMRQ 360
QY 361 GEFNLYDMLGVNGDEGLKFPDGIVDNECVTPRDPSPYSNFPDNIYGPREGDTRRET 420
DB 361 GEFNLYDMLGVNGDEGLKFPDGIVDNECVTPRDPSPYSNFPDNIYGPREGDTRRET 420
QY 421 IKFMYTMDADKENDETRRKTTLVALFTDQWAPAVAADLHAQYGSPTYFAFYHHCOSEM 480
DB 421 IKFMYTMDADKENDETRRKTTLVALFTDQWAPAVAADLHAQYGSPTYFAFYHHCOSEM 480
QY 481 KPSWADSAHGDEVPYVFGIPIWIGFTELPSCNFSKNDVMSAVVTTWTFNAKTGDPKQPV 540
DB 481 KPSWADSAHGDEVPYVFGIPIWIGFTELPSCNFSKNDVMSAVVTTWTFNAKTGDPKQPV 540
QY 541 PODTKFIHTKRNREEVAMSKYNPKDQLYHIGLKPVRDHYRATKYAFMLELVPHLAM 600
DB 541 PODTKFIHTKRNREEVAMSKYNPKDQLYHIGLKPVRDHYRATKYAFMLELVPHLAM 600
QY 601 NEIFQVYSTTKVPDPMTSPFVGTGRSPAKIWTTRPAITPANPKSKDPKHTGPD 660
DB 601 NEIFQVYSTTKVPDPMTSPFVGTGRSPAKIWTTRPAITPANPKSKDPKHTGPD 660
QY 661 TTULIETKQYISTSLSTIANGASLLFNILAPALYKDKRHRHTRRSPQKRNTHD 720
DB 661 TTULIETKQYISTSLSTIANGASLLFNILAPALYKDKRHRHTRRSPQKRNTHD 720
QY 721 IAHQNEEIMSLQKQJLEHDEHCESLQAHDTLRITCPEYTLTTRRSPDQPLMTPTWT 780
DB 721 IAHQNEEIMSLQKQJLEHDEHCESLQAHDTLRITCPEYTLTTRRSPDQPLMTPTWT 780
QY 781 MIPNTLTXQPLHFTNTPSGQGNSTNLPFGHSTTRV 816
DB 781 MIPNTLTXQPLHFTNTPSGQGNSTNLPFGHSTTRV 816

RESULT 33
US-10-013-926A-375
Sequence 375, Application US/10013926A
Publication No. US20030187241A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geiber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.

```

APPLICANT: Napier, Mary A.
APPLICANT: Pan, James F.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C80
CURRENT APPLICATION NUMBER: US/10/013,926A
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO: 375
LENGTH: 816
TYPE: PRT
ORGANISM: Homo sapiens
US-10-013-926A-375

Query Match 100.0%; Score 816; DB 12; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MINSVLLMLTALAKFTLIDSOAQYPVNTNYSKIRGRLPLENELIGVEQYIGVPA 60
DB 1 MINSVLLMLTALAKFTLIDSOAQYPVNTNYSKIRGRLPLENELIGVEQYIGVPA 60
QY 61 SEPTGERRCPEPSSWTGIRNTTOGAAYCPQHLDESLHMLPWFNANDLTXTYV 120
DB 61 SEPTGERRCPEPSSWTGIRNTTOGAAYCPQHLDESLHMLPWFNANDLTXTYV 120
QY 121 COQNEDELYINIVETEDGANTKKNADDTSDNRGEDEDIHQSKSPVXYIHGSYME 180
DB 121 COQNEDELYINIVETEDGANTKKNADDTSDNRGEDEDIHQSKSPVXYIHGSYME 180
QY 181 GTGNMIDGSLASYNVIVITINELGLGLSLSTGCKAKKNGGLQICQALKRETEENVG 240
DB 181 GTGNMIDGSLASYNVIVITINELGLGLSLSTGCKAKKNGGLQICQALKRETEENVG 240
QY 241 AFGDPKRVTFIGSGAGASCVLTLTSHVSSGDFQKATIGSGTALSMANVYCPAXYTRI 300
DB 241 AFGDPKRVTFIGSGAGASCVLTLTSHVSSGDFQKATIGSGTALSMANVYCPAXYTRI 300
QY 301 LADKVGCMMDTDMVECLRNKVKELIQTTTPATYHIAFGVYIDGVTFDDPCQIMEG 360
DB 301 LADKVGCMMDTDMVECLRNKVKELIQTTTPATYHIAFGVYIDGVTFDDPCQIMEG 360
QY 361 GEFLNYDMLGYNCGEGSKFYDGTIVENSDGVCPNDPFFSVSNFPMN:YGYPEGGDTLRET 420
DB 361 GEFLNYDMLGYNCGEGSKFYDGTIVENSDGVCPNDPFFSVSNFPMN:YGYPEGGDTLRET 420

QY 421 IKFMYTMDADKENETRKTLVALFTDQWVAPVADLHAYGSPTYFYAFYHHQSEM 480
DB 421 IKFMYTMDADKENETRKTLVALFTDQWVAPVADLHAYGSPTYFYAFYHHQSEM 480
QY 481 KPSWADSAHGEVYVVGIPMGITTELFSCNFSKNDVMLSANMTWTNRAKGC2RNPV 540
DB 481 KPSWADSAHGEVYVVGIPMGITTELFSCNFSKNDVMLSANMTWTNRAKGC2RNPV 540
QY 541 PDCFKIHTKRNREEVAMSKYNKCDQLYLHIGKPRVRCCHYATKVAFMLVPHLNL 600
DB 541 PDCFKIHTKRNREEVAMSKYNKCDQLYLHIGKPRVRCCHYATKVAFMLVPHLNL 600
QY 601 NEIPQYVSTTKVPPDMTSPPYGTRSPAKIMPTTRPAITPANNPKSKDCHKGPED 660
DB 601 NEIPQYVSTTKVPPDMTSPPYGTRSPAKIMPTTRPAITPANNPKSKDCHKGPED 660
QY 661 TVVLETRKDYSTEASTIAVGALELNLIAFAALYKDKKRRHETRRSPORNTND 720
DB 661 TVVLETRKDYSTEASTIAVGALELNLIAFAALYKDKKRRHETRRSPORNTND 720
QY 721 IAHIONERIMSQKOLEHDECSLOAHDTLRLCTCPDYTLTLRSGPDDIPATNTNIT 780
DB 721 IAHIONERIMSQKOLEHDECSLOAHDTLRLCTCPDYTLTLRSGPDDIPATNTNIT 780
QY 781 MIPNTLTMQPLHTFNTFSGQNSTNLPKHSSTRV 816
DB 781 MIPNTLTMQPLHTFNTFSGQNSTNLPKHSSTRV 816

RESULT 34
US-10-145-017A-375
Sequence 375, Application US/10145017A
Publication No. US20030196365A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dar
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Giang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C82
CURRENT APPLICATION NUMBER: US/10/145,017A
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03

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PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077453
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See file wrapper or PAM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 375
LENGTH: 816
TYPE: PRT
ORGANISM: Homo sapiens
US-10-145-017A-375

```

```

Query Match      100.0% Score 816; DB 12; Length 816;
Best Local Similarity 100.0% Pred No 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CY 1 MENSVLMTALAIKETLIDSOQVPPVNTNYGKIRGRTPLNEILCPVEQYGVPA 60
DB 1 MENSVLMTALAIKETLIDSOQVPPVNTNYGKIRGRTPLNEILCPVEQYGVPA 60
CY 61 SPPTGERPQPEPPSSWTGINTTQFAAVCPQRLDERSLHMLPMTALDLNCTV 120
DB 61 SPPTGERPQPEPPSSWTGINTTQFAAVCPQRLDERSLHMLPMTALDLNCTV 120
CY 121 QDQNECDLVNIYPTEDGANTKNADITSDRGEDIDHONSKRPVYVHGSGYK 180
DB 121 QDQNECDLVNIYPTEDGANTKNADITSDRGEDIDHONSKRPVYVHGSGYK 180
CY 181 GTGNTDGSILASGNVITITVRLGICFLSTPCQAKNGYGLDQIQALRWLENG 240
DB 181 GTGNTDGSILASGNVITITVRLGICFLSTPCQAKNGYGLDQIQALRWLENG 240
CY 241 AFGSDPKRVTIFSGAGASCVSLLTSHVSEGLFOYATIGSTALSSKAWYQPKYTI 300
DB 241 AFGSDPKRVTIFSGAGASCVSLLTSHVSEGLFOYATIGSTALSSKAWYQPKYTI 300
CY 301 LADKVGCMJDTTDMVECLRNKRYKELIQITTPATYHIAFGVIDGEVIPPDPQLMEQ 360
DB 301 LADKVGCMJDTTDMVECLRNKRYKELIQITTPATYHIAFGVIDGEVIPPDPQLMEQ 360
CY 361 GEFUNYVIMGVNQGELKFDGIVNEGCVTENDDESVSNVCKLVGYPGKCTJLET 420
DB 361 GEFUNYVIMGVNQGELKFDGIVNEGCVTENDDESVSNVCKLVGYPGKCTJLET 420
CY 421 IKRYWTMADEKNEPEPRKTJVALFTDQWVAVAVAADHACQSPFTYVAYVHHCSEY 480
DB 421 IKRYWTMADEKNEPEPRKTJVALFTDQWVAVAVAADHACQSPFTYVAYVHHCSEY 480
CY 481 KPSWADSAAGDEYVYVIGYIPIPTLEFSCNFSKKNVYLSAVVYTWTFATCGPNQYV 540
DB 481 KPSWADSAAGDEYVYVIGYIPIPTLEFSCNFSKKNVYLSAVVYTWTFATCGPNQYV 540
CY 541 PCQTRFHTKPNRFEFAWGNPKQOLYHIGLKPVRCHVYATGVAFMLEVPELNT 600
DB 541 PCQTRFHTKPNRFEFAWGNPKQOLYHIGLKPVRCHVYATGVAFMLEVPELNT 600
CY 601 NEIFQVSTTKVPPDPYISFPYGRSSPAKIWTTKRPAITPAHPKSKCPKCTGPEQ 660
DB 601 NEIFQVSTTKVPPDPYISFPYGRSSPAKIWTTKRPAITPAHPKSKCPKCTGPEQ 660
CY 661 TTVLIEFKRDTSLSTLAVGASLLFLNLAFAAYKKDKRKHETHRPSPQNTTND 720
DB 661 TTVLIEFKRDTSLSTLAVGASLLFLNLAFAAYKKDKRKHETHRPSPQNTTND 720

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CY 721 IAIHQEIMSLQKLEHDECESQAADTALTCPEYTLTARSPDIPANTPTIT 780
DB 721 IAIHQEIMSLQKLEHDECESQAADTALTCPEYTLTARSPDIPANTPTIT 780
CY 781 MINTLTGMQPLHTFTFGGQNSTNYPGHSTTRV 816
DB 781 MINTLTGMQPLHTFTFGGQNSTNYPGHSTTRV 816

RESULT 35
US-10-164-728A-375
Sequence 375, Application US/10164728A
Publication No. US20030186368A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Quang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Yary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavich, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acid Reference: P630P043
CURRENT APPLICATION NUMBER: US/10/164,728A
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See file wrapper or PAM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 375
LENGTH: 816
TYPE: PRT
ORGANISM: Homo sapiens

```

US-10-165-067A-375

Query Match 100.0%; Score 816; DB 12; Length 816;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MUNSVMMLTALAIKFTLIDSOAQYPVVNTNKGKINGLSTPPENELGPEVGYLGVPVA 60
DB 1 MUNSVMMLTALAIKFTLIDSOAQYPVVNTNKGKINGLSTPPENELGPEVGYLGVPVA 60
OY 61 SPPTGERRFQPEPPSSWTGIRNTTQFAVCPQHLDERSLHMLPIWFTANJLTMTYV 120
DB 61 SPPTGERRFQPEPPSSWTGIRNTTQFAVCPQHLDERSLHMLPIWFTANJLTMTYV 120
OY 121 ODQNEDCLYNIYVPTEDGANTKKAADITSNDRGEDEDIHDQSKKPVWVYIHGGSYME 180
DB 121 ODQNEDCLYNIYVPTEDGANTKKAADITSNDRGEDEDIHDQSKKPVWVYIHGGSYME 180
OY 181 GTGNMIDGSIILASGNYVITINRGLGLFLSTGQAAKNGYGLDQIQALRWIFENYV 240
DB 181 GTGNMIDGSIILASGNYVITINRGLGLFLSTGQAAKNGYGLDQIQALRWIFENYV 240
OY 241 AFGDDPKRVTFHSGGAGAGSCVSLTSLSHYSEGUFQKALISGTAALSMWAKYGPATYR 300
DB 241 AFGDDPKRVTFHSGGAGAGSCVSLTSLSHYSEGUFQKALISGTAALSMWAKYGPATYR 300
OY 301 LADKVCNMLDTTMEVCELRKNKXKELTQOTTPATYHAFGFIYADEVIPEDDQIMBO 360
DB 301 LADKVCNMLDTTMEVCELRKNKXKELTQOTTPATYHAFGFIYADEVIPEDDQIMBO 360
OY 361 GEFLLNIDIMGVNCGESGKFFVQGVENEDGYTPHDFPFSVSNFKINXGPECKTLRET 420
DB 361 GEFLLNIDIMGVNCGESGKFFVQGVENEDGYTPHDFPFSVSNFKINXGPECKTLRET 420
OY 421 IKFMYTMAADKENDETRKTVALFTDQWAPAVAAADLAKQGSFYFAFYHHCSEY 480
DB 421 IKFMYTMAADKENDETRKTVALFTDQWAPAVAAADLAKQGSFYFAFYHHCSEY 480
OY 481 KPSWADSAGDEVPVFGIPMIGTTELPSCNFSGNJNSAVNTYWTNFAKGDQRPV 540
DB 481 KPSWADSAGDEVPVFGIPMIGTTELPSCNFSGNJNSAVNTYWTNFAKGDQRPV 540
OY 541 PDDTFHTKPNRFEVAVMSKYNPKDCYLHIGLKPVRCHYRATXVAPLELVPHLNL 600
DB 541 PDDTFHTKPNRFEVAVMSKYNPKDCYLHIGLKPVRCHYRATXVAPLELVPHLNL 600
OY 601 NEIPQVASTTKVPPDMTSPFYGTRRSFPAKIMPTTSPATTPANPKHSDKHKTSPED 660
DB 601 NEIPQVASTTKVPPDMTSPFYGTRRSFPAKIMPTTSPATTPANPKHSDKHKTSPED 660
OY 661 TTULIETKRDYSTEISVIAVAGASLLFLNITAFALYYKKDKRHHETHRRSPQKRTND 720
DB 661 TTULIETKRDYSTEISVIAVAGASLLFLNITAFALYYKKDKRHHETHRRSPQKRTND 720
OY 721 ZAHIONEEIMSJOMQLEHDECESLQAHDTLRJCTCPDYTLTLRRSPDDIPLMTPTT 780
DB 721 ZAHIONEEIMSJOMQLEHDECESLQAHDTLRJCTCPDYTLTLRRSPDDIPLMTPTT 780
OY 781 MIPNTLTQMQLHTINTSGQNSGNTLPHGSHSTRV 816
DB 781 MIPNTLTQMQLHTINTSGQNSGNTLPHGSHSTRV 816

```

RESULT 36

US-10-165-067A-375

Sequence 375, Application US/10165067A

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desrochers, Luc

APPLICANT: Eaton, Dan

```

APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William J.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C42
CURRENT APPLICATION NUMBER: US/10/165,067A
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/062253
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 375
LENGTH: 816
TYPE: PRT
ORGANISM: Homo sapiens
US-10-165-067A-375
Query Match 100.0%; Score 816; DB 12; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 161 GTGMDGSLASGAGNVITINRLILGSLTGDOAKMIGLLDQIALRMIEENVG 240
Cy 241 AFGGDPKRVITIFSGAGASCVSLLTSHYSEGLFOKAIIOSGALSSMAVNYCPAKYTRI 300
Db 241 AFGGDPKRVITIFSGAGASCVSLLTSHYSEGLFOKAIIOSGALSSMAVNYCPAKYTRI 300
Cy 301 LADRVGCMMLDTTDMVCECLRNKYNKELIQQITIPATYHIAFGVYIGGVYIPDDFCQILMEQ 360
Db 301 LADRVGCMMLDTTDMVCECLRNKYNKELIQQITIPATYHIAFGVYIGGVYIPDDFCQILMEQ 360
Cy 361 GEFNYNDIMGVNCGESLKFDVGVNDEDEVTPNDFPSVSNFVDNLYGFEGKDTRET 420
Db 361 GEFNYNDIMGVNCGESLKFDVGVNDEDEVTPNDFPSVSNFVDNLYGFEGKDTRET 420
Cy 421 IKFMYTDMADKXENPETERKTLVALFTDHQVAVAAADLHAQYGSPTFYAFYHHCOSEM 480
Db 421 IKFMYTDMADKXENPETERKTLVALFTDHQVAVAAADLHAQYGSPTFYAFYHHCOSEM 480
Cy 481 KPSWADSAHGDDEVYVVGIMIGPTELFSGNSEKNDVMSAVVMTYTNAPKAGDPPQPV 540
Db 481 KPSWADSAHGDDEVYVVGIMIGPTELFSGNSEKNDVMSAVVMTYTNAPKAGDPPQPV 540
Cy 541 PDKTFHTKRNFEFEVAAWSKYNPKQCYLHICLPRVDHVSATKVAEMLEVFRLHNL 600
Db 541 PDKTFHTKRNFEFEVAAWSKYNPKQCYLHICLPRVDHVSATKVAEMLEVFRLHNL 600
Cy 601 NEIFQVYSTTKVPPPDYISFPYGRSSPAKIMPTTKRPAITPAKPKSKODPKTGPE 660
Db 601 NEIFQVYSTTKVPPPDYISFPYGRSSPAKIMPTTKRPAITPAKPKSKODPKTGPE 660
Cy 661 TTVLETRKRYSTELSTAVGASLLFLNLAFAAYKKDKRRECHRRPSSQKNTYND 720
Db 661 TTVLETRKRYSTELSTAVGASLLFLNLAFAAYKKDKRRECHRRPSSQKNTYND 720
Cy 721 IAHIONEIMSLQKOLEHDECEESLOAHDLRLTQPPVTLTLRRSPDDIPANCPNIT 780
Db 721 IAHIONEIMSLQKOLEHDECEESLOAHDLRLTQPPVTLTLRRSPDDIPANCPNIT 780
Cy 781 MIPNLTGNOPLATRTFSGGONSTNLPKHSITRY 816
Db 781 MIPNLTGNOPLATRTFSGGONSTNLPKHSITRY 816

RESULT 37
US-10-145-124A-375
Sequence 375, Application: US/10145124A
Publication No. US2001019770.A1
GENERAL INFORMATION:
APPLICANT: Ashkezazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botschtein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Flivarsoff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlsem, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Gurney, Austin D.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavira, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James J.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2610P1C44
CURRENT APPLICATION NUMBER: US/10/145,124A
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 09/919585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062253
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064245
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 375
LENGTH: 816
TYPE: PRT
ORGANISM: Homo sapiens
US-10-145-124A-375

Query Match 100.0%; Score 816; DB 12; Length 816;
Best local similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MUNSNNVLLMLTALAIKRTLLIDSOAOYFVNTNNGKIRGLFTPLNNEILGVEQYLGYPYA 60
Db 1 MUNSNNVLLMLTALAIKRTLLIDSOAOYFVNTNNGKIRGLFTPLNNEILGVEQYLGYPYA 60
Cy 61 SPTGERRFPQPEPSSWTGIRNTQFAAVCPQHLDBRSLLHMLPMTFANIDTLNTYV 120
Db 61 SPTGERRFPQPEPSSWTGIRNTQFAAVCPQHLDBRSLLHMLPMTFANIDTLNTYV 120
Cy 121 QQONEDCLYNIYVFTEDGANTKKNADITSNRGEDEDIDQNSKKPVVYIHGGSYME 180
Db 121 QQONEDCLYNIYVFTEDGANTKKNADITSNRGEDEDIDQNSKKPVVYIHGGSYME 180
Cy 181 GTGMDGSLASGAGNVITINRLILGSLTGDOAKMIGVGLDQIALRMIEENVG 240
Db 181 GTGMDGSLASGAGNVITINRLILGSLTGDOAKMIGVGLDQIALRMIEENVG 240
Cy 241 AFGGDPKRVITIFSGAGASCVSLLTSHYSEGLFOKAIIOSGALSSMAVNYCPAKYTRI 300
Db 241 AFGGDPKRVITIFSGAGASCVSLLTSHYSEGLFOKAIIOSGALSSMAVNYCPAKYTRI 300
Cy 301 LADRVGCMMLDTTDMVCECLRNKYNKELIQQITIPATYHIAFGVYIGGVYIPDDFCQILMEQ 360
Db 301 LADRVGCMMLDTTDMVCECLRNKYNKELIQQITIPATYHIAFGVYIGGVYIPDDFCQILMEQ 360
Cy 361 GEFNYNDIMGVNCGESLKFDVGVNDEDEVTPNDFPSVSNFVDNLYGFEGKDTRET 420
Db 361 GEFNYNDIMGVNCGESLKFDVGVNDEDEVTPNDFPSVSNFVDNLYGFEGKDTRET 420
Cy 421 IKFMYTDMADKXENPETERKTLVALFTDHQVAVAAADLHAQYGSPTFYAFYHHCOSEM 480
Db 421 IKFMYTDMADKXENPETERKTLVALFTDHQVAVAAADLHAQYGSPTFYAFYHHCOSEM 480
Cy 481 KPSWADSAHGDDEVYVVGIMIGPTELFSGNSEKNDVMSAVVMTYTNAPKAGDPPQPV 540
Db 481 KPSWADSAHGDDEVYVVGIMIGPTELFSGNSEKNDVMSAVVMTYTNAPKAGDPPQPV 540

DB 481 KPSWADSAHGDEVPYVFGIMIGTELFSCNFSXNDVMLSAVMTWTNTEAKTGDPKPV 540
QY 541 PDKTFIHTKPRREEVAVMSKYNPCQCLYHIGLKPRRCHYRATKAFFMLELPHLHNL 600
DB 541 PDKTFIHTKPRREEVAVMSKYNPCQCLYHIGLKPRRCHYRATKAFFMLELPHLHNL 600
QY 601 NEIFQVSTTTKVPDPMTSPFYGTRRSPAKIMPTTKRPAITPANNPKSKDPKGPED 660
DB 601 NEIFQVSTTTKVPDPMTSPFYGTRRSPAKIMPTTKRPAITPANNPKSKDPKGPED 660
QY 661 TTVLETKRDVSTELSVTIAGASLLFLNLIAFALYKDKRHHETRRSPQRNTND 720
DB 661 TTVLETKRDVSTELSVTIAGASLLFLNLIAFALYKDKRHHETRRSPQRNTND 720
QY 721 IAHIONEELMSLOMKOLEHDEHCESLQAHJTLRITCPEPYTLTLRRSPDIPMTPTIT 780
DB 721 IAHIONEELMSLOMKOLEHDEHCESLQAHJTLRITCPEPYTLTLRRSPDIPMTPTIT 780
QY 781 MIPNTLTGMQPLHTFNTFSGGNSINLPHGSHSTRV 816
DB 781 MIPNTLTGMQPLHTFNTFSGGNSINLPHGSHSTRV 816

RESULT 38
US-10-160-502A-375
Sequence 375, Application US/10160302A
General Information:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin P.
APPLICANT: Rotstein, David
APPLICANT: Desnoyers, Inc
APPLICANT: Satoh, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Ford, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary R.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavitt, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunes, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC57
CURRENT APPLICATION NUMBER: US/10160, 502A
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632

PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See file wrapper or PAM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO: 375
LENGTH: 816
TYPE: PRT
ORGANISM: Homo sapiens
US-10-160-502A-375

Query Match 100.0%; Score 816; DB 12; Length 816;
Best Local Similarity 100.0%; Pct. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MANSVLEMLTALAIKFTLIDSOAQYVWNTNNGIKRGLRTPPLNEILGVECYLGPVA 60
1 MANSVLEMLTALAIKFTLIDSOAQYVWNTNNGIKRGLRTPPLNEILGVECYLGPVA 60
QY 61 SPTGERRFOPEPPSSNTG:RNTQFANCPHLDERSLHMLTINFTALUDLTMTY 120
DB 61 SPTGERRFOPEPPSSNTG:RNTQFANCPHLDERSLHMLTINFTALUDLTMTY 120
QY 121 QDQNECCLYLNTYPTEDGANTKKAADTSNRSSEDEJHDCNSKKPWVYIHSSYME 180
DB 121 QDQNECCLYLNTYPTEDGANTKKAADTSNRSSEDEJHDCNSKKPWVYIHSSYME 180
QY 121 QDQNECCLYLNTYPTEDGANTKKAADTSNRSSEDEJHDCNSKKPWVYIHSSYME 180
DB 121 QDQNECCLYLNTYPTEDGANTKKAADTSNRSSEDEJHDCNSKKPWVYIHSSYME 180
QY 241 GTGNMIDGSIASGVNIVTTINRGLIGLSTGQAKKNGLLDQIALRWIEENNG 240
DB 241 GTGNMIDGSIASGVNIVTTINRGLIGLSTGQAKKNGLLDQIALRWIEENNG 240
QY 241 GTGNMIDGSIASGVNIVTTINRGLIGLSTGQAKKNGLLDQIALRWIEENNG 240
DB 241 GTGNMIDGSIASGVNIVTTINRGLIGLSTGQAKKNGLLDQIALRWIEENNG 240
QY 241 AFGGPKRVITFGSGAGASCVSLLTSHYSEGLFOKAIIOSGATLSMAVNPAYATC 300
DB 241 AFGGPKRVITFGSGAGASCVSLLTSHYSEGLFOKAIIOSGATLSMAVNPAYATC 300
QY 301 LADKVGCMMLDTTDMVCLRNKVKELIQCTITPATYHIAFGVIGDVYFDPPQILMEQ 360
DB 301 LADKVGCMMLDTTDMVCLRNKVKELIQCTITPATYHIAFGVIGDVYFDPPQILMEQ 360
QY 361 GEPINYOIMGVNCGEGLKFDVG:VNDDEGVTDNDPFSNSNVCM:YGPPEKCLTRET 420
DB 361 GEPINYOIMGVNCGEGLKFDVG:VNDDEGVTDNDPFSNSNVCM:YGPPEKCLTRET 420
QY 421 IKFMYTDWADKENETRRKTLVALFTDQWVAVAVADLAQYGSFTFYAFYHGCSEK 480
DB 421 IKFMYTDWADKENETRRKTLVALFTDQWVAVAVADLAQYGSFTFYAFYHGCSEK 480
QY 481 KPSWADSAHGDEVPYVFGIMIGTELFSCNFSXNDVMLSAVMTWTNTEAKTGDPKPV 540
DB 481 KPSWADSAHGDEVPYVFGIMIGTELFSCNFSXNDVMLSAVMTWTNTEAKTGDPKPV 540
QY 541 PDKTFIHTKPRREEVAVMSKYNPCQCLYHIGLKPRRCHYRATKAFFMLELPHLHNL 600
DB 541 PDKTFIHTKPRREEVAVMSKYNPCQCLYHIGLKPRRCHYRATKAFFMLELPHLHNL 600
QY 601 NEIFQVSTTTKVPDPMTSPFYGTRRSPAKIMPTTKRPAITPANNPKSKDPKGPED 660
DB 601 NEIFQVSTTTKVPDPMTSPFYGTRRSPAKIMPTTKRPAITPANNPKSKDPKGPED 660
QY 661 TTVLETKRDVSTELSVTIAGASLLFLNLIAFALYKDKRHHETRRSPQRNTND 720
DB 661 TTVLETKRDVSTELSVTIAGASLLFLNLIAFALYKDKRHHETRRSPQRNTND 720
QY 721 IAHIONEELMSLOMKOLEHDEHCESLQAHJTLRITCPEPYTLTLRRSPDIPMTPTIT 780
DB 721 IAHIONEELMSLOMKOLEHDEHCESLQAHJTLRITCPEPYTLTLRRSPDIPMTPTIT 780
QY 781 MIPNTLTGMQPLHTFNTFSGGNSINLPHGSHSTRV 816
DB 781 MIPNTLTGMQPLHTFNTFSGGNSINLPHGSHSTRV 816

Db 781 MIPNTLTGMOPLHTFNTFFSGGQNSTNLPHGSTRV 816

RESULT 39

US-10-165-247A-375

Sequence 375, Application US/10165247A

Publication No. US20030290321A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Bacon, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gettisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Grimaldi, C. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavich, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Nadler, Mary A.
APPLICANT: Pan, James J.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acid Reference: P26302C41

CURRENT APPLICATION NUMBER: US/10/165,247A

CURRENT FILING DATE: 2001-10-19

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/077450

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077641

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077649

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077791

PRIOR FILING DATE: 1998-03-12

Remaining Prior Application data removed - See File Wrapper or PAJX.

NUMBER OF SEQ ID NOS: 624

SEQ ID NO 375

LENGTH: 816

TYPE: PRT

ORGANISM: Homo sapiens

US-10-165-247A-375

Query Match

Best Local Similarity 100.0%; Score 816; DB 12; Length 816;

Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSNVLLMTALAIKFTLIDSCAQYFVNTNYGKIRGLRPLPNEILGVEQYLCVPYA 60

Db 781 MIPNTLTGMOPLHTFNTFFSGGQNSTNLPHGSTRV 816

QY 1 MNSNVLLMTALAIKFTLIDSCAQYFVNTNYGKIRGLRPLPNEILGVEQYLCVPYA 60

Db 61 SPTGERRPOPEPSSWTGIRNTCTQPAACPOHDEBSLHMDLIPFANIDTLYTV 120

Db 61 SPTGERRPOPEPSSWTGIRNTCTQPAACPOHDEBSLHMDLIPFANIDTLYTV 120

QY 121 CDQNEDELINIVPTEDGANTKKANADINSNGEDEDHDQNSKKPVVYVHGGSYME 180

Db 121 CDQNEDELINIVPTEDGANTKKANADINSNGEDEDHDQNSKKPVVYVHGGSYME 180

QY 181 GTGNMIGSLASTGNYVITITNYRGLICFLSTGDOAKNGYGLDQICACNIEBNG 240

Db 181 GTGNMIGSLASTGNYVITITNYRGLICFLSTGDOAKNGYGLDQICACNIEBNG 240

QY 241 AFGGCPKRVTFPSGAGASCVSLLTSVSEGGFGXKIIOSGTALSSMAVYCPAKTR 300

Db 241 AFGGCPKRVTFPSGAGASCVSLLTSVSEGGFGXKIIOSGTALSSMAVYCPAKTR 300

QY 301 LADKVGCMMLDITDMEVCELRNKYKELIQOTTPATYHAFGVINDVLPDPOQLMEQ 360

Db 301 LADKVGCMMLDITDMEVCELRNKYKELIQOTTPATYHAFGVINDVLPDPOQLMEQ 360

QY 361 GEFUNYDIMGVNGGELKFEVDGIVNEDGVTNDEPFSVSNFVNDLYGIPBCKDLRET 420

Db 361 GEFUNYDIMGVNGGELKFEVDGIVNEDGVTNDEPFSVSNFVNDLYGIPBCKDLRET 420

QY 421 IKFMYTMDADKENETRRKTLVALFTDHQVAVADVAADLHAQYGSPTYFYAFYHCOSEM 480

Db 421 IKFMYTMDADKENETRRKTLVALFTDHQVAVADVAADLHAQYGSPTYFYAFYHCOSEM 480

QY 481 KPSWADSAHGDVPEYVGMIGTLELPSGNSKNDVMISAVMTYTNPAKTGDPNOY 540

Db 481 KPSWADSAHGDVPEYVGMIGTLELPSGNSKNDVMISAVMTYTNPAKTGDPNOY 540

QY 541 PDKRFHTKPNRREZVAMSKYNDLYHIGAKPVDRHYEATKVAFLYVPHLNL 600

Db 541 PDKRFHTKPNRREZVAMSKYNDLYHIGAKPVDRHYEATKVAFLYVPHLNL 600

QY 601 NEIFQVSTTKVPPTSPFPGYTRSPAKIMPTTRPAITPANNPKSHKDPKGPED 660

Db 601 NEIFQVSTTKVPPTSPFPGYTRSPAKIMPTTRPAITPANNPKSHKDPKGPED 660

QY 661 TTVLETRKDDSTELSTIAVAGSLFLNLAFPAIYKDKRRHETRRPSPORNTND 720

Db 661 TTVLETRKDDSTELSTIAVAGSLFLNLAFPAIYKDKRRHETRRPSPORNTND 720

QY 721 IASIQNEIINSLOKQLEHDECESLQANDTLRLTGPDDYTLRLRSPPDIPTCTPYTIT 780

Db 721 IASIQNEIINSLOKQLEHDECESLQANDTLRLTGPDDYTLRLRSPPDIPTCTPYTIT 780

QY 781 MIPNTLTGMOPLHTFNTFFSGGQNSTNLPHGSTRV 816

Db 781 MIPNTLTGMOPLHTFNTFFSGGQNSTNLPHGSTRV 816

RESULT 40

US-09-978-194A-375

Sequence 375, Application US/09978194A

Publication No. US20030195339A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Ferrara, Napoleone

APPLICANT: Filaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gettisen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin J.
APPLICANT: Hilari, Kenneth J.
APPLICANT: K.Javin, Ivar C.
APPLICANT: Kuo, Sophia S.
APPLICANT: Nadier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C10
CURRENT APPLICATION NUMBER: US/03/978,194A
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 03/9,8585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062253
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064245
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-23
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
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PRIOR FILING DATE: 1998-03-26
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PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
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PRIOR APPLICATION NUMBER: 60/079663
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
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PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
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PRIOR APPLICATION NUMBER: 60/081952
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PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
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PRIOR APPLICATION NUMBER: 60/083496
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PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05

[illegible]

/ PRIOR APPLICATION NUMBER: 60/085689
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085579
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085560
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085573
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085704
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 816; DB 12; Length 816;
Best Local Similarity 100.0%; Pct. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 MUNSVMMLTALAKFTLIDSOQYPPVNTNNGKIRGLRTPJNEILGVEOYLGPYA 60
DB 1 MUNSVMMLTALAKFTLIDSOQYPPVNTNNGKIRGLRTPJNEILGVEOYLGPYA 60
QY 61 SEPTGERRFPQPEPPSSWTGIRNTTQFAAVCPQHLDRSLHDLPIWFTANJDTMTYV 120
DB 61 SEPTGERRFPQPEPPSSWTGIRNTTQFAAVCPQHLDRSLHDLPIWFTANJDTMTYV 120
QY 121 QDQNEDCYLNIYVTEGANTKKNADITSNDRGEEDHDOQSKKPVVYIHGGSYME 180
DB 121 QDQNEDCYLNIYVTEGANTKKNADITSNDRGEEDHDOQSKKPVVYIHGGSYME 180
QY 181 GTGNMIDGSIASGNNVITINRGLIGLSTGDOAKNGVLLDQIALRWIEENVG 240
DB 181 GTGNMIDGSIASGNNVITINRGLIGLSTGDOAKNGVLLDQIALRWIEENVG 240
QY 241 AFGGPKRVTIFGSGAGASCVSLLTSHYSBGLFQKAIQSGTALSSMAVNYQPAKTYRI 300
DB 241 AFGGPKRVTIFGSGAGASCVSLLTSHYSBGLFQKAIQSGTALSSMAVNYQPAKTYRI 300
QY 301 LADKVGCMMLDTTMDVECLRNKYNKELIQCTITPATYHIAFGPIVDDGVPDDPQILMEQ 360
DB 301 LADKVGCMMLDTTMDVECLRNKYNKELIQCTITPATYHIAFGPIVDDGVPDDPQILMEQ 360
QY 361 GEFLLNVDIMLGVOQEGIKFVNDGIVDNEEDGVPNDPFSVSNFVNDLYGPEBKDTLRET 420
DB 361 GEFLLNVDIMLGVOQEGIKFVNDGIVDNEEDGVPNDPFSVSNFVNDLYGPEBKDTLRET 420
QY 421 IKFMYTDMADKENPETRKRKTLYALFTDQONTAPRAYADLHAGYSSPTFYAFHRCQSEM 480
DB 421 IKFMYTDMADKENPETRKRKTLYALFTDQONTAPRAYADLHAGYSSPTFYAFHRCQSEM 480
QY 481 KPSWADSAHGDVPPVFGIPWIGPTEJSCNFSKNDVLSAVMTYWTNFAKTCQDPQPV 540
DB 481 KPSWADSAHGDVPPVFGIPWIGPTEJSCNFSKNDVLSAVMTYWTNFAKTCQDPQPV 540
QY 541 PODTKEHTKPRFEVAVMSKYNPKDQYLHIGLKPRVCHVRAKTAAPMELVPHLANT 600
DB 541 PODTKEHTKPRFEVAVMSKYNPKDQYLHIGLKPRVCHVRAKTAAPMELVPHLANT 600
QY 601 NEIFQYVSTTTPVPPDMTSFPGTRRSPAKIMPTTSPATTPANNRHSKDPKICPED 660
DB 601 NEIFQYVSTTTPVPPDMTSFPGTRRSPAKIMPTTSPATTPANNRHSKDPKICPED 660
QY 661 TTVLLETKADYSTELSVTIAVGASLLFNLAFALYKXDKRREHREPSQORNTND 720
DB 661 TTVLLETKADYSTELSVTIAVGASLLFNLAFALYKXDKRREHREPSQORNTND 720
QY 721 IAHIONEELMSQKQLEHHECESQASHDRLRLTCCPDYTLIARRSPDCLPMTPTIT 780
DB 721 IAHIONEELMSQKQLEHHECESQASHDRLRLTCCPDYTLIARRSPDCLPMTPTIT 780
QY 781 MIPNTLGCQPLHTNTRFGSGONSTNLPHGSTRV 816
DB 781 MIPNTLGCQPLHTNTRFGSGONSTNLPHGSTRV 816

RESULT 42

US-09-999-829A-375

/ Sequence 375; Application US/0999829A

/ Publication No. US20030195344A1

/ GENERAL INFORMATION:

/ APPLICANT: Ashkenazi, Avi

/ APPLICANT: Baker Kevin P.

/ APPLICANT: Bostein, David

/ APPLICANT: Desnoyers, Luc

/ APPLICANT: Eaton, Dan

/ APPLICANT: Ferrara, Napoleon

/ APPLICANT: Filvaroff, Ellen

/ APPLICANT: Fong, Sherman

/ APPLICANT: Gao, Wei-Qiang

/ APPLICANT: Geber, Hanspeter

/ APPLICANT: Gottstein, Mary E.

/ APPLICANT: Goddard, Audrey

/ APPLICANT: Grimaldi, C. Christopher

/ APPLICANT: Guiney, Austin L.

/ APPLICANT: Hillman, Kenneth J.

/ APPLICANT: Kijavini, Ivar J.

/ APPLICANT: Kuo, Sophia S.

/ APPLICANT: Napier, Mary A.

/ APPLICANT: Pan, James

/ APPLICANT: Paonni, Nicholas F.

/ APPLICANT: Roy, Margaret Ann

/ APPLICANT: Shelton, David L.

/ APPLICANT: Stewart, Timothy A.

/ APPLICANT: Tumas, Daniel

/ APPLICANT: Williams, P. Mickey

/ APPLICANT: Wood, William I.

/ APPLICANT: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

/ TITLE OF INVENTION: Acids Encoding the Same

/ FILE REFERENCE: P2630P1C61

/ CURRENT APPLICATION NUMBER: US/09/999, 829A

/ NUMBER OF SEQ ID NOS: 624

/ Prior Application removed - See File Wrapper or Palm

/ SEQ ID NO 375

/ LENGTH: 816

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ US-09-999-829A-375

Query Match 100.0%; Score 816; DB 12; Length 816;
Best Local Similarity 100.0%; Pct. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 MUNSVMMLTALAKFTLIDSOQYPPVNTNNGKIRGLRTPJNEILGVEOYLGPYA 60
DB 1 MUNSVMMLTALAKFTLIDSOQYPPVNTNNGKIRGLRTPJNEILGVEOYLGPYA 60
QY 61 SEPTGERRFPQPEPPSSWTGIRNTTQFAAVCPQHLDRSLHDLPIWFTANJDTMTYV 120
DB 61 SEPTGERRFPQPEPPSSWTGIRNTTQFAAVCPQHLDRSLHDLPIWFTANJDTMTYV 120
QY 121 QDQNEDCYLNIYVTEGANTKKNADITSNDRGEEDHDOQSKKPVVYIHGGSYME 180
DB 121 QDQNEDCYLNIYVTEGANTKKNADITSNDRGEEDHDOQSKKPVVYIHGGSYME 180
QY 181 GTGNMIDGSIASGNNVITINRGLIGLSTGDOAKNGVLLDQIALRWIEENVG 240
DB 181 GTGNMIDGSIASGNNVITINRGLIGLSTGDOAKNGVLLDQIALRWIEENVG 240
QY 241 AFGGPKRVTIFGSGAGASCVSLLTSHYSBGLFQKAIQSGTALSSMAVNYQPAKTYRI 300
DB 241 AFGGPKRVTIFGSGAGASCVSLLTSHYSBGLFQKAIQSGTALSSMAVNYQPAKTYRI 300
QY 301 LADKVGCMMLDTTMDVECLRNKYNKELIQCTITPATYHIAFGPIVDDGVPDDPQILMEQ 360
DB 301 LADKVGCMMLDTTMDVECLRNKYNKELIQCTITPATYHIAFGPIVDDGVPDDPQILMEQ 360

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QY 361 GEFLLNDIMLVNCGEGKLFVDGIVDNEEDGVTPNDPDESNSNVDNLYGEGKOLIRET 420
| | | | |
DB 361 GEFLLNDIMLVNCGEGKLFVDGIVDNEEDGVTPNDPDESNSNVDNLYGEGKOLIRET 420
QY 421 IKFVYTDMDKSNPETERKTYLALTTDHCXYAPAYALDLAQYOSPTVYFVYHHCOSEM 480
| | | | |
DB 421 IKFVYTDMDKSNPETERKTYLALTTDHCXYAPAYALDLAQYOSPTVYFVYHHCOSEM 480
QY 481 KPSMADSAHGEDEVYVFGTSMIGPTELSGNSKQDWLQSAVWYMYNTRFKTDDPPQV 540
| | | | |
DB 481 KPSMADSAHGEDEVYVFGTSMIGPTELSGNSKQDWLQSAVWYMYNTRFKTDDPPQV 540
QY 541 PCQYKZHTKPMRFEVWASKYNNPCQLYJHGLKPRVDHYRAIKYAFWELVPHLBN 600
| | | | |
DB 541 PCQYKZHTKPMRFEVWASKYNNPCQLYJHGLKPRVDHYRAIKYAFWELVPHLBN 600
QY 601 NEIFQVSTTKVPPEDMSPFYGRBSPAKIMPTTKPATTPANRFGSGCERKTPED 660
| | | | |
DB 601 NEIFQVSTTKVPPEDMSPFYGRBSPAKIMPTTKPATTPANRFGSGCERKTPED 660
QY 661 TVLLETRKDYSTEASVTIAGASLLFTNLLAFALYKKRKRHETRRSPQRATCND 720
| | | | |
DB 661 TVLLETRKDYSTEASVTIAGASLLFTNLLAFALYKKRKRHETRRSPQRATCND 720
QY 721 IAHICNEEYNSIQMKQLEHDECESELQAHOTLRCPEDYTLTLRSPEDLPKTPYTT 780
| | | | |
DB 721 IAHICNEEYNSIQMKQLEHDECESELQAHOTLRCPEDYTLTLRSPEDLPKTPYTT 780
QY 781 MIPNTLTGMQZHTFNTSGGQNSNINLPHGSHSTRY 816
| | | | |
DB 781 MIPNTLTGMQZHTFNTSGGQNSNINLPHGSHSTRY 816

RESULT 43
US-10-013-922A-375
/ Sequence 375, Application US/10013922A
/ Publication No. US20030195345A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botsstein, David
/ APPLICANT: Resnovers, Inc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Nardo, Inc
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gottlieb, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Guiney, Austin L.
/ APPLICANT: Hillan, Kenneth J
/ APPLICANT: Kijavlin, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paori, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE OF INVENTION: Acids Encoding the Same
/ FILE REFERENCE: P2630P/C91
/ CURRENT APPLICATION NUMBER: US/10/013,922A
/ CURRENT FILING DATE: 2001-10-25
/ PRIOR APPLICATION NUMBER: 09/918585
/ PRIOR FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: 60/062250

/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/064249
/ PRIOR FILING DATE: 1997-11-03
/ PRIOR APPLICATION NUMBER: 60/065311
/ PRIOR FILING DATE: 1997-11-13
/ PRIOR APPLICATION NUMBER: 60/066364
/ PRIOR FILING DATE: 1997-11-21
/ PRIOR APPLICATION NUMBER: 60/077450
/ PRIOR FILING DATE: 1998-03-10
/ PRIOR APPLICATION NUMBER: 60/077632
/ PRIOR FILING DATE: 1998-03-11
/ PRIOR APPLICATION NUMBER: 60/077641
/ PRIOR FILING DATE: 1998-03-11
/ PRIOR APPLICATION NUMBER: 60/077649
/ PRIOR FILING DATE: 1998-03-11
/ PRIOR APPLICATION NUMBER: 60/077791
/ PRIOR FILING DATE: 1998-03-12
/ PRIOR APPLICATION NUMBER: 60/078004
/ PRIOR FILING DATE: 1998-03-13
/ PRIOR APPLICATION NUMBER: 60/078886
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: 60/078936
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: 60/078910
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: 60/078939
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: 60/079294
/ PRIOR FILING DATE: 1998-03-25
/ PRIOR APPLICATION NUMBER: 60/079656
/ PRIOR FILING DATE: 1998-03-26
/ PRIOR APPLICATION NUMBER: 60/079664
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/079663
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/079728
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/079786
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/079920
/ PRIOR FILING DATE: 1998-03-30
/ PRIOR APPLICATION NUMBER: 60/079923
/ PRIOR FILING DATE: 1998-03-30
/ PRIOR APPLICATION NUMBER: 60/080105
/ PRIOR FILING DATE: 1998-03-31
/ PRIOR APPLICATION NUMBER: 60/080107
/ PRIOR FILING DATE: 1998-03-31
/ PRIOR APPLICATION NUMBER: 60/080165
/ PRIOR FILING DATE: 1998-03-31
/ PRIOR APPLICATION NUMBER: 60/080194
/ PRIOR FILING DATE: 1998-03-31
/ PRIOR APPLICATION NUMBER: 60/080327
/ PRIOR FILING DATE: 1998-04-01
/ PRIOR APPLICATION NUMBER: 60/080328
/ PRIOR FILING DATE: 1998-04-01
/ PRIOR APPLICATION NUMBER: 60/080333
/ PRIOR FILING DATE: 1998-04-01
/ PRIOR APPLICATION NUMBER: 60/080334
/ PRIOR FILING DATE: 1998-04-01
/ PRIOR APPLICATION NUMBER: 60/081070
/ PRIOR FILING DATE: 1998-04-08
/ PRIOR APPLICATION NUMBER: 60/081049
/ PRIOR FILING DATE: 1998-04-08
/ PRIOR APPLICATION NUMBER: 60/081071
/ PRIOR FILING DATE: 1998-04-08
/ PRIOR APPLICATION NUMBER: 60/081195
/ PRIOR FILING DATE: 1998-04-08
/ PRIOR APPLICATION NUMBER: 60/081203
/ PRIOR FILING DATE: 1998-04-09
/ PRIOR APPLICATION NUMBER: 60/081229
/ PRIOR FILING DATE: 1998-04-09
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PRIOR APPLICATION NUMBER: 60/081955
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081817
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081815
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081952
 PRIOR FILING DATE: 1998-04-15
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 PRIOR APPLICATION NUMBER: 60/085568
 PRIOR FILING DATE: 1998-04-21
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 PRIOR FILING DATE: 1998-04-22
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 PRIOR APPLICATION NUMBER: 60/083496
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 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/084441
 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/084637
 PRIOR FILING DATE: 1998-05-07
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 PRIOR APPLICATION NUMBER: 60/084640
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084598
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084627
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084643
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/085339
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085338
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085323

	Query Match	Best Local Similarity	100.0%	Score 816	DB 12	Length 816
	Matches	816	Conservative	0	Mismatches	0
					Indels	Gaps
QY	1	MANSNVLZMLTALAIKFTLLDSQAQYVWNTYKIRGRTPLNBIIGFVQYIGVPA	60			
DB	1	MLNSNVLMLTALAIKFTLLDSQAQYVWNTYKIRGRTPLNBIIGFVQYIGVPA	60			
CY	61	SPPTGERFPQPEPPSSWTG:RNTOPAVCPQHLDERSLJHMLPLWFTANDLXTIV	120			
DB	61	SPPTGERFPQPEPPSSWTG:RNTOPAVCPQHLDERSLJHMLPLWFTANDLXTIV	120			
QY	121	QONEDCLYNTIYPTDGNATKKNADITSNRGEDEJHDONSKKPVWVIHGSYME	180			
DB	121	QONEDCLYNTIYPTDGNATKKNADITSNRGEDEJHDONSKKPVWVIHGSYME	180			
CY	181	GTGMNIDGSLIASYGVIVTTINRGLIGFJSTGDAKQNYGLDDOICALZWIENVG	240			
DB	181	GTGMNIDGSLIASYGVIVTTINRGLIGFJSTGDAKQNYGLDDOICALZWIENVG	240			
QY	241	AFGGDPKRVTFSGSAGASCVSLLTSHYSEGLFQKAIOSGRLSSMAVNYQPAKTRI	300			
DB	241	AFGGDPKRVTFSGSAGASCVSLLTSHYSEGLFQKAIOSGRLSSMAVNYQPAKTRI	300			
CY	301	LADRVGCMULTTDMVECLRNKYKELIQOTITPATYHIAFGVIDDVIIPDDQILMEQ	360			
DB	301	LADRVGCMULTTDMVECLRNKYKELIQOTITPATYHIAFGVIDDVIIPDDQILMEQ	360			
QY	361	GEFLNYDGMGVNCGEGLKFDVGVNDXEDGTPDFPVSNFVDNLVGYRBEKDTLRET	420			
DB	361	GEFLNYDGMGVNCGEGLKFDVGVNDXEDGTPDFPVSNFVDNLVGYRBEKDTLRET	420			
CY	421	IKFMYTMDADKENETRRKTIYALFTHOMVAPAVADLAQVSPYFYAFYHHQSEM	480			
DB	421	IKFMYTMDADKENETRRKTIYALFTHOMVAPAVADLAQVSPYFYAFYHHQSEM	480			
QY	481	KPSWADSAHGEVYVYVGIPIWIGTELPSCNFSKNDVLSAVVMTYTNNAKGDPPQVY	540			
DB	481	KPSWADSAHGEVYVYVGIPIWIGTELPSCNFSKNDVLSAVVMTYTNNAKGDPPQVY	540			
CY	541	PODKFHKTRNREFEVYVYVGIPIWIGTELPSCNFSKNDVLSAVVMTYTNNAKGDPPQVY	600			
DB	541	PODKFHKTRNREFEVYVYVGIPIWIGTELPSCNFSKNDVLSAVVMTYTNNAKGDPPQVY	600			
QY	601	NEFOYVSTTKVPPPMSTSFYVSTRSPAKIWTTPRAIIPANNKSHKDPHTKZPED	660			
DB	601	NEFOYVSTTKVPPPMSTSFYVSTRSPAKIWTTPRAIIPANNKSHKDPHTKZPED	660			
CY	661	TTVLLETRKDYSTELSTIYVAGSLLENLIAFALYKCKRSHETRRSPORNTND	720			
DB	661	TTVLLETRKDYSTELSTIYVAGSLLENLIAFALYKCKRSHETRRSPORNTND	720			
QY	721	IAHIONERIMSLQKOLEHDEHCESLQADHDTLRITCPDDYTITLRSPPDDIPLATPTIT	780			
DB	721	IAHIONERIMSLQKOLEHDEHCESLQADHDTLRITCPDDYTITLRSPPDDIPLATPTIT	780			

QY 781 MIPNTLTGMQPLHTFNTFSGGQNSTNLPHGSHSTRV 816
DB 781 MIPNTLTGMQPLHTFNTFSGGQNSTNLPHGSHSTRV 816

RESULT 44

US-10-017-086A-375
Sequence 375, Application US//0017086A
Publication No. US20030194744A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Paoni, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David J.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C4
CURRENT APPLICATION NUMBER: US//10/017,086A
PRIORITY FILING DATE: 2002-04-30
Prior Application removed - See File Wrapper or Paim
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 375
LENGTH: 816
TYPE: PRT
ORGANISM: Homo sapiens
US-10-017-086A-375

Query Match : 100.0%; Score 816; DB 12; Length 816;
Best Local Similarity : 100.0%; Pred. No. C; Idels C; Gaps 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MINSNVLMITAIKFTLIDSOAQYVNTNGKRGSLTPPLNELIGFEVQYLGVPYA 60
DB 1 MINSNVLMITAIKFTLIDSOAQYVNTNGKRGSLTPPLNELIGFEVQYLGVPYA 60
QY 61 SPTGERRFQPPPEPSSWTG:RNTTGFPAVCPQHLERSJ:HMJF:WFAANDJLMTTY 120
DB 61 SPTGERRFQPPPEPSSWTG:RNTTGFPAVCPQHLERSJ:HMJF:WFAANDJLMTTY 120
QY 121 QDNEDC:YLNIYVPTSGANTKXADJITNSDEGEDEJHDQSKKPMVYHGGSYME 180
DB 121 QDNEDC:YLNIYVPTSGANTKXADJITNSDEGEDEJHDQSKKPMVYHGGSYME 180
QY 181 GTGNMIDGSIASGNYVITINRGLGLSTGDOAAXGNYGLDQIOALRWIEENWG 240
DB 181 GTGNMIDGSIASGNYVITINRGLGLSTGDOAAXGNYGLDQIOALRWIEENWG 240
QY 241 AFGGDPKRVTFSGGAGACVSLT:SHYSGLFCKX:ISGTLSSKAVNYOPAKYTRI 300
DB 241 AFGGDPKRVTFSGGAGACVSLT:SHYSGLFCKX:ISGTLSSKAVNYOPAKYTRI 300

QY 301 LADKGCNMJLDTDMVECLSNKXYKELIQCTT:BATYH:AFGPYIDGDVLPDDQILMEQ 360
DB 301 LADKGCNMJLDTDMVECLSNKXYKELIQCTT:BATYH:AFGPYIDGDVLPDDQILMEQ 360
QY 361 GEFNLNYDMLGVNCGEGK:FDG:VVDNEDGYTPNDPDSVSNFVDN:YGPBEGXDTLRET 420
DB 361 GEFNLNYDMLGVNCGEGK:FDG:VVDNEDGYTPNDPDSVSNFVDN:YGPBEGXDTLRET 420
QY 421 IKFMYTDMADKENPETRKTLYA:FTDHWVAPAAADLHAQYSSPTFYAFYHHCOSX 480
DB 421 IKFMYTDMADKENPETRKTLYA:FTDHWVAPAAADLHAQYSSPTFYAFYHHCOSX 480
QY 481 KPSWADSAHGDEVPYFGI:PMIGTELFSCNFSKNDVYLSAVMTYTNFAKTGDPNQPV 540
DB 481 KPSWADSAHGDEVPYFGI:PMIGTELFSCNFSKNDVYLSAVMTYTNFAKTGDPNQPV 540
QY 541 PODTKEITKRNRFEEVMSKYNKDDLYLH:GLKPRVRDHYRATKAFMELVPHLNL 600
DB 541 PODTKEITKRNRFEEVMSKYNKDDLYLH:GLKPRVRDHYRATKAFMELVPHLNL 600
QY 601 NEIFQYVSTTKVPDPDWTSPYGRSPAK:APTTRPATTPANNPKSKDPKGTGED 660
DB 601 NEIFQYVSTTKVPDPDWTSPYGRSPAK:APTTRPATTPANNPKSKDPKGTGED 660
QY 661 TTVLIETGRDYSTELSTVITANGAS:JFLNIAFAAL:YKKDKRHEHTRRSPGRNTTND 720
DB 661 TTVLIETGRDYSTELSTVITANGAS:JFLNIAFAAL:YKKDKRHEHTRRSPGRNTTND 720
QY 721 IAHIONEIMSLQMKOLEHDECESSLOAHOTLRLTCPPDYTLT:RRSPDOLP:WTPNIT 780
DB 721 IAHIONEIMSLQMKOLEHDECESSLOAHOTLRLTCPPDYTLT:RRSPDOLP:WTPNIT 780
QY 781 MIPNTLTGMQPLHTFNTFSGGQNSTNLPHGSHSTRV 816
DB 781 MIPNTLTGMQPLHTFNTFSGGQNSTNLPHGSHSTRV 816

RESULT 45

US-10-145-097A-375
Sequence 375, Application US//10145097A
Publication No. US20030194410A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Paoni, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David J.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C47

CURRENT APPLICATION NUMBER: US/10/145,387A
CURRENT FILING DATE: 2001-03-18
PRIOR APPLICATION NUMBER: 09/918885
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066254
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-21
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-21
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-21
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See file wrapper or FAX.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 375
LENGTH: 816
TYPE: PRT
ORGANISM: Homo sapiens
US-10-145-087A-375
Query Match 100.0%; Score 816; EB 12; Length 816;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNSNVLMITATAIKETLIDSOQYVNTNNGKRGJRTPLPNEILSPVOCYLPYA 60
DB 1 MNSNVLMITATAIKETLIDSOQYVNTNNGKRGJRTPLPNEILSPVOCYLPYA 60
QY 61 SPPTGERFQPPPEPSSWTGIRNTQFAVCPQHLDERSLJHMLTIFALIDTMTTV 120
DB 61 SPPTGERFQPPPEPSSWTGIRNTQFAVCPQHLDERSLJHMLTIFALIDTMTTV 120
QY 121 ODQNECCYLNIVPTDGGATKKNADITSNDRGEDEHDONSKKPPVYIHGSSYME 180
DB 121 ODQNECCYLNIVPTDGGATKKNADITSNDRGEDEHDONSKKPPVYIHGSSYME 180
QY 181 GTGMIDGSLIAGNYVITINRILGILGISTGQAKNGYGLDQIQALWIEVNG 240
DB 181 GTGMIDGSLIAGNYVITINRILGILGISTGQAKNGYGLDQIQALWIEVNG 240
QY 241 AFGSDPKRTIFSGGAGASCVSILTSNHYSEHFOKXIIOSGTALSSMAYVQPAVTEI 300
DB 241 AFGSDPKRTIFSGGAGASCVSILTSNHYSEHFOKXIIOSGTALSSMAYVQPAVTEI 300
QY 301 LADRVGNNMLDTTQVCELRANKYKEICQITIPATYHAFGVIIDGVIPDDPCILMEQ 360
DB 301 LADRVGNNMLDTTQVCELRANKYKEICQITIPATYHAFGVIIDGVIPDDPCILMEQ 360
QY 361 GEFINYDINLVGNGBELKFDGVYCNEDGVITNDPSSVSNVYKULXGTFEKTILAE 420
DB 361 GEFINYDINLVGNGBELKFDGVYCNEDGVITNDPSSVSNVYKULXGTFEKTILAE 420
QY 421 IKFMYTMADEKNEPRTKTLVALFTCHQVAVAPVAAADJAAQGSPTLYFAFHHGQSEN 480
DB 421 IKFMYTMADEKNEPRTKTLVALFTCHQVAVAPVAAADJAAQGSPTLYFAFHHGQSEN 480
QY 481 KPSWADSAHGDDEVYVYFIMIGTELFSQNFSGKDEMAVVMYTWYJPAKTCGQNCQV 540
DB 481 KPSWADSAHGDDEVYVYFIMIGTELFSQNFSGKDEMAVVMYTWYJPAKTCGQNCQV 540
QY 541 POCCKEHTKRNFEFEAMSKYKSCQLYHJGLKPRVDRHYATKVAATWLEVPJLHL 600
DB 541 POCCKEHTKRNFEFEAMSKYKSCQLYHJGLKPRVDRHYATKVAATWLEVPJLHL 600

QY 601 NEIFQVSTTKKPPPMPTSPFYGTRRSAPAKIWPITKRAPAITPANNPKESKDBAKTGPE 660
DB 601 NEIFQVSTTKKPPPMPTSPFYGTRRSAPAKIWPITKRAPAITPANNPKESKDBAKTGPE 660
QY 661 TTUVEFKRDYSTELSTIIVAGASLFLNLILAFALYKKOKRRECHRRPSQORNTND 720
DB 661 TTUVEFKRDYSTELSTIIVAGASLFLNLILAFALYKKOKRRECHRRPSQORNTND 720
QY 721 IAHQNEEIMSLOKQOEHHECESLQAHDTLRLGCFEDTLTPRSFDDIPMTPTIT 780
DB 721 IAHQNEEIMSLOKQOEHHECESLQAHDTLRLGCFEDTLTPRSFDDIPMTPTIT 780
QY 781 MIPNTLQXPLHTFNTFSGQNSTLPHGSHSTRV 816
DB 781 MIPNTLQXPLHTFNTFSGQNSTLPHGSHSTRV 816
RESULT 46
US-10-164-829A-375
Sequence 375, Application US/10164829A
Publication No. US20030294780A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsens, Mary E.
APPLICANT: Goodard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William J.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P263071C28
CURRENT APPLICATION NUMBER: US/10/164,829A
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: 09/918885
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066254
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-21
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-21
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-12

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/ PRIOR APPLICATION NUMBER: 60/077791
/ PRIOR FILING DATE: 1998-03-12
/ Realigning Prior Application data removed - See File Wrapper or P.A.M.
/ NUMBER OF SEQ ID NOS: 624
/ SEQ ID NO: 375
/ LENGTH: 816
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-164-929A-375

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Query Match      100.0%; Score 816; DB 12; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MNSNVLLMTALAKFTLIDSOAQYPVVNTNYGKIRSLRPLPNEILGPEYGLGVFA 60
DB 1 MNSNVLLMTALAKFTLIDSOAQYPVVNTNYGKIRSLRPLPNEILGPEYGLGVFA 60
QY 61 SEPTGERRFOPEPPSSWTGIRNTTQFAVCPQHLDESLHDMPLMFTANLDTMTYV 120
DB 61 SEPTGERRFOPEPPSSWTGIRNTTQFAVCPQHLDESLHDMPLMFTANLDTMTYV 120
QY 121 QONSDCLYNIYVETEGCATKKAADITNSDGEDEBCHIDONSKRPVWYHGGSYME 180
DB 121 QONSDCLYNIYVETEGCATKKAADITNSDGEDEBCHIDONSKRPVWYHGGSYME 180
QY 181 GTGNMIDGSLASVGNVIVITNVALGILGFESTGQQAQKNVGLDQICARWIEENVG 240
DB 181 GTGNMIDGSLASVGNVIVITNVALGILGFESTGQQAQKNVGLDQICARWIEENVG 240
QY 241 AFQSDPKAVITFGSAGASGVSLTLEHVSGLFQKAIJSGGTLSSMAKNOYAKTRI 300
DB 241 AFQSDPKAVITFGSAGASGVSLTLEHVSGLFQKAIJSGGTLSSMAKNOYAKTRI 300
QY 301 LADKYGKMLDTTEVEGECRKKNYKELIQCTTPATYIAEGPVIDEPIEDCPQIMEQ 360
DB 301 LADKYGKMLDTTEVEGECRKKNYKELIQCTTPATYIAEGPVIDEPIEDCPQIMEQ 360
QY 361 GEFLLVYDMLGVNCGEGLKPVGDIYDMEDGYTPNDFESVSNFYDNTXGPEGMDTRET 420
DB 361 GEFLLVYDMLGVNCGEGLKPVGDIYDMEDGYTPNDFESVSNFYDNTXGPEGMDTRET 420
QY 421 IKFMYTMDAKENPETRRKTLVACLTCHQWAPVAVAAJHACVSPFYFAFYHHCSEK 480
DB 421 IKFMYTMDAKENPETRRKTLVACLTCHQWAPVAVAAJHACVSPFYFAFYHHCSEK 480
QY 481 KFSMAASAAGCEVYVFGIPLYGPTLEFSCNFSKNDVYLSAVMTYVTPAKTGDNPQV 540
DB 481 KFSMAASAAGCEVYVFGIPLYGPTLEFSCNFSKNDVYLSAVMTYVTPAKTGDNPQV 540
QY 541 POCFKFHTKNEEEVAVASKVNPFCQYLHIGLKPRGRDHYAKTAAFMLELVFSAHL 600
DB 541 POCFKFHTKNEEEVAVASKVNPFCQYLHIGLKPRGRDHYAKTAAFMLELVFSAHL 600
QY 601 NEIFQVSTTTKVPDPDXTSPFYGRSRSPAKIWPRTKSPATTPANNPHGSCPKTQPED 660
DB 601 NEIFQVSTTTKVPDPDXTSPFYGRSRSPAKIWPRTKSPATTPANNPHGSCPKTQPED 660
QY 661 TVVLETKKRDVSTESVITIAGASLFLNIIAFALYKKRKHETHRRSPSCRNNTND 720
DB 661 TVVLETKKRDVSTESVITIAGASLFLNIIAFALYKKRKHETHRRSPSCRNNTND 720
QY 721 IAHICNEIYSLOMQLEHDEHCELSLOAHDTLRJCPEDYLLTLRRSPDDPLMTPMTIT 780
DB 721 IAHICNEIYSLOMQLEHDEHCELSLOAHDTLRJCPEDYLLTLRRSPDDPLMTPMTIT 780
QY 781 MIENITLGMQPLATENTFSGQGNSTNLPHGSHSTRV 816
DB 781 MIENITLGMQPLATENTFSGQGNSTNLPHGSHSTRV 816

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RESULT 47
US-10-164-929A-375

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/ Sequence 375, Application US/70164929A
/ Publication No. US20030194781A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Bolstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Geiber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Guiney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kijavira, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Pao, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2630P1C36
/ CURRENT FILING DATE: 2001-10-19
/ PRIOR APPLICATION NUMBER: 09/91585
/ PRIOR FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/064249
/ PRIOR FILING DATE: 1997-11-03
/ PRIOR APPLICATION NUMBER: 60/065311
/ PRIOR FILING DATE: 1997-11-13
/ PRIOR APPLICATION NUMBER: 60/066364
/ PRIOR FILING DATE: 1997-11-21
/ PRIOR APPLICATION NUMBER: 60/077450
/ PRIOR FILING DATE: 1998-03-10
/ PRIOR APPLICATION NUMBER: 60/077632
/ PRIOR FILING DATE: 1998-03-11
/ PRIOR APPLICATION NUMBER: 60/077641
/ PRIOR FILING DATE: 1998-03-11
/ PRIOR APPLICATION NUMBER: 60/077649
/ PRIOR FILING DATE: 1998-03-11
/ PRIOR APPLICATION NUMBER: 60/077791
/ PRIOR FILING DATE: 1998-03-12
/ Realigning Prior Application data removed - See File Wrapper or P.A.M.
/ NUMBER OF SEQ ID NOS: 624
/ SEQ ID NO: 375
/ LENGTH: 816
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-164-929A-375

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Query Match      100.0%; Score 816; DB 12; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNSNVLLMTALAKFTLIDSOAQYPVVNTNYGKIRSLRPLPNEILGPEYGLGVFA 60
DB 1 MNSNVLLMTALAKFTLIDSOAQYPVVNTNYGKIRSLRPLPNEILGPEYGLGVFA 60
QY 61 SEPTGERRFOPEPPSSWTGIRNTTQFAVCPQHLDESLHDMPLMFTANLDTMTYV 120

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Db	61	SPTGERRRQPPPPSSMTGIRKTTQPAVCPQHLDBRS.LHDM.LIWTANLTLNTV	120	APPLICANT: Kuo, Sophia S.
Qy	121	OCQEDCLYLNIVPTTEGAGATKKNAADITSDRGEDEDHONSKRPVVYTHGSSVME	180	APPLICANT: Napier, Mary A.
Db	121	OCQEDCLYLNIVPTTEGAGATKKNAADITSDRGEDEDHONSKRPVVYTHGSSVME	180	APPLICANT: Pan, James.
Qy	181	GTGNYDGSILASVGVVITINRGLIGFELSTGQAAXNGLLDQIALRWIEENQ	240	APPLICANT: Paoni, Nicholas F.
Db	181	GTGNYDGSILASVGVVITINRGLIGFELSTGQAAXNGLLDQIALRWIEENQ	240	APPLICANT: Roy, Margaret Ann
Qy	241	AFGGDPKRVTFGSGAGASCUS.LTSHVSEGLFOKALIOSGALSSMAYVQPAKVTI	300	APPLICANT: Shelton, David L.
Db	241	AFGGDPKRVTFGSGAGASCUS.LTSHVSEGLFOKALIOSGALSSMAYVQPAKVTI	300	APPLICANT: Stewart, Timothy A.
Qy	301	LADKVCNMLDTTCVYECJRNKVKELICQTTTFAVHAFGVVIDGVYIPDFQILMEQ	360	APPLICANT: Thomas, Daniel
Db	301	LADKVCNMLDTTCVYECJRNKVKELICQTTTFAVHAFGVVIDGVYIPDFQILMEQ	360	APPLICANT: Williams, P. Mickey
Qy	361	GEFLNYTLMGVNQGEGELKRVGIVNEDGVTPNDFDPSVSNFVDMLYVPEKCTLPET	420	APPLICANT: Wood, William I.
Db	361	GEFLNYTLMGVNQGEGELKRVGIVNEDGVTPNDFDPSVSNFVDMLYVPEKCTLPET	420	APPLICANT: Wood, William I.
Qy	421	IKFMYTDMADKENPEZTRKTLVALFTDHCQVAPAVAADJHAQVGSFTYFVAFVHQCSEK	480	APPLICANT: Wood, William I.
Db	421	IKFMYTDMADKENPEZTRKTLVALFTDHCQVAPAVAADJHAQVGSFTYFVAFVHQCSEK	480	APPLICANT: Wood, William I.
Qy	481	KPSWADSAHGDVPPVYFGIMISGTELFSCNFSKQDVM.SAVVMTYVNTFAKTDGQGV	540	APPLICANT: Wood, William I.
Db	481	KPSWADSAHGDVPPVYFGIMISGTELFSCNFSKQDVM.SAVVMTYVNTFAKTDGQGV	540	APPLICANT: Wood, William I.
Qy	541	PODTEHTKRNPEEFAKSKNPKDOLYHIGLKRVRVCHVATVAFVLEVPILNVL	600	APPLICANT: Wood, William I.
Db	541	PODTEHTKRNPEEFAKSKNPKDOLYHIGLKRVRVCHVATVAFVLEVPILNVL	600	APPLICANT: Wood, William I.
Qy	601	NEIFQVSTTKVPPPMTSPFYGTRSPAKIMPTKRAPIITANNPKSKXDEHKTCPED	660	APPLICANT: Wood, William I.
Db	601	NEIFQVSTTKVPPPMTSPFYGTRSPAKIMPTKRAPIITANNPKSKXDEHKTCPED	660	APPLICANT: Wood, William I.
Qy	661	TVLIEFKRDYSTELSTIYVAGSLFLNLAPALVYKXKDRHETRRPSPQRTTND	720	APPLICANT: Wood, William I.
Db	661	TVLIEFKRDYSTELSTIYVAGSLFLNLAPALVYKXKDRHETRRPSPQRTTND	720	APPLICANT: Wood, William I.
Qy	721	IAMONEEISLQKQEHDSCESLQAHDLTLRCPDVTLLRSPDIPMTENTT	780	APPLICANT: Wood, William I.
Db	721	IAMONEEISLQKQEHDSCESLQAHDLTLRCPDVTLLRSPDIPMTENTT	780	APPLICANT: Wood, William I.
Qy	781	MIPTLTGMQPLHTFNTFSGQNS.TNLPCHSTTRV	846	APPLICANT: Wood, William I.
Db	781	MIPTLTGMQPLHTFNTFSGQNS.TNLPCHSTTRV	846	APPLICANT: Wood, William I.

RESULT 48

US-09-978-299A-375

Sequence 375, Application US/09978299A

Publication No. US20030199435A1

GENERAL INFORMATION:

APPLICANT: Askrenazi, Avi

APPLICANT: Baker, Kevin P.

APPLICANT: Bolstein, David

APPLICANT: Ceenoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Geritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Guiney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijavini, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James.

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Thomas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2636P.C3

CURRENT APPLICATION NUMBER: US/09/978,299A

PRIOR FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/066250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/077450

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632

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PRIOR APPLICATION NUMBER: 60/077641

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PRIOR APPLICATION NUMBER: 60/077649

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PRIOR FILING DATE: 1998-03-31

PRIOR APPLICATION NUMBER: 60/080327

PRIOR FILING DATE: 1998-04-01

PRIOR APPLICATION NUMBER: 60/080328
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PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
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PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/083366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084411
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
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PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0% Score 816; DB 12; Length 816;
Rest Local Similarity 100.0%; Prec. No. 0; Indels 0; Gaps 0;
Matches 816; Conservative 0; Mismatches 0

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121 QONEDCLYLNYYTTEGANTKCAADITSNDGEDEDDHONSKKPVVYIHGSIYME 180
181 GTGNVYIDGILASYNVIVITINVRBLGILGFLSTGDAKAKNYGLDQICLRWIEENVG 240
181 GTGNVYIDGILASYNVIVITINVRBLGILGFLSTGDAKAKNYGLDQICLRWIEENVG 240
241 AFGSDPKRYTIFGSSAGASCVSLLTSHYSECFOKAIGSGTALSSAANVQPAKRYR 300
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361 GEFUNYDMLGNVQGEGLKFVUGIVDNEGCVTPRPFDESVSNFVNLYGYEBSKOTLRET 420
361 GEFUNYDMLGNVQGEGLKFVUGIVDNEGCVTPRPFDESVSNFVNLYGYEBSKOTLRET 420
421 IKFYTDWADKXENPETRRTKTLVALFTDQOMVPAVAADLEAGQSGPTFYFAFYHHCQSEM 480
421 IKFYTDWADKXENPETRRTKTLVALFTDQOMVPAVAADLEAGQSGPTFYFAFYHHCQSEM 480
421 IKFYTDWADKXENPETRRTKTLVALFTDQOMVPAVAADLEAGQSGPTFYFAFYHHCQSEM 480
481 KPSWADSAGDEVVPVFGIPMIGTELFSCNFSKXQVNLAVVMTYTNFAKTGDPNPV 540
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Db 541 POCXFIHFKRNFEEVAMSKYKPKXQYLIHIGLKPVRVDHVRATKVAFMLEQVPEHNL 600
QY 601 NEFFOVSTTKYKPPDMTSFPGYGRSRPAKIMPTTKKALTPANNPKSKPKHKTGPED 660
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QY 661 TVLITKRDYSTELSVTLAVGASLFLFNLAFALYKSKXEPHETRRPSPQRTYTD 720
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QY 721 IAHQNEEINSLMKOLEHDECESLQADHTLRLTGPYTLTLPSPDPCPLXTENTT 780
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QY 781 KIPNLTGMQPLHTFNTFSGGKSTLYLPHGASTRY 816
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RESULT 49
US-09-978-544A-375
Sequence 375, Application US/09978544A
Publication No. US2003019435A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Batoni, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvarole, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlesen, Kary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaud, J. Christopher
APPLICANT: Gutney, Austin L.
APPLICANT: Hillier, Kenneth J.
APPLICANT: Kijavna, Ivar C.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2630P1C3
CURRENT APPLICATION NUMBER: US/09/978,544A
PRIOR FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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Query Match 100.0%; Score 816; DB 12; Length 816;
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DB 61 SPTGERPQPEPPSSWTGIRNTQFAVCPQLDERSLHDLPLMTNLTMTYV 120
QY 121 QDQNEDECLYN-YVPTEDGANTKKNADDITSENGEDEDHDSKXKPVWYIHGSYME 180
DB 121 QDQNEDECLYN-YVPTEDGANTKKNADDITSENGEDEDHDSKXKPVWYIHGSYME 180
QY 181 GTGNMIDGSI-LASGVNVTITINRLGIGLSTGDOAKNGYGLDQIALRMIEENVG 240
DB 181 GTGNMIDGSI-LASGVNVTITINRLGIGLSTGDOAKNGYGLDQIALRMIEENVG 240
QY 241 AFQGDPRKVTTFGSGAGASCYSLTTLSHYSEGLFOKAIIOGSLASSAANVYOPAKYTRI 300
DB 241 AFQGDPRKVTTFGSGAGASCYSLTTLSHYSEGLFOKAIIOGSLASSAANVYOPAKYTRI 300
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DB 301 LADKVGCMNLDITDMVSECLRNKRYKELIOCTITPATYHIAFPVIDGVIPDDPQIMEQ 360
QY 361 GEFLLNYDMLVNGOEGKFEVDSIVENEDGTPNDPSPSVENFNDNLYGREGDTRRET 420
DB 361 GEFLLNYDMLVNGOEGKFEVDSIVENEDGTPNDPSPSVENFNDNLYGREGDTRRET 420
QY 421 IKFMYTDMADKENPEIRRRKTLVAFTDHWVAFVAADLMAOVSPTVFYAFYHRCSEM 480
DB 421 IKFMYTDMADKENPEIRRRKTLVAFTDHWVAFVAADLMAOVSPTVFYAFYHRCSEM 480
QY 481 KESANDASGDEVPRVFGIPKIGTELFSCNFSKQDNLSTVMTYTNFAKTGDPQPV 540
DB 481 KESANDASGDEVPRVFGIPKIGTELFSCNFSKQDNLSTVMTYTNFAKTGDPQPV 540
QY 541 POSTKFHTKPRFEFEVAMSKYNPRDQYLHIGKFRYRDYATKVAFMLEVPHLNL 600
DB 541 POSTKFHTKPRFEFEVAMSKYNPRDQYLHIGKFRYRDYATKVAFMLEVPHLNL 600
QY 601 NEIPQYVSTTKVPPDMTSPFYGRSFRPAKIWTCKRPA.TTPANNPSSHSCDPRKTGED 660
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QY 661 TVLLETQBDYSTEIVTIAVGASLFLNKLAFAALYKXKRREHETRRSPORNTND 720
DB 661 TVLLETQBDYSTEIVTIAVGASLFLNKLAFAALYKXKRREHETRRSPORNTND 720
QY 721 IAHIONEZIMSLOKQLEHDEGES:CAZD7LRITCOPDYLTJRSRSDCIPLMTPTIT 790
DB 721 IAHIONEZIMSLOKQLEHDEGES:CAZD7LRITCOPDYLTJRSRSDCIPLMTPTIT 790
QY 781 MIPNLTGMOPLHTNTSGGQNSNLPHGSTRV 816
DB 781 MIPNLTGMOPLHTNTSGGQNSNLPHGSTRV 816

RESULT 50
US-09-978-665A-375
Sequence 375, Application US/09978665A
Publication No. US20030199437A1
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnuyers, Juc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Palvaroff, Ellen
APPLICANT: Pong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaudi, J. Christopher
APPLICANT: Gurney, Austin J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuc, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David J.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P.C19
CURRENT APPLICATION NUMBER: US/09/975,665A
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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Query Match      100.0%  Score 816:  DB 12:  Length 816:
Best Local Similarity 100.0%  Pred. No. 0:
Matches 816:  Conservative  0:  Mismatches  0:  Indels  0:  Gaps  0:

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DB 241 AFGDPRKRVIIIFSGAGASCVSLTLISHYSEGLFQKAIIGSGTASSAWVYQAKYTR 300
QY 301 LADKVGCMNLDTTMEWCLLNKKYKEIIQOTTPRAYHAFGVIDGVYRDDPQILMEQ 360
DB 301 LADKVGCMNLDTTMEWCLLNKKYKEIIQOTTPRAYHAFGVIDGVYRDDPQILMEQ 360
QY 361 GEFUNYDMGVNGDEGLKFDVGVNDDECVTNCPEFSNSNVNDLXGPECKTJREC 420
DB 361 GEFUNYDMGVNGDEGLKFDVGVNDDECVTNCPEFSNSNVNDLXGPECKTJREC 420
QY 421 IKFWYTDWADKENPETRRKTLVALFTDQWVAEVAADLHAQYGSPTFYAFYHQCSEM 480
DB 421 IKFWYTDWADKENPETRRKTLVALFTDQWVAEVAADLHAQYGSPTFYAFYHQCSEM 480
QY 481 KPSWADSHGDEGVYVGIIMIGPTELFSNBSKNDVMASAVMTYWTWFAKTGDPNPV 540
DB 481 KPSWADSHGDEGVYVGIIMIGPTELFSNBSKNDVMASAVMTYWTWFAKTGDPNPV 540
QY 541 PDKTKFHTKXNREFEVAMSKYNEKQQLYHIGLKPVEDRHYRATKVAEMLVLPHJNL 600
DB 541 PDKTKFHTKXNREFEVAMSKYNEKQQLYHIGLKPVEDRHYRATKVAEMLVLPHJNL 600
QY 601 NEIFQVSTTKVPPDMTGFPPYSTRSPAKTPTTKRPAITPANNPKSKDPKTKGPD 660
DB 601 NEIFQVSTTKVPPDMTGFPPYSTRSPAKTPTTKRPAITPANNPKSKDPKTKGPD 660
QY 661 TVVLIETKRDYSTELSTIYVAGASLFLNLTALFAAYKKCKRHHETRRSPQRTTND 720
DB 661 TVVLIETKRDYSTELSTIYVAGASLFLNLTALFAAYKKCKRHHETRRSPQRTTND 720
QY 721 IAHIONEISLQWKCIEHBECESLCAHDTLPLTCEPDTTTLRRSPDDIPLMTNTIT 780
DB 721 IAHIONEISLQWKCIEHBECESLCAHDTLPLTCEPDTTTLRRSPDDIPLMTNTIT 780
QY 781 MIPNLTSCPLFTFNTFSGGNSINLPHGSHSTRV 816
DB 781 MIPNLTSCPLFTFNTFSGGNSINLPHGSHSTRV 816

RESULT 51
US-09-978-802A-375
Sequence 375, Application US/0997802A
Publication No. US20030199674A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geider, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gueney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kluvin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pat, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

```

FILE REFERENCE: P2630P1C20
CURRENT FILING DATE: 2001-10-16
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
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PRIOR APPLICATION NUMBER: 60/077791
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PRIOR FILING DATE: 1998-05-07

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? PRIOR APPLICATION NUMBER: 60/084643
? PRIOR FILING DATE: 1998-05-07
? PRIOR APPLICATION NUMBER: 60/085339
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? PRIOR APPLICATION NUMBER: 60/085573
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085704
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085697

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Query Match 100.0%; Score 816; DB 12; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MUNSVMMLTALAKPTLIDSOAYPVVNTYGRKRGRLTPEILGVEGYLAPVA 60
DB 1 MUNSVMMLTALAKPTLIDSOAYPVVNTYGRKRGRLTPEILGVEGYLAPVA 60
QY 61 SPTGERRFPQPEPSSWTGIRNTTQFAVCPQGLERSLJHMLPMTANDTMTYV 120
DB 61 SPTGERRFPQPEPSSWTGIRNTTQFAVCPQGLERSLJHMLPMTANDTMTYV 120
QY 121 QONEDCLYLNYYVTEOGANTKKAADJTSNDGEPEDHNDQSKRPVYIHGGVYE 180
DB 121 QONEDCLYLNYYVTEOGANTKKAADJTSNDGEPEDHNDQSKRPVYIHGGVYE 180
QY 181 GTGMMFGSILASVGNVYVITINVELGIGLSTSCAKKNGVLLDQIALKKEWNG 240
DB 181 GTGMMFGSILASVGNVYVITINVELGIGLSTSCAKKNGVLLDQIALKKEWNG 240
QY 241 AFGGPKRTIFGSGAGASVSLTSHVSGGLCKNIGSGTSSMANYOAKYTRI 300
DB 241 AFGGPKRTIFGSGAGASVSLTSHVSGGLCKNIGSGTSSMANYOAKYTRI 300
QY 301 LADKVCNMEDTTCWECLRNKNYKELIQGITATATVAFGPVJDDGVJDDPQILMEQ 360
DB 301 LADKVCNMEDTTCWECLRNKNYKELIQGITATATVAFGPVJDDGVJDDPQILMEQ 360
QY 361 GEFVYVJLVGNVQEGIKFVDGIVCNEDGYTPNDPESVSNVDNNGVPEKCTJRET 420
DB 361 GEFVYVJLVGNVQEGIKFVDGIVCNEDGYTPNDPESVSNVDNNGVPEKCTJRET 420
QY 421 IKFVYTCMAKCKENPSTRKKTUVALFTTHQVAFVAAADLNAVQSPSTYFAVFNHCOSEM 480
DB 421 IKFVYTCMAKCKENPSTRKKTUVALFTTHQVAFVAAADLNAVQSPSTYFAVFNHCOSEM 480
QY 481 KPSWADSAHGDVPPVFGIEMGPTELSCNPSKQDVLSAVCTVTWTPAKTGDNQPV 540
DB 481 KPSWADSAHGDVPPVFGIEMGPTELSCNPSKQDVLSAVCTVTWTPAKTGDNQPV 540
QY 541 PDDTFFHTKPRFEFVAVMSKYNPCDQYCYJHGLKPRVADHYATKTAFAVLELPHLJNT 600
DB 541 PDDTFFHTKPRFEFVAVMSKYNPCDQYCYJHGLKPRVADHYATKTAFAVLELPHLJNT 600
QY 601 NEIFQVSTTTKVPDPDXTSPFYGIRASPAKIWTNKAETTPANNPESGDPKXTPEP 660
DB 601 NEIFQVSTTTKVPDPDXTSPFYGIRASPAKIWTNKAETTPANNPESGDPKXTPEP 660
QY 661 TVLIETKRDYSTEJSTIAVGSLLFNLIAFALALYKCKRKHETHRSSPQRNTINC 720

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DB 661 TVLIETKRDYSTEJSTIAVGSLLFNLIAFALALYKCKRKHETHRSSPQRNTINC 720
QY 721 IAH1QNEEIMSLOKQLEHDECEESQADHTLRLTCTPPPYTLTRRSPDIPLXPNIT 780
DB 721 IAH1QNEEIMSLOKQLEHDECEESQADHTLRLTCTPPPYTLTRRSPDIPLXPNIT 780
QY 781 MIPNLTGMPLEHTEPFGSGONSTYLPCHSTTRV 816
DB 781 MIPNLTGMPLEHTEPFGSGONSTYLPCHSTTRV 816

RESULT 52
US-10-013-924A-375
? Sequence 375, Application US/10013924A
? Publication No. US20030199021A1
? GENERAL INFORMATION:
? APPLICANT: Ashkenazi, Avi
? APPLICANT: Baker Kevin P.
? APPLICANT: Bostein, David
? APPLICANT: Desnoyers, Luc
? APPLICANT: Eaton, Dan
? APPLICANT: Ferrara, Napoleon
? APPLICANT: Filvaroff, Ellen
? APPLICANT: Fong, Sherman
? APPLICANT: Gao, Wei-Qiang
? APPLICANT: Gerber, Hanspeter
? APPLICANT: Gerritsen, Mary E.
? APPLICANT: Goddard, Audrey E.
? APPLICANT: Godowski, Paul J.
? APPLICANT: Grimaldi, J. Christopher
? APPLICANT: Guiney, Austin L.
? APPLICANT: Hillan, Kenneth J.
? APPLICANT: Kiljavin, Ivar J.
? APPLICANT: Kuo, Sophia S.
? APPLICANT: Nadler, Mary A.
? APPLICANT: Pan, James
? APPLICANT: Paoni, Nicholas F.
? APPLICANT: Roy, Margaret Ann
? APPLICANT: Shelton, David L.
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tumas, Daniel
? APPLICANT: Williams, P. Mickey
? APPLICANT: Wood, William I.
? TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
? TITLE OF INVENTION: Acids Encoding the Same
? FILE REFERENCE: P2630P1C76
? CURRENT APPLICATION NUMBER: US/10/013, 924A
? PRIOR FILING DATE: 2002-12-10
? PRIOR APPLICATION NUMBER: 09/518585
? PRIOR FILING DATE: 2001-07-30
? PRIOR APPLICATION NUMBER: 60/062250
? PRIOR FILING DATE: 1997-10-17
? PRIOR APPLICATION NUMBER: 60/064249
? PRIOR FILING DATE: 1997-11-03
? PRIOR APPLICATION NUMBER: 60/065311
? PRIOR FILING DATE: 1997-11-13
? PRIOR APPLICATION NUMBER: 60/066364
? PRIOR FILING DATE: 1997-11-21
? PRIOR APPLICATION NUMBER: 60/077450
? PRIOR FILING DATE: 1998-03-10
? PRIOR APPLICATION NUMBER: 60/077632
? PRIOR FILING DATE: 1998-03-11
? PRIOR APPLICATION NUMBER: 60/077641
? PRIOR FILING DATE: 1998-03-11
? PRIOR APPLICATION NUMBER: 60/077649
? PRIOR FILING DATE: 1998-03-11
? PRIOR APPLICATION NUMBER: 60/077791
? PRIOR FILING DATE: 1998-03-12
? PRIOR FILING DATE: 1998-03-12
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 624
? SEQ ID NO 375
? LENGTH: 816

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TYPE: PRT
ORGANISM: Homo sapiens
US-10-013-924A-375

Query Match      100.0%; Score 816; DB 12; Length 846;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MNSNVLLMLTALAIFKFLIDSOAQYPVNTNYSKIRGLRPLPNEILIGVEQYLGYPYA 63
DB 1 MNSNVLLMLTALAIFKFLIDSOAQYPVNTNYSKIRGLRPLPNEILIGVEQYLGYPYA 63
CY 61 SPTGERPFPQPEPSSKGTGINTQFAPACPOHLEDESLHMLPTEFNLDITMTYV 123
DB 61 SPTGERPFPQPEPSSKGTGINTQFAPACPOHLEDESLHMLPTEFNLDITMTYV 123
CY 121 QQWEDCLVLTNYVTEEGANTKKNAADITSDSGEDFDHDSKXKPMVYVIGSSYME 163
DB 121 QQWEDCLVLTNYVTEEGANTKKNAADITSDSGEDFDHDSKXKPMVYVIGSSYME 163
CY 121 GTANVIGDSIASIGNNVYVITINRGLGLSTSTGDAKAKRYLLDQICALLRIEENVG 243
DB 121 GTANVIGDSIASIGNNVYVITINRGLGLSTSTGDAKAKRYLLDQICALLRIEENVG 243
CY 181 GTGNVIGDSIASIGNNVYVITINRGLGLSTSTGDAKAKRYLLDQICALLRIEENVG 243
DB 181 GTGNVIGDSIASIGNNVYVITINRGLGLSTSTGDAKAKRYLLDQICALLRIEENVG 243
CY 241 AFGSDPKRVTTFSGAGAGCYSLTCSHYSSECFKXATIGSTALSSKAAVYCRAXYTRI 300
DB 241 AFGSDPKRVTTFSGAGAGCYSLTCSHYSSECFKXATIGSTALSSKAAVYCRAXYTRI 300
CY 301 LADKVGCMVLDITTMWELRNKRYEELQCTITPAVYAFAPVYEDGVIPDDPQILMEQ 360
DB 301 LADKVGCMVLDITTMWELRNKRYEELQCTITPAVYAFAPVYEDGVIPDDPQILMEQ 360
CY 361 GEFLLNYDMLGNGQESCKFYDGIYDNDGVTPRDFDSNPNFQNLKYGREGDILSEI 423
DB 361 GEFLLNYDMLGNGQESCKFYDGIYDNDGVTPRDFDSNPNFQNLKYGREGDILSEI 423
CY 421 IKFMYTCMAKXENPTEKRTIYALFTDHWVAPAAVLAHQQVSPYFYVAFYHCGSEM 483
DB 421 IKFMYTCMAKXENPTEKRTIYALFTDHWVAPAAVLAHQQVSPYFYVAFYHCGSEM 483
CY 481 KPSWADSAHGDVPPVFSIPIMGPLELSCNFSKQDVLAHVMTWTNFAKIDSPQPV 540
DB 481 KPSWADSAHGDVPPVFSIPIMGPLELSCNFSKQDVLAHVMTWTNFAKIDSPQPV 540
CY 541 PODTKFIHTKPRFEVAVMSKYNPKDQYLHIGLPRVRDHYRATKVAFWLELVPHLNL 600
DB 541 PODTKFIHTKPRFEVAVMSKYNPKDQYLHIGLPRVRDHYRATKVAFWLELVPHLNL 600
CY 601 NEIFCYVSTTTKVPPEKTSPPYGRSRPAKIMPTTKAPATTPANNPQHSKDPKGTGED 660
DB 601 NEIFCYVSTTTKVPPEKTSPPYGRSRPAKIMPTTKAPATTPANNPQHSKDPKGTGED 660
CY 661 TTVLLETGVDSTELSVTIANGASLLFNILAPALVYKKKRRHETRRSPQNTTND 723
DB 661 TTVLLETGVDSTELSVTIANGASLLFNILAPALVYKKKRRHETRRSPQNTTND 723
CY 721 IAHIONEELMSQKQLEHDEHCESELCAHDTLRCLCEPDYTLTARSPDQJELMTPTTIT 783
DB 721 IAHIONEELMSQKQLEHDEHCESELCAHDTLRCLCEPDYTLTARSPDQJELMTPTTIT 783
CY 781 MIPNTLTGMQPLHTENTFSGGNSNINLPHGHSITRV 816
DB 781 MIPNTLTGMQPLHTENTFSGGNSNINLPHGHSITRV 816

```

```

APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferreira, Napoleon
APPLICANT: Filvarcoff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillen, Kenneth C.
APPLICANT: Kijavon, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C74
CURRENT APPLICATION NUMBER: US/0/020,445A
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/362250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27

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RESULT 53
US-10-020-445A-375
Sequence 375, Application US/10020445A
Publication No. US20030138994A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David

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/ PRIOR APPLICATION NUMBER: 60/079920
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/ PRIOR APPLICATION NUMBER: 60/079923
/ PRIOR FILING DATE: 1998-03-30
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/ PRIOR FILING DATE: 1998-03-31
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/ PRIOR FILING DATE: 1998-03-31
/ PRIOR APPLICATION NUMBER: 60/080165
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/ PRIOR FILING DATE: 1998-04-15
/ PRIOR APPLICATION NUMBER: 60/081617
/ PRIOR FILING DATE: 1998-04-15
/ PRIOR APPLICATION NUMBER: 60/081819
/ PRIOR FILING DATE: 1998-04-15
/ PRIOR APPLICATION NUMBER: 60/081952
/ PRIOR FILING DATE: 1998-04-15
/ PRIOR APPLICATION NUMBER: 60/081638
/ PRIOR FILING DATE: 1998-04-15
/ PRIOR APPLICATION NUMBER: 60/082563
/ PRIOR FILING DATE: 1998-04-21
/ PRIOR APPLICATION NUMBER: 60/082569
/ PRIOR FILING DATE: 1998-04-21
/ PRIOR APPLICATION NUMBER: 60/082704
/ PRIOR FILING DATE: 1998-04-22
/ PRIOR APPLICATION NUMBER: 60/082804
/ PRIOR FILING DATE: 1998-04-22
/ PRIOR APPLICATION NUMBER: 60/082700
/ PRIOR FILING DATE: 1998-04-22
/ PRIOR APPLICATION NUMBER: 60/082797
/ PRIOR FILING DATE: 1998-04-22
/ PRIOR APPLICATION NUMBER: 60/082795
/ PRIOR FILING DATE: 1998-04-23
/ PRIOR APPLICATION NUMBER: 60/083336
/ PRIOR FILING DATE: 1998-04-27
/ PRIOR APPLICATION NUMBER: 60/083322
/ PRIOR FILING DATE: 1998-04-25
/ PRIOR APPLICATION NUMBER: 60/083392
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083495
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083496
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083499
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083545
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083554
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083558

/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083559
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083500
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083742
/ PRIOR FILING DATE: 1998-04-30
/ PRIOR APPLICATION NUMBER: 60/084366
/ PRIOR FILING DATE: 1998-05-05
/ PRIOR APPLICATION NUMBER: 60/084414
/ PRIOR FILING DATE: 1998-05-06
/ PRIOR APPLICATION NUMBER: 60/084441
/ PRIOR FILING DATE: 1998-05-06
/ PRIOR APPLICATION NUMBER: 60/084637
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084639
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084640
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084598
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084600
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084627
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084643
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/085339
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085338
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085323
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085582
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085700
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085669
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085579
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085580
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085573
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085704
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0% Score 816; DB 12; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MNSNVLMITAIATFTTIDSOAQPVVNTYKTRGRTPLNEILGPVEQYLSVPA 60
Db 1 MNSNVLMITAIATFTTIDSOAQPVVNTYKTRGRTPLNEILGPVEQYLSVPA 60
Cy 61 SPTGREROPPEPESEKWTGINTTOFAVCCGCHLDERSLDHMLPIWFTANLDTMTYV 120
Db 61 SPTGREROPPEPESEKWTGINTTOFAVCCGCHLDERSLDHMLPIWFTANLDTMTYV 120
Cy 121 QDQNEDELYINIVPTPEDGANTKCNADITSDRGEDDIDQNSKKPVVYIHGGSYWE 180
Db 121 QDQNEDELYINIVPTPEDGANTKCNADITSDRGEDDIDQNSKKPVVYIHGGSYWE 180
Cy 181 GTGNMIDGSLASYGVNVIYTTINRIGLIGFLSTGCAKKNVGLLDQCALRMIEENVG 240
Db 181 GTGNMIDGSLASYGVNVIYTTINRIGLIGFLSTGCAKKNVGLLDQCALRMIEENVG 240
Cy 241 AFGGDPKRVITIFSGAGASCVSLLTSHYSEGAFQYAIQSGTALSSMAVNYQPAKYTRI 300
Db 241 AFGGDPKRVITIFSGAGASCVSLLTSHYSEGAFQYAIQSGTALSSMAVNYQPAKYTRI 300

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QY 301 LADKVGCMMLDTTDMTECLRNKNYKELIQCTTPATYHIAFGSVIDGVIPDDPQIMEQ 360
DB 301 LADKVGCMMLDTTDMTECLRNKNYKELIQCTTPATYHIAFGSVIDGVIPDDPQIMEQ 360
QY 361 GEFLLNDIMLVNNOGEGELKFDVIGVNDGCVTNNPDFSUSNVDMUYGVPEKQDLRET 420
DB 361 GEFLLNDIMLVNNOGEGELKFDVIGVNDGCVTNNPDFSUSNVDMUYGVPEKQDLRET 420
QY 421 IKFMYTDMADKENPETRKTLLVALFTEHQVAPAVAADLHAQGSPTFYAFYHHCQSEV 480
DB 421 IKFMYTDMADKENPETRKTLLVALFTEHQVAPAVAADLHAQGSPTFYAFYHHCQSEV 480
QY 481 KPSWADSAHGDDEVYVFGIPIMIGPTELFSCNFSKNDVMSAVVMTWKNFAKTGDNQPV 540
DB 481 KPSWADSAHGDDEVYVFGIPIMIGPTELFSCNFSKNDVMSAVVMTWKNFAKTGDNQPV 540
QY 541 PODTKFHTKPNRFEVAVMSKYNPKDCLYHIGKPRVDHRYATKVAFLVPLHLNL 600
DB 541 PODTKFHTKPNRFEVAVMSKYNPKDCLYHIGKPRVDHRYATKVAFLVPLHLNL 600
QY 601 NEIFQVYSTTKVPFPPDMTSFPYGRSPAKIMPTTRPAITFANPKSKDPPKCTGPD 660
DB 601 NEIFQVYSTTKVPFPPDMTSFPYGRSPAKIMPTTRPAITFANPKSKDPPKCTGPD 660
QY 661 TTVLIEFKQYSTELSTYIAVGASLFLFLNLAFPAALYKKCKRHEHTRRSPQNTITD 720
DB 661 TTVLIEFKQYSTELSTYIAVGASLFLFLNLAFPAALYKKCKRHEHTRRSPQNTITD 720
QY 721 IAHIONEELMSLOMKQJLHDEHCESLQAHDTLTCPPDYTLTLRRSPDDPLMTPNIT 780
DB 721 IAHIONEELMSLOMKQJLHDEHCESLQAHDTLTCPPDYTLTLRRSPDDPLMTPNIT 780
QY 781 MIPNTLTGQPLHTNTFSGGNSNLTPLHGSTTRV 916
DB 781 MIPNTLTGQPLHTNTFSGGNSNLTPLHGSTTRV 916

RESULT 54
US-10-017-094A-375
; Sequence 375, Application US/10017084A
; Publication No. US20030203402A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Socsteins, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Batson, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gogowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gunney, Austin L.
; APPLICANT: Hillan, Kenneth C.
; APPLICANT: Kijavitt, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Pacini, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William J.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C66
; CURRENT APPLICATION NUMBER: US/10-017-084A

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; CURRENT FILING DATE: 2002-04-30
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 375
; LENGTH: 816
; TYPE: FAT
; ORGANISM: Homo sapiens
US-10-017-084A-375

Query Match 100.0%; Score 816; DB 12; Length 816;
Best Local Similarity 100.0%; Pred. No. C;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MUNSVMILMTALAIKFTLIDSOAQYPVWNTYKINQLRFLFNEILGVECYLGVPA 60
DB 1 MUNSVMILMTALAIKFTLIDSOAQYPVWNTYKINQLRFLFNEILGVECYLGVPA 60
QY 61 SPTGERFOPPEPSSWTGIRNTGPAACVCPHLDRSLJHDMPLMFTNTLTMTYV 120
DB 61 SPTGERFOPPEPSSWTGIRNTGPAACVCPHLDRSLJHDMPLMFTNTLTMTYV 120
QY 121 QDQNEDECLYLNIVPTEDGANTKKKADDTISNDRGEDDHCQSKKPVWYHGSSEYE 180
DB 121 QDQNEDECLYLNIVPTEDGANTKKKADDTISNDRGEDDHCQSKKPVWYHGSSEYE 180
QY 181 GTKNKIDGSIASGVNIVITNRLGIGLSGQPAKGNFGLDQICALRIEENVG 240
DB 181 GTKNKIDGSIASGVNIVITNRLGIGLSGQPAKGNFGLDQICALRIEENVG 240
QY 241 AFGDPRKVTIFSGGAGSCVSLTSGVSGFLGCKTSSQGTLSGSAVAYGPARYRI 300
DB 241 AFGDPRKVTIFSGGAGSCVSLTSGVSGFLGCKTSSQGTLSGSAVAYGPARYRI 300
QY 301 LADKVGCMMLDTTDMTECLRNKNYKELIQCTTPATYHIAFGSVIDGVIPDDPQIMEQ 360
DB 301 LADKVGCMMLDTTDMTECLRNKNYKELIQCTTPATYHIAFGSVIDGVIPDDPQIMEQ 360
QY 361 GEFLLNDIMLVNNOGEGELKFDVIGVNDGCVTNNPDFSUSNVDMUYGVPEKQDLRET 420
DB 361 GEFLLNDIMLVNNOGEGELKFDVIGVNDGCVTNNPDFSUSNVDMUYGVPEKQDLRET 420
QY 421 IKFMYTDMADKENPETRKTLLVALFTEHQVAPAVAADLHAQGSPTFYAFYHHCQSEV 480
DB 421 IKFMYTDMADKENPETRKTLLVALFTEHQVAPAVAADLHAQGSPTFYAFYHHCQSEV 480
QY 481 KPSWADSAHGDDEVYVFGIPIMIGPTELFSCNFSKNDVMSAVVMTWKNFAKTGDNQPV 540
DB 481 KPSWADSAHGDDEVYVFGIPIMIGPTELFSCNFSKNDVMSAVVMTWKNFAKTGDNQPV 540
QY 541 PODTKFHTKPNRFEVAVMSKYNPKDCLYHIGKPRVDHRYATKVAFLVPLHLNL 600
DB 541 PODTKFHTKPNRFEVAVMSKYNPKDCLYHIGKPRVDHRYATKVAFLVPLHLNL 600
QY 601 NEIFQVYSTTKVPFPPDMTSFPYGRSPAKIMPTTRPAITFANPKSKDPPKCTGPD 660
DB 601 NEIFQVYSTTKVPFPPDMTSFPYGRSPAKIMPTTRPAITFANPKSKDPPKCTGPD 660
QY 661 TTVLIEFKQYSTELSTYIAVGASLFLFLNLAFPAALYKKCKRHEHTRRSPQNTITD 720
DB 661 TTVLIEFKQYSTELSTYIAVGASLFLFLNLAFPAALYKKCKRHEHTRRSPQNTITD 720
QY 721 IAHIONEELMSLOMKQJLHDEHCESLQAHDTLTCPPDYTLTLRRSPDDPLMTPNIT 780
DB 721 IAHIONEELMSLOMKQJLHDEHCESLQAHDTLTCPPDYTLTLRRSPDDPLMTPNIT 780
QY 781 MIPNTLTGQPLHTNTFSGGNSNLTPLHGSTTRV 916
DB 781 MIPNTLTGQPLHTNTFSGGNSNLTPLHGSTTRV 916

RESULT 55
US-10-017-085A-375
; Sequence 375, Application US/10017085A

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/ Publication No. US20030204055A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Boesstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kijavir, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Acids and Transmembrane polypeptides and Nucleic
/ TITLE OF INVENTION: Acids Encoding the Same
/ FILE REFERENCE: P2630P1C73
/ CURRENT APPLICATION NUMBER: US/10/017.085A
/ PRIOR FILING DATE: 2002-04-30
/ Prior Application removed - File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 624
/ SEQ ID NO 375
/ LENGTH: 816
/ TYPE: prt
/ ORGANISM: Homo sapiens
/ US-10-017-085A-375

Query Match      100.0% Score 816; DB 12; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MUNSVMKLTALAKFPIIISQAOYFVNTNRYGKIRLKPENEGVECYLSPYA 60
DB 1 MUNSVMKLTALAKFPIIISQAOYFVNTNRYGKIRLKPENEGVECYLSPYA 60
QY 61 SPTGRRPQPEPPSSSWTGIINTTQFANVCCCHLDFSLJHDMLPZMFMTANLDTLTYY 123
DB 61 SPTGRRPQPEPPSSSWTGIINTTQFANVCCCHLDFSLJHDMLPZMFMTANLDTLTYY 123
QY 121 CQNEDECLVNIYVTEDEANTKKNADDTISNDSCEDEDHONSKKPVMYIHGSGYME 190
DB 121 CQNEDECLVNIYVTEDEANTKKNADDTISNDSCEDEDHONSKKPVMYIHGSGYME 190
QY 122 CQNEDECLVNIYVTEDEANTKKNADDTISNDSCEDEDHONSKKPVMYIHGSGYME 180
DB 122 CQNEDECLVNIYVTEDEANTKKNADDTISNDSCEDEDHONSKKPVMYIHGSGYME 180
QY 131 GTGNTDGSILASVGNVYITINRYLGLGFLSTSCQAKKNYGLDIOIALKTEENVG 240
DB 131 GTGNTDGSILASVGNVYITINRYLGLGFLSTSCQAKKNYGLDIOIALKTEENVG 240
QY 181 GTGNTDGSILASVGNVYITINRYLGLGFLSTSCQAKKNYGLDIOIALKTEENVG 240
DB 181 GTGNTDGSILASVGNVYITINRYLGLGFLSTSCQAKKNYGLDIOIALKTEENVG 240
QY 241 AFGGPKRYVTFGGSGAGASVSLTLTSHVSEGLFQKALIGSTALSSAAVYQAKYTRI 300
DB 241 AFGGPKRYVTFGGSGAGASVSLTLTSHVSEGLFQKALIGSTALSSAAVYQAKYTRI 300
QY 301 LADKVGCMMLDTTDMVECLRNKRYKELIQOTTPATYHAGSPVJDSGVIPDDPQILYEO 360
DB 301 LADKVGCMMLDTTDMVECLRNKRYKELIQOTTPATYHAGSPVJDSGVIPDDPQILYEO 360
QY 361 GEFUNVDIMLGVNCQEGKFEVDGIVDNEDGVTPNDFEVSVPVNLGVYEGKCTLRET 420
DB 361 GEFUNVDIMLGVNCQEGKFEVDGIVDNEDGVTPNDFEVSVPVNLGVYEGKCTLRET 420
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QY 421 IKFMYTCWADKENPEBRKLTVALFTDQWAVPAADLHAQYGSPTYFAFYHHGQSEM 480
DB 421 IKFMYTCWADKENPEBRKLTVALFTDQWAVPAADLHAQYGSPTYFAFYHHGQSEM 480
QY 481 KPSWADSAGSEVPYVFGIPVIGTETLFCNCFKNDVMSAVVYTYTNTAKTGDNPQV 540
DB 481 KPSWADSAGSEVPYVFGIPVIGTETLFCNCFKNDVMSAVVYTYTNTAKTGDNPQV 540
QY 541 FQCTFEHTRKPRFEVYVMSKYNKQDLYHIGKPRVDRHTATKAFWLEJYVPHNL 600
DB 541 FQCTFEHTRKPRFEVYVMSKYNKQDLYHIGKPRVDRHTATKAFWLEJYVPHNL 600
QY 601 NEIFGVSTTKVPPDMTSPFYGRSPAKIMPTKRPAITPANNPKSKDPKHTGPD 660
DB 601 NEIFGVSTTKVPPDMTSPFYGRSPAKIMPTKRPAITPANNPKSKDPKHTGPD 660
QY 661 TTULIETKRDYSTELSVTANGASLLFLNLAFAALYKKCKRKHETRRSPQKNTND 720
DB 661 TTULIETKRDYSTELSVTANGASLLFLNLAFAALYKKCKRKHETRRSPQKNTND 720
QY 721 IAHIONEIMSCKMKOLEHDECSLOADTLRLCTCPDYTLTLRSPPDIPLMTPKTT 780
DB 721 IAHIONEIMSCKMKOLEHDECSLOADTLRLCTCPDYTLTLRSPPDIPLMTPKTT 780
QY 781 MIPNTLTOMOLHRTNFTSGGQNSTNLPHGSTRV 816
DB 781 MIPNTLTOMOLHRTNFTSGGQNSTNLPHGSTRV 816

RESULT 56
US-10-017-085A-375
/ Sequence 375, Application US/10017081A
/ Publication No. US20030049684A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Boesstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kijavir, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Acids and Transmembrane polypeptides and Nucleic
/ TITLE OF INVENTION: Acids Encoding the Same
/ FILE REFERENCE: P2630P1C69
/ CURRENT APPLICATION NUMBER: US/10/017.081A
/ PRIOR FILING DATE: 2002-04-30
/ Prior Application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 624
/ SEQ ID NO 375
/ LENGTH: 816
/ TYPE: prt
/ ORGANISM: Homo sapiens
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US-10-017-081a-375

Query Match 100.0%; Score 816; DB 15; Length 816;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MLNSNVLMTLALAIKFTLIDSOAYPVVNTNGIKRGLETFLEINELGVEGYLGVPYA 63
DB 1 MLNSNVLMTLALAIKFTLIDSOAYPVVNTNGIKRGLETFLEINELGVEGYLGVPYA 63
QY 61 SPTGERRFOPEPPSSMTGIRNTTQFAAVCPQHLDESLJHDMPLWFTANLDTLMTYV 120
DB 61 SPTGERRFOPEPPSSMTGIRNTTQFAAVCPQHLDESLJHDMPLWFTANLDTLMTYV 120
QY 121 QONEDCLYNTIYVTEEGANTKKKADDTISNDGDEEDIDHDSKKPVMVYIHGGSYME 180
DB 121 QONEDCLYNTIYVTEEGANTKKKADDTISNDGDEEDIDHDSKKPVMVYIHGGSYME 180
QY 181 GTGNMIDGSIILASGVNIVITINRGLGFLSTGDAKAGNYGLDQIQALRWIEENVG 240
DB 181 GTGNMIDGSIILASGVNIVITINRGLGFLSTGDAKAGNYGLDQIQALRWIEENVG 240
QY 241 AFGADPRKRVITFSSGAGASCYSLTLTSHVSEGLFOKALIGSGTALSQAVNYGFAVYTRI 300
DB 241 AFGADPRKRVITFSSGAGASCYSLTLTSHVSEGLFOKALIGSGTALSQAVNYGFAVYTRI 300
QY 301 LADRYGCMCLDTTDMVEELRNKYEKLCQITTPATVHAFGPIIDCVIPDDQIIMEQ 360
DB 301 LADRYGCMCLDTTDMVEELRNKYEKLCQITTPATVHAFGPIIDCVIPDDQIIMEQ 360
QY 361 GEELNYDINKGVNGEGIKFYDGLVNDGDVTPNDEPRSSNFRNLYGSEKCTIREE 420
DB 361 GEELNYDINKGVNGEGIKFYDGLVNDGDVTPNDEPRSSNFRNLYGSEKCTIREE 420
QY 421 IKFYTDMADKENETPRKTLVALFTDCHQWAPAAVADLHCQSPFYFAFHHCSSEY 480
DB 421 IKFYTDMADKENETPRKTLVALFTDCHQWAPAAVADLHCQSPFYFAFHHCSSEY 480
QY 481 KPSWADSAHGDEVYVYVGIEMIGTBELFCSCFNQNDVMSLVMTVYTNPAKTGDPNPV 540
DB 481 KPSWADSAHGDEVYVYVGIEMIGTBELFCSCFNQNDVMSLVMTVYTNPAKTGDPNPV 540
QY 541 POCFKFHTKPRREEEYAKSKYNPKDCLYJHGLKPRRHYVATKAFPLEYVPHANL 600
DB 541 POCFKFHTKPRREEEYAKSKYNPKDCLYJHGLKPRRHYVATKAFPLEYVPHANL 600
QY 601 NEIFQVSTTTKVPSPMTSEPYGTRSPAKIMPTTTPAIPANNDKSKDPMKTSPEE 660
DB 601 NEIFQVSTTTKVPSPMTSEPYGTRSPAKIMPTTTPAIPANNDKSKDPMKTSPEE 660
QY 661 TTUULETKRQVSTELSTIYVAGASLLFLNIIAPALYYKKDKRHHETRRPSPQNTND 720
DB 661 TTUULETKRQVSTELSTIYVAGASLLFLNIIAPALYYKKDKRHHETRRPSPQNTND 720
QY 721 IAHIONEEMSLQKOLEHDEGESIQAHETLRJCCPPDZTLTLRRSPDDIPLMTPTIT 780
DB 721 IAHIONEEMSLQKOLEHDEGESIQAHETLRJCCPPDZTLTLRRSPDDIPLMTPTIT 780
QY 781 XIPNLTIGMCPHLTFNTSSGQNSTNLPHGSHSTRV 816
DB 781 XIPNLTIGMCPHLTFNTSSGQNSTNLPHGSHSTRV 816

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RESULT 57
 US-10-167-749-375

; Sequence 375; Application US/10:67749

; Publication No. US20030356137A1

; GENERAL INFORMATION:

; APPLICANT: Askenazi, Av;

; APPLICANT: Baker Kevin P.

; APPLICANT: Bostein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

```

; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geider, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David W.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane polypeptides and Nucleic
; TYPE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC60
; CURRENT APPLICATION NUMBER: US/10/167,749
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-27
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077921
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO: 375
; LENGTH: 816
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-10-167-749-375

Query Match 100.0%; Score 816; DB 15; Length 816;
 Best Local Similarity 100.0%; Pred. No. 0;
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DB 1 MLNSNVLMTLALAIKFTLIDSOAYPVVNTNGIKRGLETFLEINELGVEGYLGVPYA 60
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DB 181 GTGNMIDGSIILASGVNIVITINRGLGFLSTGDAKAGNYGLDQIQALRWIEENVG 240

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Db 661 TTVL:ETKRDYSTE:SVTIAVGASLL:ETNILA:FAALYKCKRRETHRRSP:FORNTND 720
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Qy 781 MIPNLTGMQPLHPTFTSGGNSNLPKSHSTTV 840
Db 781 MIPNLTGMQPLHPTFTSGGNSNLPKSHSTTV 840

APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P084
CURRENT APPLICATION NUMBER: US/0/013,922-A
PRIOR FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
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PRIOR APPLICATION NUMBER: 60/077450
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PRIOR APPLICATION NUMBER: 60/077632
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PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
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PRIOR FILING DATE: 1998-03-13
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RESULT 59
US-10-013-929A-375
Sequence 375, Application US/13013929A
Publication No. US20030372745A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desroyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvarsoff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gettlesen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavitt, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Najler, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoletti, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2630P1C89
CURRENT APPLICATION NUMBER: US/10/013, 929A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064243
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PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
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PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
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PRIOR FILING DATE: 1998-04-01
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PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
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PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
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PRIOR APPLICATION NUMBER: 60/081838
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PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22

PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
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PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084365
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PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 816; DB 15; Length 816;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNSNVLTWZCALAKFTLLDSQAOYPVVNTYKIRGLRPLPNEIJCPEVOYGVPA 60
Db 1 MNSNVLTWLTALAKFTLLDSQAOYPVVNTYKIRGLRPLPNEIJCPEVOYGVPA 60
QY 61 SEPTGRRRQPEPPSSWTGIRNTTQFAVCCOHLDESLHDMJPIWFTANLDTMTYV 120
Db 61 SEPTGRRRQPEPPSSWTGIRNTTQFAVCCOHLDESLHDMJPIWFTANLDTMTYV 120
QY 122 QONNEDCYLNIYVPEZGANTKXADDTISNDRGDEIHPQNSKKPMVYIHGSSYE 180
Db 122 QONNEDCYLNIYVPEZGANTKXADDTISNDRGDEIHPQNSKKPMVYIHGSSYE 180
QY 181 GTGNMIDGILASXGVNIVITINRILGILFSTGBOAKNGVJLDCQALRWIEENVG 240
Db 181 GTGNMIDGILASXGVNIVITINRILGILFSTGBOAKNGVJLDCQALRWIEENVG 240
QY 241 AFGGDPKRVITIGSGAGASCVSLLTSLHSEGLFCXAIIQSGTALSSMAVNYCPAAYT81 300
Db 241 AFGGDPKRVITIGSGAGASCVSLLTSLHSEGLFCXAIIQSGTALSSMAVNYCPAAYT81 300
QY 301 LADKVGCMMLDTEDVVEGCRNKNYKELIQOTITPATYHAFGVVIDGVIPDAPQILXEQ 360
Db 301 LADKVGCMMLDTEDVVEGCRNKNYKELIQOTITPATYHAFGVVIDGVIPDAPQILXEQ 360
QY 361 GEFLLNYDMLGVNQGEGKFPVDGIYDNEGVTPENDEFSVSNFVDMJYGPBGKJLRET 420
Db 361 GEFLLNYDMLGVNQGEGKFPVDGIYDNEGVTPENDEFSVSNFVDMJYGPBGKJLRET 420
QY 421 IKXYTDMADCKENPETRRKCTVALFTDQWVAPAAADLHAQYSPTYFAFYHCOQSM 480
Db 421 IKXYTDMADCKENPETRRKCTVALFTDQWVAPAAADLHAQYSPTYFAFYHCOQSM 480
QY 481 KPSMADSAGDEVYFPGIPMIGFELFCFNSKXDVMSAVVYTYWTFNFAKTPGNCQV 540
Db 481 KPSMADSAGDEVYFPGIPMIGFELFCFNSKXDVMSAVVYTYWTFNFAKTPGNCQV 540
QY 541 PODTKFIHTKPRFEEVANSKYNPKDQVLYHGLKPRVDEYRAIKVAWJCVPHLENY 600
Db 541 PODTKFIHTKPRFEEVANSKYNPKDQVLYHGLKPRVDEYRAIKVAWJCVPHLENY 600
QY 601 NEFYVSTTTKVPPEPDMSPFYGRSPAKMPTTKRAIIPANNPKSKXDPHKTGPE 660
Db 601 NEFYVSTTTKVPPEPDMSPFYGRSPAKMPTTKRAIIPANNPKSKXDPHKTGPE 660
QY 661 TVLLETKRQDYSELSTLAVGASLFLNIIAFAALYKKDKRREHETARRPSORVTTND 720
Db 661 TVLLETKRQDYSELSTLAVGASLFLNIIAFAALYKKDKRREHETARRPSORVTTND 720
QY 721 IAHIONEELKSLQKOLEHDEHCESLQANDTLRLTCPEPYTITLRRSPDIDPLMTFNITT 780
Db 721 IAHIONEELKSLQKOLEHDEHCESLQANDTLRLTCPEPYTITLRRSPDIDPLMTFNITT 780
QY 791 MIPNLTGMOPLHTEYTFSGGONSTNLPHGSHSTRY 816
Db 791 MIPNLTGMOPLHTEYTFSGGONSTNLPHGSHSTRY 816
RESULT 60
US-10-016--77A-375
Sequence 375, Application US/10016:77A
Publication No. US20030073131A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desrochers, Luc
APPLICANT: Eaton, Dar.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman

```

/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Geritsen, Mary F.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, G. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kijavir, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James I.
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2630PIC90
/ CURRENT APPLICATION NUMBER: US/10/016,77A
/ PRIOR FILING DATE: 2002-04-30
/ PRIOR APPLICATION: removed - See File Wrapper or Pam
/ NUMBER OF SEQ ID NOS: 624
/ SEQ ID NO 375
/ LENGTH: 816
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-016-77A-375

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Query Match      100.0%  Score 816;  EB 15;  Length 816;
Best Local Similarity 100.0%;  Fred. No. 0;
Matches 816;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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QY 1 MUNSVMKLTALAKETLLDSQAGYVAVNTNYSKIGSLRPLNELIGVEYLGGEYA 60
DB 1 MUNSVMKLTALAKETLLDSQAGYVAVNTNYSKIGSLRPLNELIGVEYLGGEYA 60
QY 61 SPTGERRFPQPEPSSWTGIRNTQFAVCPHLDERSLLHDMPLWETANLCTLTYY 120
DB 61 SPTGERRFPQPEPSSWTGIRNTQFAVCPHLDERSLLHDMPLWETANLCTLTYY 120
QY 121 CQMEDCLYINLYVTEEGANTKKAADCTSDNREGRDIDQSKSRVYVYHIGSSYVE 180
DB 121 CQMEDCLYINLYVTEEGANTKKAADCTSDNREGRDIDQSKSRVYVYHIGSSYVE 180
QY 181 GTSNVIGSILASYNVYVITINRYLGLGFLSTGDAQAKNGYGLDQICAFRIEENYG 240
DB 181 GTSNVIGSILASYNVYVITINRYLGLGFLSTGDAQAKNGYGLDQICAFRIEENYG 240
QY 241 AGGCPFKVYITIGSSAGASCVSLTLHSRSEGLPEKATIGGTLSSAAVNYGAKYTRI 300
DB 241 AGGCPFKVYITIGSSAGASCVSLTLHSRSEGLPEKATIGGTLSSAAVNYGAKYTRI 300
QY 301 LADKYGCMNLETTMWECLAKNGYKELLCQITATATVIAAGPVYDGPVDPDECIYNEQ 360
DB 301 LADKYGCMNLETTMWECLAKNGYKELLCQITATATVIAAGPVYDGPVDPDECIYNEQ 360
QY 361 GEFNVDIMAGVNGEGELKFDVGIYDNEGVTPNFDSVSNFVDNIYGVPESEKDTLRET 420
DB 361 GEFNVDIMAGVNGEGELKFDVGIYDNEGVTPNFDSVSNFVDNIYGVPESEKDTLRET 420
QY 421 IKFYATMADKENPETRRKTLYALFTBQWAAFAVAALHAYQSSPTFYAFYHIGGSEM 480
DB 421 IKFYATMADKENPETRRKTLYALFTBQWAAFAVAALHAYQSSPTFYAFYHIGGSEM 480
QY 481 KPSMADSAHGEDEVYVFGIPIWIGPTELFSQNSKYDYLSAVYTWYTWNPFKCTCPQPV 540
DB 481 KPSMADSAHGEDEVYVFGIPIWIGPTELFSQNSKYDYLSAVYTWYTWNPFKCTCPQPV 540
QY 541 POCFTFHTKPNRFEVAVMSKYNPRDQCYLHIGLKPRVRCFYRTKVAFWLEJVPJHNL 600

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DB 541 POCFTFHTKPNRFEVAVMSKYNPRDQCYLHIGLKPRVRCFYRTKVAFWLEJVPJHNL 600
QY 601 NEIFQVSTTTKVPDPMDTSFPYGRBPATWETTKRPAITTPANPNHSDPKPTGED 660
DB 601 NEIFQVSTTTKVPDPMDTSFPYGRBPATWETTKRPAITTPANPNHSDPKPTGED 660
QY 661 TVLLIETKRDYSTELSVIAGASLFLNIAFALYKKDKRRECHTRRRSPQRTNTD 720
DB 661 TVLLIETKRDYSTELSVIAGASLFLNIAFALYKKDKRRECHTRRRSPQRTNTD 720
QY 721 IAHIONEELMSQMKOLEHCECELSQADTLRLCTPPDYTLTRSPDDIPLMTPTIT 780
DB 721 IAHIONEELMSQMKOLEHCECELSQADTLRLCTPPDYTLTRSPDDIPLMTPTIT 780
QY 781 MIPNTLTGMOPHTENTSGGQNSTNLEPHGSTIRV 816
DB 781 MIPNTLTGMOPHTENTSGGQNSTNLEPHGSTIRV 816

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RESULT 61

US-13-166-709A-375

Sequence 375, Application US/10166709A

Publication No. US20030104536A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Geritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, G. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijavir, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James I.

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2630PIC90

CURRENT APPLICATION NUMBER: US/10/166, 709A

PRIOR FILING DATE: 2001-10-13

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2003-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/07450

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077642

PRIOR FILING DATE: 1998-03-11

[illegible]

FILE APPLICATION NUMBER: 60/085704
CURRENT FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 816; DB 15; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MUNSVMWLTALAIKFTLLDSOAGYPTNTNKGKSGJPLPNEILSPVEQYGVFA 60
DB 1 MUNSVMWLTALAIKFTLLDSOAGYPTNTNKGKSGJPLPNEILSPVEQYGVFA 60

QY 61 SPTGERRFQPPPESSMTGIRNCTGPAVCPQHLDBERSLHDMPLIFETANCTLWY 120
DB 61 SPTGERRFQPPPESSMTGIRNCTGPAVCPQHLDBERSLHDMPLIFETANCTLWY 120

QY 121 QGQNEDECLYNIIVFTEGANTKKAACDITSDRGEDIEHCNKKRWMYTHGSGTNE 180
DB 121 QGQNEDECLYNIIVFTEGANTKKAACDITSDRGEDIEHCNKKRWMYTHGSGTNE 180

QY 181 GTGNTDGSILASGVNVIYTIIVRLGJLSTSDQAKKNVGLDQIALWLEENVG 240
DB 181 GTGNTDGSILASGVNVIYTIIVRLGJLSTSDQAKKNVGLDQIALWLEENVG 240

QY 241 AFGDPRKVTTFSSGAGASCVSLLTSHSEGLFQKALIQSTLSSKAAVQPKATRI 300
DB 241 AFGDPRKVTTFSSGAGASCVSLLTSHSEGLFQKALIQSTLSSKAAVQPKATRI 300

QY 301 LADKVGCMDDTTDMECELRNKKYKELIQOTTPATYHAFGPVADGVPDDEPOLWEO 360
DB 301 LADKVGCMDDTTDMECELRNKKYKELIQOTTPATYHAFGPVADGVPDDEPOLWEO 360

QY 361 GEFINDIMAGVQSGKLFVDSIVNEDGVTPNDPSSVFNUNYGYEGCKTLRET 420
DB 361 GEFINDIMAGVQSGKLFVDSIVNEDGVTPNDPSSVFNUNYGYEGCKTLRET 420

QY 421 IKEMYTDMADKXENPERRKTVALFTCHQWVAFAVAADLAQVGSPTFYFVYHGCQSEM 480
DB 421 IKEMYTDMADKXENPERRKTVALFTCHQWVAFAVAADLAQVGSPTFYFVYHGCQSEM 480

QY 481 KPSWADSAGDEVPYFGJPMIGPTELFSCNFKNDVMSAVVMTYKTNFAKGTGPNCPV 540
DB 481 KPSWADSAGDEVPYFGJPMIGPTELFSCNFKNDVMSAVVMTYKTNFAKGTGPNCPV 540

QY 541 POSTKFIHTKPNRFEVAVSKYKPKDCLJHGLKPRVZCHRAKVAFWELVSHLHN 600
DB 541 POSTKFIHTKPNRFEVAVSKYKPKDCLJHGLKPRVZCHRAKVAFWELVSHLHN 600

QY 601 NEIFQVSTTKVPPDMTSFPYGRSPAKIMPTIKRPAITPANPKHSHKPKHTGSED 660
DB 601 NEIFQVSTTKVPPDMTSFPYGRSPAKIMPTIKRPAITPANPKHSHKPKHTGSED 660

QY 661 TTVALTEKRDYSELVTAIVAGSLLFLKILAFALYKCKXERHETRRPSPQNTND 720
DB 661 TTVALTEKRDYSELVTAIVAGSLLFLKILAFALYKCKXERHETRRPSPQNTND 720

QY 721 IAHIONEIMSLCKOLFHDCESELIQANDTLRITCPPEYTLTUBRSSPDIFLWTPNIT 780
DB 721 IAHIONEIMSLCKOLFHDCESELIQANDTLRITCPPEYTLTUBRSSPDIFLWTPNIT 780

QY 781 KIENTLTGQPLTEFTVFSGGQSTNLPHGSHTRV 816
DB 781 KIENTLTGQPLTEFTVFSGGQSTNLPHGSHTRV 816

FILE REFERENCE: 10448-058001
CURRENT APPLICATION NUMBER: US/09/875,353
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/209,949
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 816
TYPE: PRT
ORGANISM: Homo sapiens
US-09-875-353-2

Query Match 40.0%; Score 326; DB 10; Length 816;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 546; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 163 QNSKRWMTYHGSSTYBETGMIDGSLASGVNVIYTNVETGLGFLSTGQAKGN 222
DB 162 QNSKRWMTYHGSSTYBETGMIDGSLASGVNVIYTNVETGLGFLSTGQAKGN 221

QY 223 YGLDQIQALRMEENVGAFGDPRKVTTFSSGAGASCVSLLTSHSEGLFQKALIQSG 282
DB 222 YGLDQIQALRMEENVGAFGDPRKVTTFSSGAGASCVSLLTSHSEGLFQKALIQSG 281

QY 283 TALSKAAVYQPAKATRIILADKVGCMDDTTDMECELRNKKYKELIQOTTPATYHAFG 342
DB 282 TALSKAAVYQPAKATRIILADKVGCMDDTTDMECELRNKKYKELIQOTTPATYHAFG 341

QY 343 PYDGVIPDDPQILMEGSEFLNDIMAGVQSGKLFVDSIVNEDGVTPNDPSSVFN 402
DB 342 PYDGVIPDDPQILMEGSEFLNDIMAGVQSGKLFVDSIVNEDGVTPNDPSSVFN 401

QY 403 FVDNLYGYEGCKTLRETIKEMYTDMADKXENPERRKTVALFTCHQWVAFAVAADLA 461
DB 402 FVDNLYGYEGCKTLRETIKEMYTDMADKXENPERRKTVALFTCHQWVAFAVAADLA 460

QY 462 CYGSPFYFAFYHHCQSEKPSMAHAGDEVYFGJPMIGPTELFSCNFKNDVMSA 521
DB 462 CYGSPFYFAFYHHCQSEKPSMAHAGDEVYFGJPMIGPTELFSCNFKNDVMSA 520

QY 522 VMTYTNFAKTGDPNPVODTKFIHTKPNRFEVAVSKYKPKDCLJHGLKPRVZCH 581
DB 522 VMTYTNFAKTGDPNPVODTKFIHTKPNRFEVAVSKYKPKDCLJHGLKPRVZCH 580

QY 582 YAKTKVAFLEIVPHLNLNEIFQVSTTKVPPDMTSFPYGRSPAKIMPTIKRPAI 641
DB 582 YAKTKVAFLEIVPHLNLNEIFQVSTTKVPPDMTSFPYGRSPAKIMPTIKRPAI 640

QY 642 TPANNPKSHKDPKHTGPEDTVLLETKRDYSELVTAIVAGSLLFLNIIAFALYKCK 701
DB 642 TPANNPKSHKDPKHTGPEDTVLLETKRDYSELVTAIVAGSLLFLNIIAFALYKCK 700

QY 702 KRRHETRR 709
DB 702 KRRHETRR 709

RESULT 62
US-09-875-353-2
Sequence 2, Application US/09875353
Patent No. US20020168713A1
GENERAL INFORMATION:
APPLICANT: Curtiss, Roy A. J.
TITLE OF INVENTION: 46980, A NOVEL HUMAN NEURULIGIN FAMILY
TITLE OF INVENTION: MEYER AND USES THEREOF

RESULT 63
US-09-934-323-6
Sequence 6, Application US/09934323
Patent No. US20020150910A1
GENERAL INFORMATION:
APPLICANT: Curtiss, Roy A. J.
TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYL ESTERASE
FILE REFERENCE: 10448-081001
CURRENT APPLICATION NUMBER: US/09/934,323
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/226,774
PRIOR FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 6
LENGTH: 550
TYPE: PRT
ORGANISM: Homo sapiens
US-09-934-323-6

Query Match: 5.9%; Score 48; DB 10; Length 550;
Best Local Similarity 100.0%; Pred. No. 3.5e-40;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 CNFSKNDVMSAVVMTYNTNFAKTGDPNQPVPQDTKFIHTKRNREEV 557
DB 236 CNFSKNDVMSAVVMTYNTNFAKTGDPNQPVPQDTKFIHTKRNREEV 283

RESULT 64
US-10-274-694-12
Sequence 12, Application US/12274694
Publication No. US20030143565A1
GENERAL INFORMATION:
APPLICANT: EAVSHER, Mariah R.
APPLICANT: BRUNS, Christopher M.
APPLICANT: DAS, Deeporitya
APPLICANT: CING, Li
APPLICANT: ELIOTT, Vicki S.
APPLICANT: GANDHI, Ameena R.
APPLICANT: HAFALIA, April J.A.
APPLICANT: KEARNEY, Liam
APPLICANT: KHAN, Farrah A.
APPLICANT: LAU, Preeti G.
APPLICANT: LEE, Ernestine A.
APPLICANT: LU, Dying Aina M.
APPLICANT: LU, Yan
APPLICANT: NGUYEN, Dannie B.
APPLICANT: PATTERSON, Chandra S.
APPLICANT: RAYKCAR, Jayalaxmi
APPLICANT: RING, Heijun Z.
APPLICANT: SAMUNMALA, Madhusudan M.
APPLICANT: TANG, Y. Tom
APPLICANT: THANGAVELU, Kavitha
APPLICANT: THORNTON, Michael B.
APPLICANT: TRIBOULEY, Catherine M.
APPLICANT: WALIA, Narinder K.
APPLICANT: XU, Yuming
APPLICANT: YANG, Junming
APPLICANT: YAO, Monique G.
APPLICANT: YUE, Henry
TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
FILE REFERENCE: PI-0151 USA
CURRENT APPLICATION NUMBER: US/10/274,694
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 60/222,837
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/220,037
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: 60/218,946
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US01/21324
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/216,804
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PERL Program
SEQ ID NO 12
LENGTH: 801
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Ircyle ID No. US20030143565A1 7473875CD;
US-10-274-694-12
Query Match: 5.9%; Score 45; DB 12; Length 801;

Best Local Similarity 100.0%; Pred. No. 5e-40;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 CNFSKNDVMSAVVMTYNTNFAKTGDPNQPVPQDTKFIHTKRNREEV 557
DB 521 CNFSKNDVMSAVVMTYNTNFAKTGDPNQPVPQDTKFIHTKRNREEV 568

RESULT 65
US-09-934-323-2

Sequence 2, Application US/09934323
Patent No. US20020150910A1

GENERAL INFORMATION:

APPLICANT: Curtis, Roy A. C.

TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYESTERASE

FILE REFERENCE: 10448-081001

CURRENT APPLICATION NUMBER: US/09/934,323

CURRENT FILING DATE: 2001-08-21

PRIOR FILING DATE: 2000-06-21

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 835

TYPE: PRT

ORGANISM: Homo sapiens

US-09-934-323-2

Query Match: 5.9%; Score 48; DB 10; Length 835;

Best Local Similarity 100.0%; Pred. No. 5.2e-40;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 CNFSKNDVMSAVVMTYNTNFAKTGDPNQPVPQDTKFIHTKRNREEV 557
DB 521 CNFSKNDVMSAVVMTYNTNFAKTGDPNQPVPQDTKFIHTKRNREEV 568

RESULT 66
US-09-934-323-5

Sequence 5, Application US/09934323

Patent No. US20020150910A1

GENERAL INFORMATION:

APPLICANT: Curtis, Roy A. C.

TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYESTERASE

FILE REFERENCE: 10448-081001

CURRENT APPLICATION NUMBER: US/09/934,323

CURRENT FILING DATE: 2001-08-21

PRIOR FILING DATE: 2000-06-21

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5

LENGTH: 836

TYPE: PRT

ORGANISM: Rattus norvegicus

US-09-934-323-5

Query Match: 5.9%; Score 48; DB 10; Length 836;

Best Local Similarity 100.0%; Pred. No. 5.2e-40;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 CNFSKNDVMSAVVMTYNTNFAKTGDPNQPVPQDTKFIHTKRNREEV 557
DB 521 CNFSKNDVMSAVVMTYNTNFAKTGDPNQPVPQDTKFIHTKRNREEV 568

RESULT 67

US-09-964-761-46697

Sequence 46697, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:

```
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David R.
/ APPLICANT: Hanzel, David K.
/ APPLICANT: Chen, Mensheng
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
/ FILE REFERENCE: AEWICA-X-1
/ CURRENT APPLICATION NUMBER: US/09/864,761
/ CURRENT FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: US 60/250,312
/ PRIOR FILING DATE: 2003-02-04
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2003-05-26
/ PRIOR APPLICATION NUMBER: US 69/632,366
/ PRIOR FILING DATE: 2003-08-03
/ PRIOR APPLICATION NUMBER: GB 24263,6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2003-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00672
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-22
/ PRIOR APPLICATION NUMBER: US 69/608,408
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 69/774,203
/ PRIOR FILING DATE: 2001-01-29
/ NUMBER OF SEQ ID NOS: 43177
/ SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 46697
/ LENGTH: 49
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURES:
/ OTHER INFORMATION: MAP TO AC010979.1
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.9
/ OTHER INFORMATION: EST HUMAN HIT: BE46544E.1, EVALU 4,00e-22
/ OTHER INFORMATION: SWISSPROT HIT: Q63880, EVALU 6,00e-10
US-09-864-761-46697

Query Match 5.64; Score 46; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 4,1e-39;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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/ TITLE OF INVENTION: 46980, A NOVEL HUMAN NEUROLOGIN FAMILY
/ FILE REFERENCE: 10448-058001
/ CURRENT APPLICATION NUMBER: US/09/875,353
/ CURRENT FILING DATE: 2001-06-06
/ PRIOR APPLICATION NUMBER: US 60/209,949
/ PRIOR FILING DATE: 2000-06-06
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 5
/ LENGTH: 848
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
US-09-875-353-5

Query Match 3.94; Score 32; DB 10; Length 848;
Best Local Similarity 100.0%; Pred. No. 1,4e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 69
US-10-029-386-31666
/ Sequence 31666, Application US/10023386
/ Publication No. US20030194704A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David R.
/ APPLICANT: Hanzel, David K.
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
/ FILE REFERENCE: AEWICA-X-2
/ CURRENT APPLICATION NUMBER: US/10/029,386
/ CURRENT FILING DATE: 2001-12-20
/ NUMBER OF SEQ ID NOS: 34288
/ SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 31666
/ LENGTH: 157
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURES:
/ OTHER INFORMATION: MAP TO AC010979.3
/ OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.4
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
/ OTHER INFORMATION: SWISSPROT HIT: P23795, EVALU 5,00e-16
US-10-029-386-31666

Query Match 3.44; Score 28; DB 12; Length 157;
Best Local Similarity 100.0%; Pred. No. 3,7e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 70
US-10-029-386-30476
/ Sequence 30476, Application US/10023386
/ Publication No. US20030194704A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David R.
/ APPLICANT: Hanzel, David K.
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
/ FILE REFERENCE: AEWICA-X-2
```

CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-23
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annotax Sequence Listing Engine vers. 1.1
SEQ ID NO 34276
LENGTH: 61
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC239319.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.61
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.62
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.55
OTHER INFORMATION: SWISSPROT HIT: P14943, EVALUATE 3.00e-14
US-10-029-386-30476

Query Match 2.9%; Score 24; DB 12; Length 61;
Best Local Similarity 100.0%; Pred. No. 26-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 211 FLSTGDCQAKGNVGLDQICALLRW 214
|||||
Db 1 FLSTGDCQAKGNVGLDQICALLRW 24

RESULT 71
US-09-925-297-718
Sequence 718, Application US/0925297
Patent No. US20020681559A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 718
LENGTH: 359
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-297-718

Query Match 1.5%; Score 12; DB 9; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 526 WYTNFAKTGDPN 537
|||||
Db 192 WYTNFAKTGDPN 203

RESULT 72
US-09-418-176-4
Sequence 4, Application US/09418176
Publication No. US20030040040A1
GENERAL INFORMATION:
APPLICANT: Das, Goutam
TITLE OF INVENTION: DNA Molecules for Expression of
NUMBER OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States

ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/418,176
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/624,398
FILING DATE: 04-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SE96/00318
FILING DATE: 12-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9501939-4
FILING DATE: 24-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Thelma A. Chen Cleland
REGISTRATION NUMBER: 40,948
REFERENCE/DOCKET NUMBER: 1103326-0206
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8200
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Mammary gland
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..568
OTHER INFORMATION: /label= Variant_C
PUBLICATION INFORMATION:
AUTHORS: Hansson, Lennart
AUTHORS: Blackberg, Lars
AUTHORS: Edvard, Michael
AUTHORS: Sundberg, Lennart
AUTHORS: Stromqvist, Mats
AUTHORS: Hernell, Oile
TITLE: Recombinant Human Milk Bile Salt-stimulated
TITLE: Lipase
JOURNAL: J. Biol. Chem.
VOLUME: 268
ISSUE: 35
PAGES: 26692-26698
DATE: Dec. 15-1993
US-09-418-176-4

Query Match 1.5%; Score 12; DB 11; Length 568;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 526 WYTNFAKTGDPN 537
|||||
Db 467 WYTNFAKTGDPN 478

RESULT 73
US-10-156-932-7
Sequence 7, Application US/10156932
Publication No. US20030069181A1
GENERAL INFORMATION:
APPLICANT: Wong, Albert J.
TITLE OF INVENTION: Alternative Splice Forms of Proteins as

/ TITLE OF INVENTION: Basis for Multiple Therapeutic Modalities
/ FILE REFERENCE: 8321-8-
/ CURRENT APPLICATION NUMBER: US/10/156,932
/ CURRENT FILING DATE: 2002-05-28
/ PRIOR APPLICATION NUMBER: US 60/293,791
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 82
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 7
/ LENGTH: 612
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
/ US-10-156-932-7

Query Match: 1.5%; Score 12; DB 15; Length 612;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 526 YWTFNFAKTGDPN 537
Db 467 YWTFNFAKTGDPN 478

RESULT 74
US-09-418-176-3
/ Sequence 3, Application US/09/418,76
/ Publication No. US20030040040A1
/ GENERAL INFORMATION:
/ APPLICANT: Das, Gouram
/ TITLE OF INVENTION: DNA Molecules for Expression of
/ TITLE OF INVENTION: Polypeptides
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: White & Case
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: United States
/ ZIP: 10036-2787
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/418,176
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/624,398
/ FILING DATE: 04-APR-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/SE96/00318
/ FILING DATE: 12-MAR-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: SE 9501939-4
/ FILING DATE: 24-MAY-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Thelma A. Chen Cleland
/ REGISTRATION NUMBER: 40,948
/ REFERENCE/DOCKET NUMBER: 1103326-0206
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 819-8200
/ TELEFAX: (212) 354-8113
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 722 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHEICAL: NO
/ ORIGINAL SOURCE:

/ ORGANISM: Homo sapiens
/ TISSUE TYPE: Mammary gland
/ US-09-418-176-3

Query Match: 1.5%; Score 12; DB 15; Length 722;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 526 YWTFNFAKTGDPN 537
Db 467 YWTFNFAKTGDPN 478

RESULT 75
US-09-418-176-2
/ Sequence 2, Application US/09/418,76
/ Publication No. US20030040040A1
/ GENERAL INFORMATION:
/ APPLICANT: Das, Gouram
/ TITLE OF INVENTION: DNA Molecules for Expression of
/ TITLE OF INVENTION: Polypeptides
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: White & Case
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: United States
/ ZIP: 10036-2787
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/418,176
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/624,398
/ FILING DATE: 04-APR-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/SE96/00318
/ FILING DATE: 12-MAR-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: SE 9501939-4
/ FILING DATE: 24-MAY-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Thelma A. Chen Cleland
/ REGISTRATION NUMBER: 40,948
/ REFERENCE/DOCKET NUMBER: 1103326-0206
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 819-8200
/ TELEFAX: (212) 354-8113
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 745 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-418-176-2

Query Match: 1.5%; Score 12; DB 15; Length 745;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 526 YWTFNFAKTGDPN 537
Db 490 YWTFNFAKTGDPN 501

Search completed: November 5, 2003, 15:31:29
Cob time : 46 secs

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: November 5, 2003, 15:19:28 ; Search time 41 Seconds

(without alignments)
5135.876 Million cell updates/sec

Title: US-09-978-423a-375

Perfect score: 816
Sequence: 1 XJNSNVJLMTALAIKFTLL.....TFGGQNSTNLPHGSTRV 816

Scoring table: OLIGO
Gapex 60.0, Gapext 60.0

Searched: 830525 seqs, 259352604 residues

Word size: 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 3

Maximum DB seq length: 2000000000

Post-Processing: Listing first 100 summaries

Database:

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_ornate:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	538	65.9	816	4 Q9N0W4	Q9N0W4 homo sapien
2	538	65.9	817	4 Q9ULG0	Q9ULG0 homo sapien
3	326	40.0	816	4 Q8NFZ3	Q8NFZ3 homo sapien
4	319	39.1	648	4 Q9Y2F8	Q9Y2F8 homo sapien
5	213	26.1	213	6 Q8WMC7	Q8WMC7 macaca mula
6	30	6.1	509	4 Q8N207	Q8N207 homo sapien
7	30	6.1	823	4 Q9UP12	Q9UP12 homo sapien
8	50	6.1	823	11 Q6Z765	Q6Z765 rattus norv
9	48	5.9	134	4 Q8N5B6	Q8N5B6 homo sapien
10	48	5.9	553	4 Q9P211	Q9P211 homo sapien
11	48	5.9	835	4 Q8N2Z4	Q8N2Z4 homo sapien
12	48	5.9	836	11 Q6Z888	Q6Z888 rattus norv
13	35	4.3	558	4 Q9N296	Q9N296 homo sapien
14	35	4.3	682	4 Q9P248	Q9P248 homo sapien
15	35	4.3	828	4 Q9N294	Q9N294 homo sapien
16	35	4.3	848	4 Q9N295	Q9N295 homo sapien

17	32	3.9	144	11 Q9Z4X0	Q9Z4X0 mus musculus
18	32	3.9	825	11 Q8ZYMS	Q8ZYMS mus musculus
19	32	3.9	828	4 Q9N297	Q9N297 homo sapien
20	32	3.9	848	11 Q6Z889	Q6Z889 rattus norv
21	28	3.4	202	6 Q8WMC2	Q8WMC2 macaca mula
22	28	3.4	335	4 Q8N2C0	Q8N2C0 homo sapien
23	28	3.4	383	11 Q8N2R4	Q8N2R4 homo sapien
24	24	2.2	245	11 Q9N2K10	Q9N2K10 mus musculus
25	25	1.5	612	4 Q75612	Q75612 homo sapien
26	26	1.5	742	4 Q16398	Q16398 homo sapien
27	27	1.5	745	4 Q9UP41	Q9UP41 homo sapien
28	28	1.5	998	6 Q9N1D1	Q9N1D1 gorilla gor
29	29	1.3	110	5 Q8NXX4	Q8NXX4 pluteia xy
30	30	1.3	540	5 Q23735	Q23735 culex quinq
31	31	1.3	559	11 Q8N297	Q8N297 mus musculus
32	32	1.3	559	11 Q8N248	Q8N248 mus musculus
33	33	1.3	610	5 Q97110	Q97110 coligo opai
34	34	1.3	656	5 Q9XYA9	Q9XYA9 meloidogyne
35	35	1.3	656	5 Q96529	Q96529 meloidogyne
36	36	1.3	1248	5 Q9N2K5	Q9N2K5 drosophila
37	37	1.2	134	5 Q9N2C2	Q9N2C2 tribolium c
38	38	1.2	505	5 Q23736	Q23736 culex quinq
39	39	1.2	540	5 Q91920	Q91920 culex tarsa
40	40	1.2	540	5 Q23734	Q23734 culex quinq
41	41	1.2	593	5 Q9VDP5	Q9VDP5 drosophila
42	42	1.1	288	4 Q9UXY3	Q9UXY3 homo sapien
43	43	1.1	360	5 Q9N2R1	Q9N2R1 drosophila
44	44	1.1	469	4 Q8N2C8	Q8N2C8 homo sapien
45	45	1.1	497	16 Q97TP8	Q97TP8 clostridium
46	46	1.1	503	16 Q9UYU6	Q9UYU6 neisseria m
47	47	1.1	503	16 Q9UT77	Q9UT77 neisseria m
48	48	1.1	507	5 Q9V731	Q9V731 drosophila
49	49	1.1	525	4 Q96DN9	Q96DN9 homo sapien
50	50	1.1	533	2 Q8RLUC	Q8RLUC enterobacte
51	51	1.1	541	5 Q9V1C9	Q9V1C9 drosophila
52	52	1.1	541	5 Q24197	Q24197 drosophila
53	53	1.1	545	6 Q81034	Q81034 felis sive
54	54	1.1	549	2 Q8KRZ6	Q8KRZ6 vibrio harv
55	55	1.1	554	11 Q54936	Q54936 mus musculus
56	56	1.1	554	11 Q8K125	Q8K125 mus musculus
57	57	1.1	558	11 Q8K1R0	Q8K1R0 rattus norv
58	58	1.1	558	11 Q8Q2R3	Q8Q2R3 mus musculus
59	59	1.1	559	11 Q35533	Q35533 mesocricetu
60	60	1.1	560	11 Q8R097	Q8R097 mus musculus
61	61	1.1	561	11 Q91KJ0	Q91KJ0 mus musculus
62	62	1.1	561	11 Q91W60	Q91W60 mus musculus
63	63	1.1	561	11 Q76631	Q76631 rattus norv
64	64	1.1	562	11 Q924V9	Q924V9 rattus norv
65	65	1.1	564	5 Q9VLA4	Q9VLA4 drosophila
66	66	1.1	565	4 Q8TD29	Q8TD29 homo sapien
67	67	1.1	565	5 Q23010	Q23010 caenorhabdi
68	68	1.1	565	6 Q77540	Q77540 oryzolaus
69	69	1.1	565	6 Q95N05	Q95N05 canis fami
70	70	1.1	565	6 Q97582	Q97582 sus scrofa
71	71	1.1	565	11 Q8VCC2	Q8VCC2 mus musculus
72	72	1.1	565	11 Q924V8	Q924V8 mus musculus
73	73	1.1	565	11 Q55136	Q55136 mus musculus
74	74	1.1	565	11 Q912V9	Q912V9 mus musculus
75	75	1.1	565	11 Q35534	Q35534 mesocricetu
76	76	1.1	565	11 Q8VCT4	Q8VCT4 mus musculus
77	77	1.1	565	11 P70104	P70104 cavia porce
78	78	1.1	566	4 Q96EE8	Q96EE8 homo sapien
79	79	1.1	566	6 Q46421	Q46421 macaca fasc
80	80	1.1	567	4 Q9UK77	Q9UK77 homo sapien
81	81	1.1	567	4 Q9ULY1	Q9ULY1 homo sapien
82	82	1.1	574	5 Q9BMT7	Q9BMT7 drosophila
83	83	1.1	574	5 Q9V7J2	Q9V7J2 drosophila
84	84	1.1	676	5 Q9BMJ1	Q9BMJ1 schizaphis
85	85	1.1	676	5 Q8N235	Q8N235 aphid gossy
86	86	1.1	806	5 Q81P36	Q81P36 drosophila
87	87	1.0	956	5 Q9N2K0	Q9N2K0 drosophila
88	88	1.0	106	11 Q8VE32	Q8VE32 mus musculus
89	89	1.0	106	11 Q9CYM8	Q9CYM8 mus musculus

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90      8      1.0      125      16      08PRP3
91      8      1.2      147      11      09WT01
92      8      1.2      147      5      08WY33
93      8      1.0      177      5      061695
94      8      1.0      185      10      068879
95      8      1.0      210      4      09NOC5
96      8      1.0      231      5      017964
97      8      1.0      281      5      08ST14
98      8      1.0      289      16      05RYF9
99      8      1.0      354      5      08MTF8
100     3      1.0      354      5      08MTF8

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ALIGNMENTS

RESULT 1

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Q8N0M4      PRELIMINARY:      PRT:      816 AA.
ID      Q8N0M4
AC      Q8N0M4
DT      01-OCT-2002 (Tremblrel: 22, Created)
DT      01-OCT-2002 (Tremblrel: 22, Last sequence update)
DT      01-MAR-2003 (Tremblrel: 23, Last annotation update)
DE      Neurotigin X.
CS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Strausberg R.;
RA      Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RT      12.
RP      SEQUENCE FROM N.A.
RA      Jaman S., Quach H., Pelicci X., Bourgeron T.;
RT      "Evolution and expression of the human neurotigin family, including
RT      two primate specific members on the X and Y chromosomes."
RL      Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC      -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXY-ESTERASE/LIPASE FAMILY.
DR      EMBL; BC034018; AA034018.1; .
DR      EMBL; AF376803; AA046112.1; .
DR      InterPro: IPR002018; Carboxylesterase.
DR      InterPro: IPR000460; Neurotigin.
DR      InterPro: IPR000379; Ser_estrs_site.
DR      Pfam; PF00135; Coesterase; 1.
DR      PRINTS; PRO1090; NEUROIGLN.
DR      PROSITE; PS00941; CARBOXY-ESTERASE_B_2; 1.
SQ      HYDROLASE.
KM      SEQUENCE      816 AA; 91915 MW; EA1320D630F76BD CRC64;

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Query Match:      65.9%; Score 538; DB 4; Length 816;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 658; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY      159      DHDQSKRPVYVYHGGSYMEGTGMIDGSLASGVNVTITTYRGLIGLFGSTGQA      218
DB      158      DHDQSKRPVYVYHGGSYMEGTGMIDGSLASGVNVTITTYRGLIGLFGSTGQA      217
QY      219      AKGNVGLDQIQALRKIEENVGAFGDPKRVYTFGSGAGACVSLTISHYSEGFPQAKI      278
DB      218      AKGNVGLDQIQALRKIEENVGAFGDPKRVYTFGSGAGACVSLTISHYSEGFPQAKI      277
QY      279      FOSGTA-SSWAVNCPAKYTRILADKYGCKMLDPTNVECCAPKXNYKELIQGTFITPATYH      338
DB      278      FOSGTA-SSWAVNCPAKYTRILADKYGCKMLDPTNVECCAPKXNYKELIQGTFITPATYH      337
QY      339      IAFGVDIDGVYIPDDPQILMEQGFNLVYDMLSVNGCGAKFVGGVYVNEEDGYTKNCFPF      398
DB      338      IAFGVDIDGVYIPDDPQILMEQGFNLVYDMLSVNGCGAKFVGGVYVNEEDGYTKNCFPF      397
QY      399      SYSNFVNLYGVFEGKDTIRETIKENVYTDWADKRNPEYTRPKTVALFTHQWAPAVYA      457
DB      399      SYSNFVNLYGVFEGKDTIRETIKENVYTDWADKRNPEYTRPKTVALFTHQWAPAVYA      457

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DB      398      SYSNFVNLYGVFEGKDTIRETIKENVYTDWADKRNPEYTRPKTVALFTHQWAPAVYA      457
QY      458      DLHAQYGSFTFYFAFYHHCQSEMKRSMWDSAHGDEVYVFG-PMIGTELFSQNFSDYV      517
DB      458      DLHAQYGSFTFYFAFYHHCQSEMKRSMWDSAHGDEVYVFG-PMIGTELFSQNFSDYV      517
QY      518      MISAAYVYVYTNFPAKTDGPNQVPODTSFYTHKXPRFEVMSKXNPDQULYHGLKPR      577
DB      518      MISAAYVYVYTNFPAKTDGPNQVPODTSFYTHKXPRFEVMSKXNPDQULYHGLKPR      577
QY      578      VRDPRATYVAFMLELVLPHLNLNEIFQVYSTTTPVPPDDTSFPFYSRSPAKTWPTTK      637
DB      578      VRDPRATYVAFMLELVLPHLNLNEIFQVYSTTTPVPPDDTSFPFYSRSPAKTWPTTK      637
QY      638      RPAITPANNPKSKDPBKFGPDITVLVETKRDISTE-SVITANGASLLPLN--APALY      697
DB      638      RPAITPANNPKSKDPBKFGPDITVLVETKRDISTE-SVITANGASLLPLN--APALY      697
QY      698      YKDKRHRHTHRPSPORTTNDIAHIONEELMS-LOKQLEHDECESLQADTLRLTGP      757
DB      698      YKDKRHRHTHRPSPORTTNDIAHIONEELMS-LOKQLEHDECESLQADTLRLTGP      757
QY      758      PBYTLTLRSPDDIPMTPTNTTMTPTLTGNOPLATPNTFGSGQNS-TNLRHGSTTRV      816
DB      758      PBYTLTLRSPDDIPMTPTNTTMTPTLTGNOPLATPNTFGSGQNS-TNLRHGSTTRV      816

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RESULT 2

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Q8JUGO      PRELIMINARY:      PRT:      817 AA.
ID      Q8JUGO
AC      Q8JUGO
DT      01-MAY-2000 (Tremblrel: 13, Created)
DT      01-MAY-2000 (Tremblrel: 13, Last sequence update)
DT      01-OCT-2002 (Tremblrel: 23, Last annotation update)
DE      Hypothetical protein KIAA1260 (Frogmont).
CS      KIAA1260.
OC      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      MEDLINE=20039619; PubMed=10574462;
RA      Nagase T., Ishikawa K., Kikuno R., Hirosewa X., Nemura N., Ohara O.;
RT      "Prediction of the coding sequences of unidentified human genes. XV.
RT      The complete sequences of 100 new cDNA clones from brain which code
RT      for large proteins in vitro."
RJ      DNA Res. 6:337-345(1999).
CC      -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXY-ESTERASE/LIPASE FAMILY.
DR      EMBL; AB033086; BA06574.1; .
DR      HSPD; P21835; XAA.
DR      InterPro: IPR002018; Carboxylesterase.
DR      InterPro: IPR000460; Neurotigin.
DR      InterPro: IPR000379; Ser_estrs_site.
DR      Pfam; PF00135; Coesterase; 1.
DR      PRINTS; PRO1090; NEUROIGLN.
DR      PROSITE; PS00941; CARBOXY-ESTERASE_B_2; 1.
KM      HYDROLASE.
FT      NON_TER
SQ      SEQUENCE      817 AA; 92016 MW; D991AC6BAC378763 CRC64;

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Query Match:      65.9%; Score 538; DB 4; Length 817;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 658; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY      159      DHDQSKRPVYVYHGGSYMEGTGMIDGSLASGVNVTITTYRGLIGLFGSTGQA      218
DB      159      DHDQSKRPVYVYHGGSYMEGTGMIDGSLASGVNVTITTYRGLIGLFGSTGQA      218
QY      219      AKGNVGLDQIQALRKIEENVGAFGDPKRVYTFGSGAGACVSLTISHYSEGFPQAKI      278
DB      219      AKGNVGLDQIQALRKIEENVGAFGDPKRVYTFGSGAGACVSLTISHYSEGFPQAKI      278

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QY 279 TCGCTALSSMANVYQPAKYTRILADKVGGM:LTTRWEC:LRNKYKELIQCTITETATVH 338
DB 279 TCGCTALSSMANVYQPAKYTRILADKVGGM:LTTRWEC:LRNKYKELIQCTITETATVH 338
QY 339 TACGPIIDGCVIPDDQILMEGGEF:NYCINLGVNGEGELKXPDDGIVNEDGVTNRDCEP 398
DB 339 TACGPIIDGCVIPDDQILMEGGEF:NYCINLGVNGEGELKXPDDGIVNEDGVTNRDCEP 398
QY 399 SVSNFVNDLYGYPEGKDTLRETIKMYITDMADKENPETERKTLVALFTDHQVAPAVA-A 457
DB 399 SVSNFVNDLYGYPEGKDTLRETIKMYITDMADKENPETERKTLVALFTDHQVAPAVA-A 457
QY 456 DLHAQYGSPTFYFAFHHCQSEMKPSMADSAHGDVFPYFG:PMIGPTELSGNSKNDV 517
DB 456 DLHAQYGSPTFYFAFHHCQSEMKPSMADSAHGDVFPYFG:PMIGPTELSGNSKNDV 517
QY 518 MLSAVVYTWNTWNAKTCGPNQPVQDTEKFIHTKPNFFFEVAMSKYKPKQCLYHLGLKR 577
DB 518 MLSAVVYTWNTWNAKTCGPNQPVQDTEKFIHTKPNFFFEVAMSKYKPKQCLYHLGLKR 577
QY 578 VRDHYRATKYAFLELVPHLNLNEIFQYVSTTKYPPDMTSFPYGRRSAPAKIWPTRK 637
DB 578 VRDHYRATKYAFLELVPHLNLNEIFQYVSTTKYPPDMTSFPYGRRSAPAKIWPTRK 637
QY 638 RPATPANNPKSHKDHKTGPEDTVLLETGRYSVE:SVTIAVGSLLFLNLAPALY 697
DB 638 RPATPANNPKSHKDHKTGPEDTVLLETGRYSVE:SVTIAVGSLLFLNLAPALY 697
QY 699 YKKDKRHEHTRRSPQRYTNDIAHIONEELSLCKOLEHDEHES:QANDTLRLICEP 757
DB 699 YKKDKRHEHTRRSPQRYTNDIAHIONEELSLCKOLEHDEHES:QANDTLRLICEP 757
QY 753 PLYTLRLRSPDDIP:LMKPYTIVYINVL:GNGQY:HTN:TFSGGQNSTL:PHGHS:TRV 816
DB 753 PLYTLRLRSPDDIP:LMKPYTIVYINVL:GNGQY:HTN:TFSGGQNSTL:PHGHS:TRV 816

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RESULT 3

Q9NF23 PRELIMINARY; PRT; 816 AA.

AC Q9NF23;
 DT 01-OCT-2002 (TREMBLrel. 22, Created);
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update);
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update);
 DE Neuroigin Y.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Umanin S., Quach H., Fellous X., Bourgeron T.
 RT "Evolution and expression of the human neuroigin family, including
 RT two primate specific members on the X and Y chromosomes."
 RL Submitted (MAY-2001) to the FMBL/GenBank/DBJ databases.
 CC - - SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DE EMBL: A878684; AAA4613.1; -
 DR InterPro: IPR02018; CarbesteraseB.
 DR InterPro: IPR00460; Neuroigin.
 DR InterPro: IPR00379; Ser esters _site.
 DR Pfam: PF00135; Coesterase_1.
 DR PRINTS: PR01050; NEUROIGIN.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2, 1.
 KW Hydrolase.
 SQ SEQUENCE 816 AA; 92020 MW; FB68910773B1BBF6 CRC64;

Query Match 40.8; Score 326; DB 4; Length 816;
 Best Local Similarity 99.6%; P-val: No.0;
 Matches 546; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

163 QNSKKPVMVYIHGGSYVEGTGNMIDGSLASVGNVIT:NYRLGILGFLSTGQAAKGN 222

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DB 162 QNSKKPVMVYIHGGSYVEGTGNMIDGSLASVGNVIT:NYRLGILGFLSTGQAAKGN 222
QY 223 YGLIDQIQALRMIEENGAEGDPKRVTTFGSGAGACVSLTSHSEGLFGQAL:IOSG 282
DB 223 YGLIDQIQALRMIEENGAEGDPKRVTTFGSGAGACVSLTSHSEGLFGQAL:IOSG 282
QY 282 TALSSMANVYQPAKYTRILADKVGGM:LTTRWEC:LRNKYKELIQCTITETATVH 338
DB 282 TALSSMANVYQPAKYTRILADKVGGM:LTTRWEC:LRNKYKELIQCTITETATVH 338
QY 343 PVIIGDVPDDQILMEGGEF:NYCINLGVNGEGELKXPDDGIVNEDGVTNRDCEP 398
DB 343 PVIIGDVPDDQILMEGGEF:NYCINLGVNGEGELKXPDDGIVNEDGVTNRDCEP 398
QY 399 SVSNFVNDLYGYPEGKDTLRETIKMYITDMADKENPETERKTLVALFTDHQVAPAVA-A 457
DB 399 SVSNFVNDLYGYPEGKDTLRETIKMYITDMADKENPETERKTLVALFTDHQVAPAVA-A 457
QY 456 DLHAQYGSPTFYFAFHHCQSEMKPSMADSAHGDVFPYFG:PMIGPTELSGNSKNDV 517
DB 456 DLHAQYGSPTFYFAFHHCQSEMKPSMADSAHGDVFPYFG:PMIGPTELSGNSKNDV 517
QY 518 MLSAVVYTWNTWNAKTCGPNQPVQDTEKFIHTKPNFFFEVAMSKYKPKQCLYHLGLKR 577
DB 518 MLSAVVYTWNTWNAKTCGPNQPVQDTEKFIHTKPNFFFEVAMSKYKPKQCLYHLGLKR 577
QY 578 VRDHYRATKYAFLELVPHLNLNEIFQYVSTTKYPPDMTSFPYGRRSAPAKIWPTRK 637
DB 578 VRDHYRATKYAFLELVPHLNLNEIFQYVSTTKYPPDMTSFPYGRRSAPAKIWPTRK 637
QY 638 RPATPANNPKSHKDHKTGPEDTVLLETGRYSVE:SVTIAVGSLLFLNLAPALY 697
DB 638 RPATPANNPKSHKDHKTGPEDTVLLETGRYSVE:SVTIAVGSLLFLNLAPALY 697
QY 699 YKKDKRHEHTRRSPQRYTNDIAHIONEELSLCKOLEHDEHES:QANDTLRLICEP 757
DB 699 YKKDKRHEHTRRSPQRYTNDIAHIONEELSLCKOLEHDEHES:QANDTLRLICEP 757
QY 753 PLYTLRLRSPDDIP:LMKPYTIVYINVL:GNGQY:HTN:TFSGGQNSTL:PHGHS:TRV 816
DB 753 PLYTLRLRSPDDIP:LMKPYTIVYINVL:GNGQY:HTN:TFSGGQNSTL:PHGHS:TRV 816

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RESULT 4

Q9Y2F8 PRELIMINARY; PRT; 648 AA.

AC Q9Y2F8;
 DT 01-NOV-1999 (TREMBLrel. 12, Created);
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update);
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update);
 DE Hypothetical protein KIA0951.
 GN KIA0951.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosewa M.,
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.,
 RT "The complete sequences of the coding sequences of identified human genes. XIII.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro."
 RL DNA Res. 6:63-70(1999).
 CC - - SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DE EMBL: AB023166; BA476795.1; -
 DR HSPF: P21836; IMA.
 DR InterPro: IPR02018; CarbesteraseB.
 DR InterPro: IPR00460; Neuroigin.
 DR InterPro: IPR00379; Ser esters _site.
 DR Pfam: PF00135; Coesterase_1.
 DR PRINTS: PR01050; NEUROIGIN.
 DR Hypothetical protein; Hydrolase.
 KW SEQUENCE 648 AA; 72885 MW; 1A2E6727A709BFBC CRC64;

Query Match: 39.1%; Score 319; DB 4; Length 648;
 Best Local Similarity: 99.6%; Pred. No. 0;
 Matches 539; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

DB 170 NXYTHGSGVMEGGMIDGSLASGNNVITINVEGLGLSTLSTDCAKKNGCILDG 229
 1 MVIHGGSTMEGGMIDGSLASGNNVITINVEGLGLSTDCAKKNGCILDG 60

QY 230 QALRMIEENVGAGFGDPKRTITFGSGAGASCVSLTLSHVEGLFQKAIIGSGTALSSWA 289
 DB 61 QALRMIEENVGAGFGDPKRTITFGSGAGASCVSLTLSHVEGLFQKAIIGSGTALSSWA 120

QY 290 VNYQPAKYTRILADKVGCMMLDTTDMVECCRNKXVELLIQITTPATYVIAFGPVLDGV 349
 DB 121 VNYQPAKYTRILADKVGCMMLDTTDMVECCRNKXVELLIQITTPATYVIAFGPVLDGV 180

QY 350 IPPDPQIMCEGFLVYDMLGVNCGEGLKFGVGVNEDGVTNPFCSSVNFVGNVXG 409
 DB 191 IPPDPQIMCEGFLVYDMLGVNCGEGLKFGVGVNEDGVTNPFCSSVNFVGNVXG 240

QY 410 YPEGKDTJRETIKENYTCMDAKENPECTRRKTVVAFTHQWVAFAVA-ADLRAGYGSPT 468
 DB 241 YPEGKDTJRETIKENYTCMDAKENPECTRRKTVVAFTHQWVAFAVA-ADLRAGYGSPT 300

QY 469 FVAFHHGCGSEKSPASDASHGDEYVYVGIYGTGLFSCGFSKNDVMSAVVNTYT 529
 DB 301 FVAFHHGCGSEKSPASDASHGDEYVYVGIYGTGLFSCGFSKNDVMSAVVNTYT 360

QY 529 NFAKTGDDPNQPVQDRTKFIHTKPNFEVMAKSKYKPDOLYHIGKERVDRHYATKVA 568
 DB 361 NFAKTGDDPNQPVQDRTKFIHTKPNFEVMAKSKYKPDOLYHIGKERVDRHYATKVA 420

QY 589 FWELVPHLHNLNLEIFQYVSTTKVPPDMTSFPYGTSSPAKIMWTTKRPATTPANNPK 648
 DB 421 FWELVPHLHNLNLEIFQYVSTTKVPPDMTSFPYGTSSPAKIMWTTKRPATTPANNPK 480

QY 649 HSKDPKHTGPEDEDTVLETKRDSYSELSTVTAAGSALLFLNIAFAALYKCKDKRHETH 709
 DB 481 HSKDPKHTGPEDEDTVLETKRDSYSELSTVTAAGSALLFLNIAFAALYKCKDKRHETH 540

QY 709 R 709
 DB 541 R 541

RESULT 5
 Q8MMG7 PRELIMINARY; PRT; 213 AA.
 AC Q8MMG7: 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Neuro1igin 4 (Fragment).
 OS Macaca mulatta (Rhesus macaque).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecinae; Macaca.
 NCBI_TaxID=9544;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC Tissue=Medial basar hypothalamus;
 RA Murgens A.E., O'Lea S.R.;
 RL Submitted (FRC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF462606; AAL65382.1; -;
 FT NON TER 1
 SQ SEQUENCE 213 AA; 24096 MW; 3AF21610C35C660B CRC64;

Query Match: 26.1%; Score 213; DB 6; Length 213;
 Best Local Similarity: 100.0%; Pred. No. 176-221;
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 604 EQYVSTTTXVPPDMTSFPYGTSSPAKIMWTTKRPATTPANNPKSKDPKHTGPEDETTV 663
 1 EQYVSTTTXVPPDMTSFPYGTSSPAKIMWTTKRPATTPANNPKSKDPKHTGPEDETTV 663

DB 1 EQYVSTTTXVPPDMTSFPYGTSSPAKIMWTTKRPATTPANNPKSKDPKHTGPEDETTV 60
 QY 664 LIETKRYSTELSVTIWAGSL-FLNIAFAALYKCKDKRHETHRSPFORNTDIAH 723
 DB 61 LIETKRYSTELSVTIWAGSL-FLNIAFAALYKCKDKRHETHRSPFORNTDIAH 120

QY 724 IONEIWSLQMKLEHDECEISQADDT-RLTCPPYTLTLRRSPDIPLMTPTTTP 783
 DB 121 IONEIWSLQMKLEHDECEISQADDT-RLTCPPYTLTLRRSPDIPLMTPTTTP 180

QY 784 NTLGMOPLHTFNTFSGGNSSTLPHKSTTRV 816
 DB 181 NTLGMOPLHTFNTFSGGNSSTLPHKSTTRV 213

RESULT 6
 Q8N207 PRELIMINARY; PRT; 509 AA.
 AC Q8N207: 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein FLJ90041.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC Tissue=Embryo;
 RA Tsogai T., Oca T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
 RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
 RA Masuho Y., Oso T., Okano K., Yoshikawa Y., Aoyama S., Sasaki N.,
 RA Hattori A., Okumura K., Iwayanagi T., Niromiya K.,
 RA "NEDO human cDNA sequencing project";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
 DR EMBL: AK074522; BA011039.1; -;
 DR InterPro: IPR002018; Carboxylesterase.
 DR Pfam: PF00135; Coesterase.1.
 DR PRINTS: PR01090; NEUROLOGIN.
 DR Hypothetical protein; Hydrolase.
 KW SEQUENCE 509 AA; 57793 MW; 682170A29CB77003 CRC64;

Query Match: 6.1%; Score 50; DB 4; Length 509;
 Best Local Similarity: 100.0%; Pred. No. 44-45;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 CNFSKNDVMSAVVMTWTNPAKTGDPNQPVDQTKFIHTKPNFEVAV 559
 DB 212 CNFSKNDVMSAVVMTWTNPAKTGDPNQPVDQTKFIHTKPNFEVAV 261

RESULT 7
 Q9UP72 PRELIMINARY; PRT; 823 AA.
 AC Q9UP72: 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein KIAA1070 (Neuro1igin 1).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC Tissue=Brain;
 RA MEDLINE=99397452; PubMed=10470851;
 RA Kikuno R., Nagase T., Ishikawa K., Hirose M., Miyajima N.,

RA Tanaka A., Kotani H., Nomura N., Chata O.;
 RT "Prediction of the coding sequences of unidentified human genes. XIV.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro."
 RL DNA Res. 6:197-205(1999).
 RN [2];
 RP SEQUENCE FROM N.A.
 RC TISSUE=Duodenum;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 CC EMBL: AB028993; BAA63022.1; -;
 DR EMBL: BC03555; AA82555.1; -;
 DR HSSP: P21836; 1MAA.
 DR Genew; HGNC:14291; NLGN1.
 DR InterPro; IPR002048; Carboxesterase.
 DR InterPro; IPR000460; Neuroligin.
 DR InterPro; IPR000379; Ser_estrs_site.
 DR Pfam; PF00135; Coesterase; 1.
 DR PRINTS; PRO1090; NEUROLIGIN.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hypothetical protein; Hydrolase.
 SQ SEQUENCE 823 AA; 92800 MW; EA93B8F96C1CB8A8 CRC64;

Query Match 6.1%; Score 50; DB 4; Length 823;
 Best Local Similarity 100.0%; Pred. No. 6.9e-45;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 CNEFKQVWLSAVVMTYWTNFAKTGDPQVFCQDKFHTKRNREEVAV 559
 |||
 DB 526 CNEFKQVWLSAVVMTYWTNFAKTGDPQVFCQDKFHTKRNREEVAV 573

RESULT 8

062765 PRELIMINARY; PRT: 643 AA.
 ID 062765
 AC 062765;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-FAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Neuroligin 1.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=95254653; PubMed=7736595;
 RA Ichchenko K., Hara Y., Nguyen T., Ulrich B., Miesler N., Mowaw C.,
 RA Suchof T.C.;
 RT "Neuroligin 1: a splice site-specific ligand for beta-neurexins."
 RL Cell 81:435-443(1995).
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 CC EMBL: U22952; AAA85720.1; -;
 DR HSSP: P37967; 1QZ3.
 DR InterPro; IPR002018; Carboxesterase.
 DR InterPro; IPR000460; Neuroligin.
 DR InterPro; IPR00379; Ser_estrs_site.
 DR Pfam; PF00135; Coesterase; 1.
 DR PRINTS; PRO1090; NEUROLIGIN.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolase.
 SQ SEQUENCE 843 AA; 94294 MW; 90A18540245B789D CRC64;

Query Match 6.1%; Score 50; DB 11; Length 843;
 Best Local Similarity 100.0%; Pred. No. 7e-45;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 CNEFKQVWLSAVVMTYWTNFAKTGDPQVFCQDKFHTKRNREEVAV 559
 |||
 DB 546 CNEFKQVWLSAVVMTYWTNFAKTGDPQVFCQDKFHTKRNREEVAV 595

RESULT 9
 06NSB6 PRELIMINARY; PRT: 134 AA.
 AC 06NSB6
 ID 06NSB6
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Similar to neuroligin 3 isoform.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 CC EMBL: BC032567; AA832567.1; -;
 DR InterPro; IPR002018; Carboxesterase.
 DR Pfam; PF00135; Coesterase; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolase.
 SQ SEQUENCE 134 AA; 15225 MW; 91ADC5AA38A2EBCD CRC64;

Query Match 5.9%; Score 48; DB 4; Length 134;
 Best Local Similarity 100.0%; Pred. No. 1.9e-43;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 QNSKRPVWYIHGGSYMEGTGNNIDSLASGVNVVITNREGLG 210
 |||
 DB 63 QNSKRPVWYIHGGSYMEGTGNNIDSLASGVNVVITNREGLG 107

062711 PRELIMINARY; PRT: 550 AA.
 ID 062711
 AC 062711;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2002 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein KIAA1366 (fragment).
 DE KIAA1366.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=20181126; PubMed=10728198;
 RA Nagase T., Kikuno R., Ishikawa K., Hikosawa M., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XV."
 RT The complete sequences of 150 new cDNA clones from brain which code
 RT for large proteins in vitro."
 RL DNA Res. 7:65-73(2000).
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 CC EMBL: ABC37787; BAA92604.1; -;
 DR HSSP; P21836; 1MAA.
 DR Genew; HGNC:14290; NLGN2.
 DR InterPro; IPR002018; Carboxesterase.
 DR InterPro; IPR000460; Neuroligin.
 DR InterPro; IPR002965; P_rich_extensn.
 DR Pfam; PF00135; Coesterase; 1.
 DR PRINTS; PRO1090; NEUROLIGIN.
 DR PRINTS; PRO1217; PRICHEXTENS.
 KW Hypothetical protein; Hydrolase.
 SQ SEQUENCE 550 AA; 60734 MW; 5B09C3E2323618F1 CRC64;

Query Match 5.9%; Score 48; DB 4; Length 550;
 Best Local Similarity 100.0%; Pred. No. 7.2e-43;


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      DNA Res. 7:143-150(2000).
      -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC EMBL; AB04059.3; BAA96004.1; -.
DR HSSP; F21836; IMMA.
DR InterPro; IPR002018; Carboxesterase3.
DR InterPro; IPR000460; Neurologin.
DR InterPro; IPR000379; Ser_ester_site.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR01090; NEUROLIGIN.
DR Hypothetical protein; Hydrolyase.
FT NON TER 1
SQ SEQUENCE 682 AA; 75592 MW; 9E56DBF44F5DC31 CRC64;

Query Match 4.3%; Score 35; DB 4; Length 682;
Best Local Similarity 100.0%; Pred. No. 1.4e-28;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 KPWVYIHGSGYMEGTGMIDGSLASGYNIVIT 201
DB 34 KPWVYIHGSGYMEGTGMIDGSLASGYNIVIT 68

RESULT 15
Q9NZ94 PRELIMINARY; PRT; 828 AA.
AC Q9NZ94;
LT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Neurologin 3 isoform.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=20231756; PubMed=10767552;
RA Philibert R.A., Winfield S.L., Sandhu H.K., Martin B.M., Gims E.I.;
RT "The structure and expression of the human neurologin-3 gene.";
RL Gene 246:303-310(2000).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AF217413; AAF1232.1; -.
DR HSSP; P21836; IMMA.
DR InterPro; IPR002018; Carboxesterase3.
DR InterPro; IPR000460; Neurologin.
DR InterPro; IPR000379; Ser_ester_site.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR01090; NEUROLIGIN.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolyase.
SQ SEQUENCE 828 AA; 91570 MW; E72BAF3472678692 CRC64;

Query Match 4.3%; Score 35; DB 4; Length 828;
Best Local Similarity 100.0%; Pred. No. 1.7e-28;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 KPWVYIHGSGYMEGTGMIDGSLASGYNIVIT 201
DB 180 KPWVYIHGSGYMEGTGMIDGSLASGYNIVIT 214

RESULT 16
Q9NZ95 PRELIMINARY; PRT; 848 AA.
AC Q9NZ95;
LT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Neurologin 3 isoform.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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CX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=20231756; PubMed=10767552;
RA Philibert R.A., Winfield S.L., Sandhu H.K., Martin B.M., Gims E.I.;
RT "The structure and expression of the human neurologin-3 gene.";
RL Gene 246:303-310(2000).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AF217413; AAF1233.1; -.
DR HSSP; F21836; IMMA.
DR InterPro; IPR002018; Carboxesterase.
DR InterPro; IPR000460; Neurologin.
DR InterPro; IPR000379; Ser_ester_site.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR01090; NEUROLIGIN.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolyase.
SQ SEQUENCE 848 AA; 93895 MW; B3FE2FAB7E427C82 CRC64;

Query Match 4.3%; Score 35; DB 4; Length 848;
Best Local Similarity 100.0%; Pred. No. 1.7e-28;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 KPWVYIHGSGYMEGTGMIDGSLASGYNIVIT 201
DB 200 KPWVYIHGSGYMEGTGMIDGSLASGYNIVIT 234

RESULT 17
Q924X0 PRELIMINARY; PRT; 144 AA.
AC Q924X0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Neurologin 3 protein (Fragment).
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RA Chateauet A.;
RT "mouse neurologin 3".
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AJ291730; CAC37694.1; -.
DR InterPro; IPR002018; Carboxesterase3.
DR Pfam; PF00135; Coesterase; 1.
KW Hydrolyase.
FT NON TER 1
FT NON TER 144
SQ SEQUENCE 144 AA; 16348 MW; D4618324E8AA7727 CRC64;

Query Match 3.9%; Score 32; DB 11; Length 144;
Best Local Similarity 100.0%; Pred. No. 6.2e-26;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 399 SVSNFVDNLYGYPECKDTLRETIKFMVTDMA 430
DB 34 SVSNFVDNLYGYPECKDTLRETIKFMVTDMA 65

RESULT 18
Q8BYM5 PRELIMINARY; PRT; 825 AA.
AC Q8BYM5;
LT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE NEUROLIGIN 3 isoform HNL3 homolog.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10293;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=2254683; PubMed=1266851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 426:563-573 (2002).
DR EMBL: AC039018; BAC30207.1;
SQ SEQUENCE 825 AA; 91175 MW; 33F7F939B0A44CE CRC64;

Query Match 3.9%; Score 32; DB 1; Length 825;
Best Local Similarity 100.0%; Pred. No. 3.1e-25;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 399 SVSNFVNDLYGPEGKDTRETIKFMVTDWAD 430
Db 409 SVSNFVNDLYGPEGKDTRETIKFMVTDWAD 440

RESULT 19
Q9NZ97 PRELIMINARY; PRT; 828 AA.
AC Q9NZ97;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Neurotigin 3 isoform HNL3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20231756; PubMed10767552;
RA Philibert R.A., Winfield S.L., Sandhu H.K., Martin B.M., Gims E.L.;
RT "The structure and expression of the human neurotigin-3 gene";
RL Gene 246:303-310 (2000).
CC 1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLSTERASE/LIPASE FAMILY.
DR EMBL: AF217411; AAF7230.1;
DR HSSP: P37967; IQS3.
DR InterPro: IPR002018; Carboxylsterase3.
DR InterPro: IPR000460; Neurotigin.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PRINTS: PR01090; NEUROIGIN.
DR PROSITE: PS00941; CARBOXYLSTERASE_B_2; 1.
KW Hydroilase.
SQ SEQUENCE 828 AA; 91554 MW; A896C05932678CAA CRC64;

Query Match 3.9%; Score 32; DB 4; Length 828;
Best Local Similarity 100.0%; Pred. No. 3.2e-25;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 399 SVSNFVNDLYGPEGKDTRETIKFMVTDWAD 430
Db 412 SVSNFVNDLYGPEGKDTRETIKFMVTDWAD 443

RESULT 20
Q62889 PRELIMINARY; PRT; 543 AA.
AC Q62889;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update);
DE Neurotigin.3.
OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Forebrain;
RX MEDLINE=96162010; PubMed=8576240;
RA Ichchenko K., Nguyen T., Sudhof T.C.;
RT "Structures, alternative splicing, and neurexin binding of multiple
RT neurotigin";
RL J. Biol. Chem. 271:2676-2683 (1996).
CC 1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLSTERASE/LIPASE FAMILY.
DR EMBL: U41663; AAA37871.1;
DR HSSP: P21836; 1MAA.
DR InterPro: IPR002018; CarboxylsteraseB.
DR InterPro: IPR000460; Neurotigin.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PRINTS: PR01090; NEUROIGIN.
DR PROSITE: PS00941; CARBOXYLSTERASE_B_2; 1.
KW Hydroilase.
SQ SEQUENCE 848 AA; 93888 MW; 7520653B32535750 CRC64;

Query Match 3.9%; Score 32; DB 1; Length 848;
Best Local Similarity 100.0%; Pred. No. 3.2e-25;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 399 SVSNFVNDLYGPEGKDTRETIKFMVTDWAD 430
Db 432 SVSNFVNDLYGPEGKDTRETIKFMVTDWAD 463

RESULT 21
Q8W8H2 PRELIMINARY; PRT; 202 AA.
AC Q8W8H2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Neurotigin 3 (Fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
CX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Medial basal hypothalamus;
RA Mungana A.E., Ojeda S.R.;
RT Submitted (SEP-2001) to the EMBL/Genbank/DDBJ databases.
CC 1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLSTERASE/LIPASE FAMILY.
DR EMBL: AF248501; AAL40263.1;
DR InterPro: IPR002018; CarboxylsteraseB.
DR InterPro: IPR000460; Neurotigin.
DR Pfam: PF00135; Coesterase; 1.
DR PRINTS: PR01090; NEUROIGIN.
KW Hydroilase.
FT KIN_TBR 1
FT KIN_TBR 202
SQ SEQUENCE 202 AA; 22897 MW; 99602C5B728E758 CRC64;

Query Match 3.4%; Score 28; DB 6; Length 202;
Best Local Similarity 100.0%; Pred. No. 2e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 510 CNFSKDVNLSAVVYTYWTFNFAKTGDPN 537
Db 49 CNFSKDVNLSAVVYTYWTFNFAKTGDPN 76
RESULT 22
Q8NCD0 PRELIMINARY; PRT; 335 AA.
ID Q8NCD0

AC Q8NCD0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein F190333.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isegai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hiro Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Masuhara Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Nimomiya K.;
RT "NEO human cDNA sequencing project."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJP databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
DR EMBL; AK074814; BAC11226.1; -
DR InterPro; IPR002018; Carboxylesterase.
DR InterPro; IPR000460; Neuriligin.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR01090; NEURILIGIN.
KW Hypothetical protein; Hydrolase.
SQ SEQUENCE 335 AA; 37399 MW; 3E82B66FCB5F54ED CRC64;

Query Match 3.4%; Score 28; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 3.2e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 CNFSKNDVLSAVMTYNTNFAKTGDPN 537
DB 3: CNFSKNDVLSAVMTYNTNFAKTGDPN 58

RESULT 23
Q8BXK4 PRELIMINARY; PRT; 383 AA.
AC Q8BXK4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE NEUROLOGIN 3 isoform HMD homolog (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-C57BL/6J; Tissue=retina;
RX MEDLINE=22354683; PubMed=1246651;
RA The PANTOM Consortium.
RT "The RIKEN Genome Exploration Research Group Phase I & II team:
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK044387; BAC11918.1; -
DR NCBI_TaxID=10090;
SQ SEQUENCE 383 AA; 43075 MW; D0B3E31B34D35056 CRC64;

QY 510 CNFSKNDVLSAVMTYNTNFAKTGDPN 537
DB 79 CNFSKNDVLSAVMTYNTNFAKTGDPN 106

RESULT 24
Q99K10 PRELIMINARY; PRT; 245 AA.

AC Q99K10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Similar to neuroigin 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJP databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
DR EMBL; BC005523; AAH05523.1; -
DR HSSP; P30122; 2BCE.
DR MGD; MGI:2179435; N19n1.
DR InterPro; IPR002018; Carboxylesterase.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00941; CARBOXYL-ESTERASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE 245 AA; 27130 MW; 48ED37A3433E9B5 CRC64;

Query Match 2.2%; Score 18; DB 11; Length 245;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 KPVWVYHGGSYMEGTGN 184
DB 173 KPVWVYHGGSYMEGTGN 190

RESULT 25
Q75612 PRELIMINARY; PRT; 612 AA.
AC Q75612;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Bile salt-dependent lipase oncofetal isoform (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Pancreas;
RX MEDLINE=98447673; PubMed=9774442;
RA Pasqualini E., Gallot N., Panicot L., Mas E., Llobes R.,
RA Lombard C.;
RT "Molecular cloning of the oncofetal isoform of the human pancreatic
RT bile salt-dependent lipase."
RL J. Biol. Chem. 273:28208-28218 (1998).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
DR EMBL; AF081673; AAC1012.1; -
DR HSSP; P30122; 2BCE.
DR InterPro; IPR002018; Carboxylesterase.
DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser estersite.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLINESTERASE.
DR PROSITE; PS00122; CARBOXYL-ESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYL-ESTERASE_B_2; 1.
KW Hydrolase.
FT NON TER 1
SQ SEQUENCE 612 AA; 66363 MW; A5E9092D19390826 CRC64;

Query Match 1.5%; Score 12; DB 4; Length 612;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTFNFAKTGDPN 537

Db 467 YMTNFAKTGDPN 478

RESULT 26

Q16398 PRELIMINARY; PRT; 742 AA.

AC Q16398; 01-NOV-1996 (TREMBLrel. 02, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Bile salt-dependent lipase.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP MEDLINE=6638831; PubMed=7576248;
RA Roudaut S., Miralles F., Margotat A., Escritano M.C., Lombardo E.;
RT "Bile salt-dependent lipase transcripts in human fetal tissues."
RL Biochim. Biophys. Acta 1264:141-150(1995).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: S9774; AAB35489.2; -
DR HSSP: P30122; 28CE.
DR InterPro: IPR002038; Carboxesterase.
DR InterPro: IPR003379; Ser_estr_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE 742 AA; 78317 MW; 4D7DF66772EAC07 CRC64;

Query Match 1.5%; Score 12; DB 4; Length 742;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 526 YMTNFAKTGDPN 537
Db 487 YMTNFAKTGDPN 498

RESULT 27

Q9UP41 PRELIMINARY; PRT; 745 AA.

AC Q9UP41; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Carboxyl ester lipase.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP MEDLINE=58191740; PubMed=9510636;
RA Madevski K., Lidberg U., Bjursell G., Nilsson U.;
RT "Structure and organization of the human carboxyl ester lipase
llocus."
RL Mamm. Genome 9:334-338(1998).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AF032711; AAC26514.1; -
DR HSSP: P30122; 28CE.
DR InterPro: IPR002038; Carboxesterase.
DR InterPro: IPR003379; Ser_estr_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE 745 AA; 78697 MW; 0251356CC556706A CRC64;

Query Match 1.5%; Score 12; DB 4; Length 745;

Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 526 YMTNFAKTGDPN 537
Db 490 YMTNFAKTGDPN 501

RESULT 28

Q9NID1 PRELIMINARY; PRT; 998 AA.

AC Q9NID1; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Carboxyl-ester lipase.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
OX NCBI_TaxID=9593;
RN (1)
RP MEDLINE=20018178; PubMed=13548728;
RA Madevski K., Lidberg U., Bjursell G., Nilsson U.;
RT "Characterization of the gorilla carboxyl ester lipase locus, and the
appearance of the carboxyl ester lipase pseudogene during primate
evolution."
RL Gene 239:273-282(1999).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AF206618; AAF71700.1; -
DR HSSP: P30122; 28CE.
DR InterPro: IPR002038; Carboxesterase.
DR InterPro: IPR003379; Ser_estr_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE 998 AA; 101026 MW; 3C81AD44504EBABA CRC64;

Query Match 1.5%; Score 12; DB 6; Length 998;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 526 YMTNFAKTGDPN 537
Db 490 YMTNFAKTGDPN 501

RESULT 29

Q8WXX4 PRELIMINARY; PRT; 110 AA.

AC Q8WXX4; 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Esterase (Fragment) (Diamondback moth).
OS Plutella xylostella (Diamondback moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Yponomeutoidea; Plutellidae; Plutella.
OX NCBI_TaxID=5165;
RN (1)
RP SEQUENCE FROM N.A.
RA Sten B., Qiao C.;
RT "cDNA cloning and characterization of Plutella xylostella esterase
related to phosphatase insecticides resistance."
RL Submitted (JUG-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AB059914; BAC10286.1; -
DR InterPro: IPR002018; Carboxesterase.
DR InterPro: IPR003379; Ser_estr_site.
DR Pfam: PF00135; Coesterase; 1.

KM Hydrolase. 1
 FT NON TER 1:0 1:0
 SC SEQUENCE 110 AA: 12002 MW: 89C2CC943CCCFD76 CRC64;
 Query Match 1.3%; Score 11; DB 5; Length 110;
 Best Local Similarity 100.0%; Pred. No. 0.0042;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 INVRGILGFL 212
 DB 56 INVRGILGFL 66

RESULT 30
 Q23735 PRELIMINARY; PRT; 540 AA.

AC Q23735;
 CT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DE Esterase B1 precursor (EC 3.1.1.1).
 OS *Culex quinquefasciatus* (Southern house mosquito).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culex.
 NCBI_TaxID=7176;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN=MES;
 RX MEDLINE=95134253; PubMed=7510448;
 RA Vaughan A., Rodriguez X., Hemingway C.;
 RT "The independent gene amplification of *e*-electrophoretically
 RT indistinguishable B esterases from the insecticide-resistant mosquito
 RT *Culex quinquefasciatus*."

RT Biochem. J. 335:651-658(1995).

CC -1- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON
 CC MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.

CC -1- CATALYTIC ACTIVITY: A CARBOXYLIC ESTER + H₂O = AN ALCOHOL + A
 CC CARBOXYLIC ANION.

CC -1- MISCELLANEOUS: THERE ARE TWO SUCH ESTERASES: A AND B. ALLELES OF
 CC BOTH A AND B ARE KNOWN.

CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/ESTERASE FAMILY.

DR EMBL: Z33695; CAA83644.1; -

DR HSSP: P21835; TMAA

DR InterPro: IPR002018; Carboxylesterase.

DR InterPro: IPR000997; Cholinesterase.

DR InterPro: IPR003734; Lipase.

DR InterPro: IPR003739; Ser ester _site.

DR Pfam: PF00135; Coesterase; 1.

DR PRINTS: PR00876; CHOLIN-ESTERASE.

DR PROSITE: PS00122; CARBOXYL-ESTERASE_B_1; 1.

DR PROSITE: PS00120; LIPASE_SER; 1.

KW Hydroxylase; Serine esterase; Glycoprotein; Multigene family; Signal.

FT SIGNAL 1 540

FT CHAIN 1 540

FT ACT SITE 191 191

FT ACT_SITE 442 442

FT DISULFID 68 81

FT CARBOHYD 54 54

FT CARBOHYD 485 485

SO SEQUENCE 540 AA; 60852 MW; AF4787D571EDBDCD CRC64;

Query Match 1.3%; Score 11; DB 5; Length 540.

Best Local Similarity 100.0%; Pred. No. 0.018;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 240 GAFGDPKRVY 250

DB 176 GAFGDPKRVY 186

RESULT 31

Q8BM97

ID Q8BM97 PRELIMINARY; PRT; 559 AA.
 AC Q8BM97;
 CT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DE Similar to carboxylesterase precursor.
 OS *Mus musculus* (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium.
 RA The Riken Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL: AK033563; BAC28361.1; -
 SO SEQUENCE 559 AA; 62305 MW; 8C54D21522C252C4 CRC64;

Query Match 1.3%; Score 11; DB 11; Length 559;

Best Local Similarity 100.0%; Pred. No. 0.019;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYNIYVP 135

DB 121 EDCLYNIYVP 131

RESULT 32

Q8BK48 PRELIMINARY; PRT; 559 AA.

AC Q8BK48;
 CT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DE Similar to carboxylesterase precursor.

DE Similar to carboxylesterase precursor.

OS *Mus musculus* (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN 1;
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Ovary, and Uterus;

RX MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium.

RA The Riken Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."

RL Nature 420:563-573(2002).

DR EMBL: AK077248; BAC36707.1; -

SO SEQUENCE 559 AA; 62317 MW; CC14C61034A122C3 CRC64;

Query Match 1.3%; Score 11; DB 11; Length 559;

Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYNIYVP 135

DB 121 EDCLYNIYVP 131

RESULT 33

Q97110 PRELIMINARY; PRT; 610 AA.

AC Q97110;
 CT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DE Acetylcholinesterase (Fragment).
 OS *Loligo opalescens* (California market squid).

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Acetylcholinesterase (Fragment).

OS *Loligo opalescens* (California market squid).

CC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coeloidae; Neocoleoidea;
 CC Decapodiformes; Scudiformidae; Loligo.
 OX NCBI_TaxID=31211;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Optic lobe.
 RA Talses V., Granoso M., Appagans M., Giovannini E., Romani R., Rosi G.,
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DE EMBL: AF065384; AAD15886.1; -.
 DR HSSP: P21836; IMAA.
 DR InterPro: IPR002018; Carboxesterase.
 DR InterPro: IPR000997; Cholinesterase.
 DR Pfam: PF00135; Coesterase; 1.
 DR PRINTS: PR00878; CHOLNESTRASE.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 KM Hydrolyase.
 FT NON_TER 610 610
 SQ SEQUENCE 610 AA; 69516 MW; 51EBAFFE1112063 CRC64;

Query Match 1.3%; Score 11; DB 5; Length 610;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 527 MTNFAKTGDPN 537
 DQ 506 MTNFAKTGDPN 516

RESULT 34
 C9XYA9 PRELIMINARY; PRT: 656 AA.
 ID C9XYA9
 AC C9XYA9:
 DT 01-NOV-1999 (TREMBlrel. 12, Created;
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Acetylcholinesterase (Fragment).
 SN AChE.
 OS Meloidogyne javanica (Root-knot nematode).
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
 CC Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
 OX NCBI_TaxID=6303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99270313; PubMed=10340488;
 RA Piote C., Arthaud L., Abad P., Rosso M.N.;
 RT "Molecular cloning of an acetylcholinesterase gene from the plant
 parasitic nematode, Meloidogyne incognita and Meloidogyne javanica."
 RJ Mol. Biochem. Parasitol. 99:247-256 (1999).
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DE EMBL: AF065384; AAD25921.1; -.
 DR HSSP: P21836; IMAA.
 DR InterPro: IPR002018; Carboxesterase.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR001064; Crystallin.
 DR Pfam: PF00135; Coesterase; 1.
 DR PRINTS: PR00878; CHOLNESTRASE.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; 1.
 KM Hydrolyase.
 FT NON_TER 656 656
 SQ SEQUENCE 656 AA; 76061 MW; AF90A221AERFPO0C CRC64;

Query Match 1.3%; Score 11; DB 5; Length 656;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 125 EDCLYNIYVP 135

DB 133 EDCLYNIYVP 143

RESULT 35
 C9NGK5 PRELIMINARY; PRT: 656 AA.
 ID C9NGK5
 AC C9NGK5:
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Acetylcholinesterase.
 SN AChE.
 OS Meloidogyne incognita (Southern root-knot nematode).
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
 CC Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
 OX NCBI_TaxID=6306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99270313; PubMed=10340488;
 RA Piote C., Arthaud L., Abad P., Rosso M.N.;
 RT "Molecular cloning of an acetylcholinesterase gene from the plant
 parasitic nematode, Meloidogyne incognita and Meloidogyne javanica."
 RJ Mol. Biochem. Parasitol. 99:247-256 (1999).
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DE EMBL: AF075719; AAD02835.1; -.
 DR HSSP: P21836; IMAA.
 DR InterPro: IPR002018; Carboxesterase.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR001064; Crystallin.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PRINTS: PR00878; CHOLNESTRASE.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; 1.
 KM Hydrolyase.
 FT NON_TER 656 AA; 75962 MW; 646C39B57ABDFE0 CRC64;
 SQ SEQUENCE 656 AA; 75962 MW; 646C39B57ABDFE0 CRC64;

Query Match 1.3%; Score 11; DB 5; Length 656;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYNIYVP 135
 DB 133 EDCLYNIYVP 143

RESULT 36
 C9NGK5 PRELIMINARY; PRT: 248 AA.
 ID C9NGK5
 AC C9NGK5: Q9NM73;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Neurotigin (CG13772 protein).
 SN Neurotigin (CG13772 protein).
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Pterygota;
 CC Insecta; Endopterygota; Diptera; Brachycera; Muscophora;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX Xie W., Boulianne G.L.;
 RT "cDNA (Drosophila neurotigin)."
 DT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amandides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.C., Mortan C.R., Yencel M.D., Zhang Q., Chen L.X.,
RA Brandt R.C., Rogers V.-H.C., Blazyn R.G., Campo X., Pfeiffer B.D.,
RA Mac K.H., Doyle C., Baxter S.G., Helt G., Nelson C.R., Miller G.J.G.,
RA Adair J.F., Agbayani A., An H.-D., Andrews-Plambeck C., Baldwin P.,
RA Baller R.M., Basu A., Bakende J., Bayraktaroglu U.L., Baaley E.M.,
RA Beeson K.V., Beron P.V., Bernat B.P., Bhattacharya D., Shachy S.,
RA Bokova D., Borhan M.R., Buck J., Brokstein P., Brostler P.,
RA Butts K.C., Busan D.A., Butler H., Cadiz E., Center A., Chandra I.,
RA Cherry J.M., Caley S., Darke C., Davenport J.B., Davies P.,
RA de Palos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doug L.E., Dowes M., Duran-Rocha S., Dunkov B.C., Dunn P.,
RA Dubin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischman N.,
RA Foster C., Gabrielian A.E., Gaig N.S., Gebart W.M., Glaser K.,
RA Gloder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris W.,
RA Harris N.L., Harvey D., Heiman T.C., Hernandez J.R., Holck J.,
RA Hostett D., Houston K.A., Howland T.J., Mei M.-H., Idegram C.,
RA Joell M., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Kelchum K.A.,
RA Kamel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasco P., Lee Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Martini B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris T., Mosherelli A.,
RA Mount S.W., Moy M., Murphy B., Murphy L., Wenz D.M., Nelson D.L.,
RA Neelson D.R., Nelson K.A., Nixon K., Kussern D.R., Pachet C.M.,
RA Palazzo V., Pittman G.S., Pan S., Pollard J., Putti V., Reese W.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shee B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spierkas R., Tector C., Turney R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri C.S., Zhao M., Zhang S., Zhao Q., Zheng L.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.Y., Venter C.C.,
RT "The genome sequence of *Drosophila melanogaster*" ;
RL Science 287:2123-2195(2001).
RN
R2 SEQUENCE FROM N.A.
RA Centner S.E., Adams V.D., Kronmiller B., Mac K.H., Holt R.A.,
RA Evans C.A., Goeyne J.D., Amanaidis P.G., Barton R.C., Rogers Y.,
RA Barzon J., An H., Baldwin D., Barzon C., Beeson K.V., Busan D.A.,
RA Carlson J.W., Center A., Champ M., Davenport I.B., Dietz S.W.,
RA Dodson K., Dorsett V., Doug L.E., Doyle C., Dreanok D., Farfan D.,
RA Ferreira S., Frise E., Galie R.F., Garo N.S., George R.A.,
RA Gonzalez M., Huck J., Hoskin D.A., Hostun D., Howard J.C.,
RA Izdegan C., Idaldi M., Kruse D., Li P., Melati B., Mostrelti A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo C.,
RA Paclet J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phoungvorong S., Pittman G.S., Putti V., Richards S., Schaefer P.,
RA Stapleton M., Strong R., Switaski R., Tector C., Tyler E.,
RA Williams S.M., Zaveloff S., Smith H.C., Venter C.C., Rubin G.Y.;
RT "Sequencing of *Drosophila melanogaster* genome" ;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN
R3 SEQUENCE FROM N.A.
RP Mira S., Crosby M.A., Matthews B.B., Bayraktaroglu U., Campbell K.,
RA Hradecky P., Huang Y., Kathiner C.S., Prochnik S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Bettan B., Carlson J.W., Centner S.E.,
RA Clomp M., Drysdale R., Emmert J., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Milburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smitnak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.Y., Mangali C.J., Lewis S.E.;
RT "Annotation of *Drosophila melanogaster* genome" ;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN
R4 SEQUENCE FROM N.A.
RP Adams M.D., Centner S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN
R5 SEQUENCE FROM N.A.
RP Flybase:
RL Submitted (SEP-2002) to the EMBL/GenBank/CCB databases.
CC -!- STYLARITY: BELONGS TO THE TYPE-B CARBOXYTERMINAL-LIPASE FAMILY.
DR EMBL; AF251479; AAF69455.1; --

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DR EMBL: AED03615; AAF52450.2; -.
DR HSPB; P37967; 10E3.
DR Flybase; FBgn0031866; neurColligin.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR003379; Ser esters_site.
DR Pfam; PF00135; Coesterase; 1.
DR ProSITE; PS00941; CARBOXYESTERASE_B_2; 1.
KM HydroLase.
SQ SEQUENCE 1248 AA; 136844 MW; 3F95AD4289F61DF CRC64;
Query Match
Best Local Similarity 100.0%; Score 11; DB 5; Length 1248;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 125 EDCYLNIVVP 135
|||||
Db 280 EDCYLNIVVP 290

RESULT 37
Q9GN02 PRELIMINARY; PRT; 134 AA.
ID Q9GN02
AC Q9GN02;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Alpha-esterase like protein E2 (Fragment).
OS Tribolium castaneum (Red flour beetle).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Tenebrionidae; Tribolium.
CX NCBI_TaxID=7070;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GA-1;
RA Claudianus C., Crone E., Coppin C., Russell R., Oakeshott J.;
RT Resistance to O-glycophosphates."
RL (In: Unknown A. (eds.);
RL PESTICIDE RESISTANCE - SPECIAL ACS MEETING 1999, pp.1-1,
RL Unknown Publisher (2000).
RL -1. SYMMETRY: BELONGS TO THE TYPE-B CARBOXYESTERASE/LIPASE FAMILY.
DR EMBL: AF260821; AAC020.9.1; -.
DR HSPB; P37967; 10E3.
DR InterPro; IPR002018; CarbesteraseB.
DR Pfam; PF00135; Coesterase; 1.
KM HydroLase.
FT NON TER 1 1
FT NON TER 134 134
SQ SEQUENCE 134 AA; 14749 MW; 3BBFECDE7274375 CRC64;
Query Match
Best Local Similarity 100.0%; Score 10; DB 5; Length 134;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 203 NYRGILGFL 212
|||||
Db 107 NYRGILGFL 116

RESULT 38
ID Q23736 PRELIMINARY; PRT; 505 AA.
AC Q23736;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Esterase B (EC 3.1.1.1) (Fragment).
OS Culex quinquefasciatus (Southern house mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culex.
CX NCBI_TaxID=7176;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=PELSS;
RX MEDLINE=95:34253; PubMed=7530448;
RA Vaughan A., Rodriguez M., Hemingway J.;
RT "The independent gene amplification of electrophoretically
RT indistinguishable B esterases from the insecticide-resistant mosquito
RT Culex quinquefasciatus."
R2 Biochem. J. 305:651-658(1995).
CC -1- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON
CC MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.
CC -1- CATALYTIC ACTIVITY: A CARBOXYLIC ESTER + H(2)O = AN ALCOHOL + A
CC CARBOXYLIC ANION.
CC -1- MISCELLANEOUS: THERE ARE TWO SUCH ESTERASES: A AND B. ALLELES OF
CC BOTH A AND B ARE KNOWN.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: Z22696; CAA83645.1; -.
DR HSSP: P17672; I033.
DR InterPro: IPR002018; Carbesterase.
DR InterPro: IPR000734; Lipase.
DR Pfam: PF00135; Coesterase; Ser_estr_site.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00120; Lipase_ser; 1.
KM Hydrolyase; Serine esterase; Glycoprotein; Multigene family.
FT NON_TER
FT ACT_SITE 156 156 BY SIMILARITY.
FT ACT_SITE 457 457 BY SIMILARITY.
FT DISULFID 30 46 BY SIMILARITY.
FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 417 417 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 505 AA; 56934 MW; CF3345CC86F0698 CRC64;

Query Match 1.2%; Score 10; DB 5; Length 505;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 241 AFGDPRKRYT 250
Db 142 AFGDPRKRYT 151

RESULT 39
P91920 PRELIMINARY; PRT; 540 AA.
AC P91920;
DT 01-MAY-1997 (TRENBLREL. 03, Created)
DT 01-MAY-1997 (TRENBLREL. 03, Last sequence update)
DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)
DE Esterase B3.
OS Culex tarsalis (Mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culex.
NCBI_TaxID=7177;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=97385422; PubMed=9241436;
RA Tittiger C., Walker V.K.;
RT "Isolation and characterization of an unamp-lified esterase B3 gene
RT from malathion-resistant Culex tarsalis."
R2 Biochem. Genet. 35:119-138(1997).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: U88972; AAC23391.1; -.
DR HSSP: P21836; IMAA.
DR InterPro: IPR002018; Carbesterase.
DR InterPro: IPR000734; Lipase.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
KM Hydrolyase.
SQ SEQUENCE 540 AA; 60795 MW; CFC8A843A17A558B CRC64;

Query Match 1.2%; Score 10; DB 5; Length 540;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 241 AFGDPRKRYT 250
Db 177 AFGDPRKRYT 186

RESULT 40
Q23734 PRELIMINARY; PRT; 540 AA.
AC Q23734; O02537;
DT 01-JAN-1998 (TRENBLREL. 05, Created)
DT 01-JAN-1998 (TRENBLREL. 05, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE Esterase B2 (EC 3.1.1.1).
CS Culex quinquefasciatus (Southern house mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culex.
NCBI_TaxID=7176;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=PELSS;
RX MEDLINE=95:34253; PubMed=7530448;
RA Vaughan A., Rodriguez M., Hemingway J.;
RT "The independent gene amplification of electrophoretically
RT indistinguishable B esterases from the insecticide-resistant mosquito
RT Culex quinquefasciatus."
R2 Biochem. J. 305:651-658(1995).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=94178593; PubMed=8132048;
RA Vaughan A., Ketterman A.C., Hemingway J.;
RT "Comparisons of nucleic acid sequences of esterases from resistant and
RT susceptible strains of Culex quinquefasciatus."
R2 Biochem. Soc. Trans. 21:481S-485S(1993).
CC -1- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON
CC MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.
CC -1- CATALYTIC ACTIVITY: A CARBOXYLIC ESTER + H(2)O = AN ALCOHOL + A
CC CARBOXYLIC ANION.
CC -1- MISCELLANEOUS: THERE ARE TWO SUCH ESTERASES: A AND B. ALLELES OF
CC BOTH A AND B ARE KNOWN.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: Z22694; CAA83643.1; -.
DR EMBL: Z86069; CAB06676.1; -.
DR HSSP: P21836; IMAA.
DR InterPro: IPR002018; Carbesterase.
DR InterPro: IPR000734; Lipase.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00120; Lipase_ser; 1.
KM Hydrolyase; Serine esterase; Glycoprotein; Multigene family.
FT ACT_SITE 191 191 BY SIMILARITY.
FT ACT_SITE 442 442 BY SIMILARITY.
FT DISULFID 68 81 BY SIMILARITY.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 452 452 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 540 AA; 60697 MW; IAOB40417CC2B70C CRC64;

Query Match 1.2%; Score 10; DB 5; Length 540;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 241 AFGDPRKRYT 250
Db 177 AFGDPRKRYT 186

RESULT 41
Q9VDP5 PRELIMINARY; PRT; 593 AA.
AC Q9VDP5;
DT 01-MAY-2000 (TRENBLREL. 13, Created)

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DT 01-OCT-2002 (TRENBLER). 22, Last sequence update;
CT 01-MAR-2003 (TRENBLER). 23, Last annotation update;
DE CG5030 protein.
GN CG5030.
CS Drosophila melanogaster (Fruit fly).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC Ephydroidae; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20396006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Hersenson S.N.,
RA Sutton G.G., Wortman J.E., Vandal M.D., Zhang J.X., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer V., Chapple M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., McKus G.L.G.,
RA Abrita C.F., Agbayani A., An H.-C., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Sasu A., Baxendale C., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolintsov S.,
RA Borokova D., Botchan M.R., Bouck C., Brockstein P., Brotler P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dabike C., Davenport L.S., Davies P.,
RA dePaulos B., Delcher A., Deng Z., Mays A.D., Dew J., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali N., Kalush F., Karpen G.H., Ke Z., Kenton J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matzel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mohanty C., Morris J., Moshrefi A.,
RA Mount S.W., Moy M., Murphy B., Murphy J., Muzny D.W., Nelson D.,
RA Nelson D.R., Nelson K.A., Nixon K., Ruskern D.R., Pacleb J.W.,
RA Palazolo R., Pittman G.S., Pat S., Poizard C., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shao H.,
RA Shue B.C., Siden-Klaras I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Switkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri U.S., Zhan X., Zhang G., Zhao C., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter A.C.;
RA "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K., Busam D.A.,
RA Carlson C.W., Center A., Champe M., Davenport L.P., Dietz S.M.,
RA Dodson K., Dorett V., Doup J.E., Doyle C., Dyrenke D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez K., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali N., Kruse D., Li P., Matzel B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson X.A., Nunoo C.,
RA Pacub J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouaneavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Switkas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri U.S., Smith H.O., Venter G.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Mista S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson C.W., Celniker S.E.,

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RA Clamp V., Dysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Krommiller B., Marshall B., Milburn G., Richter J., Russo S.,
RA Seale S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Murgall C.J., Lewis S.F.;
RT "Annotation of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Flybase;
RC Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AEO03729; AAF55745.2; -
DR HSSP: P21816; IMAA.
DR Flybase: FBgn0038776; CG5030.
DR InterPro: IPR002018; Carboxylesterase.
DR Pfam: PF00135; Coesterase_1.
DR PROSITE: P500941; CARBOXYLESTERASE_E_2; 1.
KM Hydrolyase.
SO SEQUENCE 593 AA; 65726 MW; F0296DC1FB98F4C CRC64;

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Query Match 1.2%; Score 10; DB 5; Length 593;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CY 203 NYRLLIGFL 212
DB 234 NYRLLIGFL 243

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RESULT 42
09UKY3 PRELIMINARY; PRT; 288 AA.

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AC 09UKY3;
DT 01-MAY-2000 (TRENBLER). 13, Created
DT 01-MAY-2000 (TRENBLER). 13, Last sequence update)
DT 01-MAR-2002 (TRENBLER). 20, Last annotation update)
DE Carboxylesterase-related protein.
OS Homo sapiens (human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;

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RN [1]
RP SEQUENCE FROM N.A.
RC Yvan B., Maceney L., Yang D.;
RA Yvan B., Maceney L., Yang D.;
RT "Human placental carboxylesterases: enzymatic characterization,
RT molecular cloning and evidence for the existence of multiple forms.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AF106005; AAF14185.1; -
DR HSSP: P37967; IQE3.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000379; Ser_estr_site.
DR Pfam: PF00135; Coesterase_1.
DR PROSITE: P500122; CARBOXYLESTERASE_B_2; 1.
KM Hydrolyase.

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SQ SEQUENCE 288 AA; 30886 MW; 8F4C3BDE531BE9E CRC64;

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Query Match 1.1%; Score 9; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CY 125 EDCGLYINLY 133
DB 116 EDCGLYINLY 124

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RA Masen T., Ciecko A., Parksey D.S., Blair E., Cline H., Clark E.B.,
RA Cotton V.D., Utterback T.R., Khouri H., Qin H., Yamathavan C.,
RA Gill J., Scarlato V., Maignant V., Pizzo M., Grandi G., Sun H.,
RA Smith H.C., Fraser C.M., Moxon E.R., Rappold R., Vetter J.C.,
RA "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MCS9."
RT Science 287:1809-1815(2000).
CC -1- CATALYTIC ACTIVITY: ATP + L-AMINO ACID + TRNA(AMINO ACID) = AMP +
CC PROPHOSPHATE + L-AMINOACYL-TRNA(AMINO ACID).
CC -1- CATALYTIC ACTIVITY: ATP + L-ASPARAGINE +
CC TRNA(ASN) = AMP + PYROPHOSPHATE + L-ASPARTYL-TRNA(ASP) (OR L-
CC ASPARAGINYL-TRNA(ASN)).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -1- SIMILARITY: BELONGS TO ASPARTYL-TRNA SYNTHETASE FAMILY.
DR EMBL: A602491; AAF41786.1; -.
DR HSSP: P14825; 1E10.
DR TIGR: MMB1425; -.
DR InterPro: IPR004364; trna-synt_2.
DR InterPro: IPR002112; trna-synt_asp.
DR InterPro: IPR002113; trna-synt_lys_2.
DR InterPro: IPR004365; trna-anti_1.
DR InterPro: IPR006195; trna-lygase_II.
DR Pfam: PF00152; trna-synt_2; 1.
DR Pfam: PF01336; trna-anti; 1.
DR PRINTS: PRO1342; TRNASYNTHASP.
DR PRINTS: PRO0982; TRNASYNTHLVS.
DR TIGRFS: TIGR04499; lys_bact; 1.
DR PROSITE: PS50862; AA TRNA_LIGASE_II; 1.
KM ATP-binding; Aminoacyl-TRNA synthetase; Ligase; Protein biosynthesis;
KM Complete proteome.
SQ SEQUENCE 503 AA; 57311 MW; 28CEC53DA02B46C6 CRC64;

Query Match 1.1%; Score 9; DB 16; Length 503;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 456 AADLHAQYG 464
|||
46 AADLHAQYG 54

RESULT 47
Q9UT77 PRELIMINARY; PRT; 503 AA.
ID Q9UT77;
AC Q9UT77;
DT 01-OCT-2003 (TrEMBLrel. 13, Created)
DT 01-OCT-2003 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Lysyl-TRNA synthetase (EC 6.1.1.6).
GN LYS OR NMA1658.
OS Neisseria meningitidis (serogroup A).
CC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
CC Neisseriaceae; Neisseria.
CX NCB1_TaxID=65699;
RN [1] TaxID=65699;
RP SEQUENCE FROM N.A.
RC STRAIN=22491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Fairhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hartlin N., Holroyd S.,
RA Jagals K., Leachter S., Moule S., Mungall K., Quail M.A.,
RA Rajandream V.A., Rutherford K.W., Simmonds M., Skelton C.,
RA Whitehead S., Spratt B.G., Baxell B.G.;
RA "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis 22491."
RT Nature 404:502-506(2000).
CC -1- CATALYTIC ACTIVITY: ATP + L-AMINO ACID + TRNA(AMINO ACID) = AMP +
CC PYROPHOSPHATE + L-AMINOACYL-TRNA(AMINO ACID).
CC -1- CATALYTIC ACTIVITY: ATP + L-ASPARAGINE +
CC TRNA(ASN) = AMP + PYROPHOSPHATE + L-ASPARTYL-TRNA(ASP) (OR L-

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CC ASPARAGINYL-TRNA(ASN)).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -1- SIMILARITY: BELONGS TO ASPARTYL-TRNA SYNTHETASE FAMILY.
DR EMBL: A163756; CAB84866.1; -.
DR HSSP: P14825; 1E10.
DR InterPro: IPR004364; trna-synt_2.
DR InterPro: IPR002112; trna-synt_asp.
DR InterPro: IPR002113; trna-synt_lys_2.
DR InterPro: IPR004365; trna-anti_1.
DR InterPro: IPR006195; trna-lygase_II.
DR Pfam: PF00152; trna-synt_2; 1.
DR Pfam: PF01336; trna-anti; 1.
DR PRINTS: PRO1042; TRNASYNTHASP.
DR PRINTS: PRO0982; TRNASYNTHLVS.
DR TIGRFS: TIGR00499; lys_bact; 1.
DR PROSITE: PS50862; AA TRNA_LIGASE_II; 1.
KM ATP-binding; Aminoacyl-TRNA synthetase; Ligase; Protein biosynthesis;
KM Complete proteome.
SQ SEQUENCE 503 AA; 57264 MW; 381891348F9D0543 CRC64;

Query Match 1.1%; Score 9; DB 16; Length 503;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 456 AADLHAQYG 464
|||
46 AADLHAQYG 54

RESULT 48
Q9V7J1 PRELIMINARY; PRT; 507 AA.
ID Q9V7J1;
AC Q9V7J1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2003 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG8424 protein.
GN CG8424.
OS Drosophila melanogaster (fruit fly).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
CC Ephydroidea; Drosophilidae; Drosophila.
CX NCB1_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams V.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Kramarcus P.G., Scherer S.E., Si P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blasei R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
RA Abril J.F., Abpayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxter D., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Brandler D., Bohnsack S.,
RA Borokova D., Botchan M.R., Boulter J., Brodeur P., Brothier P.,
RA Burris K.C., Busam D.A., Butler H., Cocke D.E., Center A., Chandra I.,
RA Cherry J.W., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Davis A.D., Dew C., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.S., Garg N.S., Gelbart W.M., Glasser K.,
RA Glick A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jhalil M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeok P., Lei Y., Levitsky A.A., Li Y., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny J.M., Nelson J.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazzolo Y., Pittman G.S., Pat S., Pollard J., Puri V., Reese Y.G.,
 RA Reinert K., Remington K., Sanders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spiedling A.C., Stapleton M., Stinson R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach C.,
 RA Williams S.W., Woodage T., Morley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.C.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 CC "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195 (2000).
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL: AEC33808; AAF58062.1; -.
 DR HSSP: P21316; IMA.
 DR Flybase: FBgn0034376; CG8424.
 DR InterPro: IPR002618; CarbesteraseB.
 DR InterPro: IPR000734; Lipase.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 DR PROSITE: PS00120; LIPASE_SER; 1.
 DR HydroBase.
 SQ SEQUENCE 507 AA: 55968 MW: 87635841854357 CRC64:

Query Match 1.1%; Score 9; DB 5; Length 507;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 168 PMVYTHGG 176
 |||||
 Db 119 PMVYTHGG 126

RESULT 49
 Q96DN9 PRELIMINARY; PRT; 525 AA.
 ID Q96DN9
 AC Q96DN9
 DT 01-DEC-2001 (TrEMBLrel. 13, Created)
 DT 01-DEC-2001 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein F131547.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homc.
 CC NCBI_TaxId=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Niimiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
 RA Furuya T., Takahashi M., Kikawa E., Omura Y., Abe K., Karihara K.,
 RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
 RA Otsuki T., Sato H., Nakatsu A., Ishii S., Yamamoto U., Isono Y.,
 RA Kawai-Hiro Y., Sato K., Nishikawa T., Kitura K., Yamashita H.,
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Muzakawa K.,
 RA Matsuhori K., Takahashi-Tajiri A., Oshima A., Sugiyama A., Kawakami B.,
 RA Suzuki Y., Sugano S., Kagahari K., Masuno Y., Nagai K., Isogai T.,
 RT NEDO human cDNA sequencing project.
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL: AK056109; BAB71094.1; -.
 DR InterPro: IPR002018; CarbesteraseB.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 DR PROSITE: PS00120; LIPASE_SER; 1.
 DR HydroBase.
 SQ SEQUENCE 525 AA: 58200 MW: 772487638422F215 CRC64:

Query Match 1.1%; Score 9; DB 4; Length 525;
 Best Local Similarity 100.0%; Pred. No. 2.8;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Cy 125 EDCYLYNY 133
 |||||
 Db 119 EDCYLYNY 127

RESULT 50
 Q9VTCO PRELIMINARY; PRT; 533 AA.
 ID Q9VTCO
 AC Q9VTCO
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Paraben-hydrolyzing esterase precursor.
 GN PRBA.
 OS Enterobacter cloacae.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Enterobacter.
 CC NCBI_TaxId=550;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA STRAIN=EM.
 RA Valkova R., Lepine F., Boile C., Dupont X., Vilmoux R.,
 RA "giba, a gene coding for an esterase hydrolyzing parabens in E.
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL: AY077721; AA482802.1; -.
 DR InterPro: IPR002018; CarbesteraseB.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 DR HydroBase; Signal.
 F- SIGNAL
 SQ SEQUENCE 533 AA: 57922 MW: 520084F96DE093BA CRC64:

Query Match 1.1%; Score 9; DB 2; Length 533;
 Best Local Similarity 100.0%; Pred. No. 2.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YMTNFAKTG 534
 |||||
 Db 476 YMTNFAKTG 486

RESULT 51
 Q9VTCO PRELIMINARY; PRT; 541 AA.
 ID Q9VTCO
 AC Q9VTCO
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE ALPHA-EST4 protein (RED07760p).
 GN ALPHA-EST4 OR CG1082.
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 CC NCBI_TaxId=7227;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA STRAIN=BERKELEY.
 RC MEDLINE=20196006; Pubmed=10711132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell C.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Baau A., Baxterdale J., Bayraktaroglu L., Beasley E.M.,

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RA Beeson K.Y., Benos P.V., Berman B.F., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dabke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Nays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Donnes M., Dugan-Rocha S., Durkin B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glaser K.,
RA Glodde A., Gong F., Gottell J.H., Gu Z., Guan P., Harris K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Hock C.,
RA Houslin D., Houshorst K.A., Howland T.J., Mei M.-H., Idenwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,
RA Kimel B.E., Kodita C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko F., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mlshina N.V., Modyury C., Morris J., Mozhart A.,
RA Mount S.M., Moy M., Murphy B., Murphy C., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet C.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Put V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spreading A.C., Stapleton M., Strong R., Sun E.,
RA Swirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Massarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.V., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan W., Zhao X., Zhao Q., Zheng L.,
RA Zheng X.H., Zheng F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
(2)
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agdayani A., Carlson J.,
RA Chame M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kromtiller B., Li P., Liao G.,
RA Miranda A., Mungall C.T., Nunco J., Paclet J., Pargass V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Ceiniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBD databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EXBL: AEO03671; AAF5405.1; -
DR EMBL: AY070981; AAL46603.1; -
DR HSSP: P30122; 2BCE.
DR Flybase: FBgn015572; alpha-Est4.
DR InterPro: IPR02018; Carboxylesterase.
DR InterPro: IPR00379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
SQ SEQUENCE 541 AA; 61305 MW; C39282265AC72EFD CRC64;
Query Match 1.1%; Score 9; DB 5; Length 541;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 168 PWMVYIHGG 176
DB 104 PWMVYIHGG 112
RESULT 52
Q24197 PRELIMINARY; PRT; 541 AA.
AC Q24197;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Alpha esterase.
GN ALPHA-EST4 OR AE4 OR CG1082.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Artropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.

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CX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Robin C.;
CC Submitted (MAR-1996) to the EMBL/GenBank/DBD databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EXBL: U51046; AAB01145.1; -
DR HSSP: P30122; 2BCE.
DR Flybase: FBgn0015572; a.alpha-Est4.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR Hydrolyase.
SQ SEQUENCE 541 AA; 61277 MW; 7C6D6BE0690A4C33 CRC64;
Query Match 1.1%; Score 9; DB 5; Length 541;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 168 PWMVYIHGG 176
DB 104 PWMVYIHGG 112
RESULT 53
Q81034 PRELIMINARY; PRT; 545 AA.
AC Q81034;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Carboxylesterase-like urinary excreted protein.
GN CAUXIN.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eulalia; Carnivora; Fissipedia; Felidae; Felis.
CX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Miyazaki M., Kamie K., Soeta S., Taiba H., Yamashita T.;
RT "Molecular cloning and characterization of a novel carboxylesterase-
RT like protein that is physiologically present at high concentrations in
RT the urine of domestic cats (Felis catus).";
RJ Biochem. J. 0:0-0(2002).
DR EXBL: AB045377; BAC22577.1; -
SQ SEQUENCE 545 AA; 60505 MW; 9F73FA693D271FA9 CRC64;
Query Match 1.1%; Score 9; DB 6; Length 545;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 125 EDCLYDNIY 133
DB 119 EDCLYDNIY 127
RESULT 54
Q3KQ26 PRELIMINARY; PRT; 549 AA.
AC Q3KQ26;
DT 01-OCT-2002 (TEMBLrel. 22, Created)
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Vest.
OS Vibrio harveyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
CX NCBI_TaxID=669;
RN [1]
RP SEQUENCE FROM N.A.
RA Teo J.W.P., Poh C.L., Zhang L.H.;
RT "Cloning and expression of Vibrio harveyi lipase.";

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RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AF521299; AAM77904.1; -.
DR InterPro: IPR002018; Carboxesterase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
KW Hydrolyase.
SQ SEQUENCE 549 AA; 60613 MW; 67CDBA5A30DC429F CRC64;

Query Match 1.1%; Score 9; DB 11; Length 549;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 EDCLYLNLY 210
DB 164 INYRLGLG 172

RESULT 55
ID 054936 PRELIMINARY; PRT; 554 AA.
AC 054936;
CT 01-AUG-1998 (TrEMBLrel. 07, Created)
CT 01-AUG-1998 (TrEMBLrel. 27, Last sequence update)
CT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Carboxylesterase precursor.
GN ESI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=CPL; TISSUE=Lung;
RC MEDLINE=99032675; PubMed=9815113;
RA Krishnasamy S., Teng A.L., Dhond R., Schultz R.M., Gross N.J.;
RT "Molecular cloning, characterization, and differential expression
RT pattern of mouse lung surfactant convertase.";
RL Am. J. Physiol. 275:1269-1275(1998).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AF034435; AAC04708.1; -.
DR HSSP: P37967; 1OE3.
DR MGD: MGI:95420; Esl.
DR InterPro: IPR002018; Carboxesterase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
DR KM Hydrolyase. Signal.
FT SIGNAL 18 POTENTIAL.
FT CHAIN 19 554 CARBOXYLESTERASE.
SQ SEQUENCE 554 AA; 61140 MW; FEFBE9A8EE74975 CRC64;

Query Match 1.1%; Score 9; DB 11; Length 554;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNLY 133
DB 114 EDCLYLNLY 122

RESULT 56
ID 08K125 PRELIMINARY; PRT; 554 AA.
AC 08K125;
CT 01-OCT-2002 (TrEMBLrel. 22, Created)
CT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
CT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to esterase 1.
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=Liver;
RA Straussberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: BC028907; AAH28907.1; -.
DR InterPro: IPR002018; Carboxesterase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
DR KM Hydrolyase.
SQ SEQUENCE 554 AA; 61020 MW; 592A9C4705FC8F5E CRC64;

Query Match 1.1%; Score 9; DB 11; Length 554;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNLY 133
DB 114 EDCLYLNLY 122

RESULT 57
ID 08K380 PRELIMINARY; PRT; 558 AA.
AC 08K380;
CT 01-OCT-2002 (TrEMBLrel. 22, Created)
CT 01-OCT-2002 (TrEMBLrel. 21, Last sequence update)
CT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Carboxylesterase isoenzyme.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RA Sarghant S.P., Davis W.J., Mahrenholz A., Boston W.F.;
RT "Identification of the members of rat liver carboxylesterase family by
RT mass spectroscopy: cloning of a new isoenzyme.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AY034877; AAK61610.1; -.
DR InterPro: IPR002018; Carboxesterase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
DR KM Hydrolyase.
SQ SEQUENCE 558 AA; 61802 MW; FB267DD19581106 CRC64;

Query Match 1.1%; Score 9; DB 11; Length 558;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNLY 133
DB 120 EDCLYLNLY 128

RESULT 58
ID 08Q2R3 PRELIMINARY; PRT; 558 AA.
AC 08Q2R3;
CT 01-JUN-2002 (TrEMBLrel. 21, Created)
CT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
CT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to carboxylesterase 2 (Intestine, liver) (Expressed sequence
DE A1266584) (Similar to liver carboxylesterase precursor).
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GN A1265984.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CX NCBI_TaxID=10090.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon, and Liver;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum;
RX MEDLINE=22354683; PubMed=246685.;
RA The FANTOM Consortium;
RL The RIKEN Genome Exploration Research Group Phase 1 & 2 Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,773 full-length cDNAs."
RJ Nature 420:563-573(2002).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; BC024491; AAH24491.1; -
DR EMBL; BC024517; AAH24517.1; -
DR EMBL; BC025537; AAH25537.1; -
DR EMBL; BC025812; AAH25812.1; -
DR EMBL; BC026643; AAH26643.1; -
DR EMBL; BC031295; AAH31295.1; -
DR EMBL; BC024082; AAH24082.1; -
DR EMBL; AK078958; BA07476.1; -
DR MGD; MGI:2142491; A2266984.
DR InterPro: IPR002013; Carboxylesterase.
DR InterPro: IPR003793; Ser_estrs_site.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE 558 AA; 61940 MW; 961A06BDC92E3FD CRC64;

Query Match 1.1%; Score 9; DB 11; Length 558;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCUYNLY 133
DB 120 EDCUYNLY 128

RESULT 59
035533 PRELIMINARY; PRT; 559 AA.
AC 035533;
DT 01-JAN-1998 (TRENBLREL 05, Created)
DT 01-JAN-1998 (TRENBLREL 05, Last sequence update)
DE Carboxylesterase precursor (EC 3.1.1.1) (Alc-esterase) (B-esterase)
DE (MONOBUITYRASE) (Cocaine esterase) (PROCAINE esterase) (METHYLBUTYRASE).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;

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CC Mesocricetus.
CX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SVR1AN GOLDEN; TISSUE=Liver;
RA Some T., Wang C.Y.;
RT "Mitochondrial amides and carboxylesterases."
RL (In) Genglerich F.P. (eds.);
RL Comprehensive toxicology, pp.3:265-281, Elsevier Science,
RL Oxford (1997).
CC -1- CATALYTIC ACTIVITY: A CARBOXYLIC ESTER + H(2)O = AN ALCOHOL + A
CC CARBOXYLIC ANION.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; D53577; BAA23605.1; -
DR HSSP; P37967; 1OE3.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000886; ER_target.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Signal.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 559 CARBOXYLESTERASE.
SQ SEQUENCE 559 AA; 62126 MW; 5B6BD4F9A47C6AD8 CRC64;

Query Match 1.1%; Score 9; DB 11; Length 559;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCUYNLY 133
DB 121 EDCUYNLY 129

RESULT 60
08R097 PRELIMINARY; PRT; 560 AA.
AC 08R097;
DT 01-JUN-2002 (TRENBLREL 21, Created)
DT 01-JUN-2002 (TRENBLREL 21, Last sequence update)
DT 01-OCT-2002 (TRENBLREL 22, Last annotation update)
DE Hypothetical 62.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; BC027185; AAH27185.1; -
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR003793; Ser_estrs_site.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hypothetical protein; Hydrolase.
SQ SEQUENCE 560 AA; 62735 MW; 3B8E56DC9FB108B5 CRC64;

Query Match 1.1%; Score 9; DB 11; Length 560;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCUYNLY 133
DB 122 EDCUYNLY 130

RESULT 61

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Q91WU0
ID Q91WU0 PRELIMINARY; PRT; 561 AA.
AC Q91WU0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical 61.6 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
CC Submitted (SEP-2001) to the EMBL/GenBank/DDJ databases.
DR EXPL: BC034479; AAH3449.1; -
DR InterPro: IPR003018; CarboxylesteraseB.
DR InterPro: IPR003086; ER_target.
DR InterPro: IPR003379; Ser_estrs_site.
DR Pfam: PF0135; Coesterase.1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
DR PROSITE: PS0014; ER_TARGET; 1.
KW Hypothetical protein; Hydrolyase.
SQ SEQUENCE 561 AA; 62612 MW; 100313143A797868 CRC64;

Query Match 1.1%; Score 9; DB 11; Length 561;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCYLNIY 133
DB 114 EDCYLNIY 122

RESULT 62
Q91WU0 PRELIMINARY; PRT; 561 AA.
AC Q91WU0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Similar to carboxylesterase 2 (intestine, liver) (Hypothetical
protein).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
CC Submitted (OCT-2001) to the EMBL/GenBank/DDJ databases.
DT [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
CC Submitted (JUN-2002) to the EMBL/GenBank/DDJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, and Colon;
RA Strausberg R.;
CC Submitted (JUL-2002) to the EMBL/GenBank/DDJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
EMBL: BC015290; AAH15290.1; -

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DR EMBL: BC024552; AAH24552.1; -
DR EMBL: BC031170; AAH31170.1; -
DR EMBL: BC034178; AAH34178.1; -
DR EMBL: BC034180; AAH34180.1; -
DR EMBL: BC034191; AAH34191.1; -
DR MGD: KGI:2385905; Cest2.
DR InterPro: IPR002018; CarboxylesteraseB.
DR InterPro: IPR003379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase.1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hypothetical protein; Hydrolyase.
SQ SEQUENCE 561 AA; 62469 MW; F793967A646EB728 CRC64;

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Query Match 1.1%; Score 9; DB 11; Length 561;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCYLNIY 133
DB 123 EDCYLNIY 131

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RESULT 63
Q76631 PRELIMINARY; PRT; 561 AA.
AC Q76631;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Carboxylesterase precursor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MISTAR; TISSUE=liver;
RA Sone T., Sawada T., Kunitomo T., Takabatake E., Wang C.Y., Isobe M.;
CC Submitted (JUN-1998) to the EMBL/GenBank/DDJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AB010635; BAA25692.1; -
DR EMBL: AB010570; BAA25690.1; -
DR EMBL: AB010589; BAA25680.1; COINED.
DR EMBL: AB010560; BAA25690.1; COINED.
DR EMBL: AB010561; BAA25690.1; COINED.
DR EMBL: AB010562; BAA25690.1; COINED.
DR EMBL: AB010563; BAA25690.1; COINED.
DR EMBL: AB010564; BAA25690.1; COINED.
DR EMBL: AB010565; BAA25690.1; COINED.
DR EMBL: AB010566; BAA25690.1; COINED.
DR EMBL: AB010567; BAA25690.1; COINED.
DR EMBL: AB010568; BAA25690.1; COINED.
DR EMBL: AB010569; BAA25690.1; JOINED.
DR HSSD: P37967; IOB3.
DR InterPro: IPR002018; CarboxylesteraseB.
DR InterPro: IPR003379; Ser_estrs_site.
DR Pfam: PF0135; Coesterase.1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolyase; Signal.
FT SIGNAL 1
FT CHAIN 27 56; POTENTIAL.
SQ SEQUENCE 561 AA; 62189 MW; 13BF365F5063379 CRC64;

Query Match 1.1%; Score 9; DB 11; Length 561;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCYLNIY 133
DB 123 EDCYLNIY 131

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RESULT 64
ID Q924V9 PRELIMINARY: PRT: 562 AA.
AC Q924V9:
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Carboxylesterase F1.
GN CESRL1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=Mistar; TISSUE=Liver;
RA Hosokawa M., Hadame A., Shirizu T., Takahashi D., Satoh T., Chiba K.;
RT "Molecular cloning and expression of cDNA encoding microsomal acyl-CoA
hydroxylase from rat liver.";
RJ Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC - SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AE023630; BA060697.1; -.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000886; ER_target.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
DR PROSITE: PS00024; ER_TARGET; 1.
KM Hydroxylase.
SQ SEQUENCE 562 AA; 62305 MW; 82475E22703BD33B CRC64;

Query Match 1.1%; Score 9; DB 1; Length 562;
Best local similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCVYENIY 133
Db 124 EDCVLYNRY 122

RESULT 65
ID Q9VLA4 PRELIMINARY: PRT: 564 AA.
AC Q9VLA4:
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE C33841 protein.
GN C33841.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscivora;
OC Sphingidae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=BKRLRY;
RA MEDJANE=20196006; PubMed=10731132;
RA Adams M.C., Cealiker S.E., Holt R.A., Evans C.A., Gocayne J.L.,
RA Amaralides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gale R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zheng X., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazey R.G., Chafee N., Pfeiffer B.D.,
RA Wan K.H., Boyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Adair J.F., Agdavi A., An H.-Y., Andrews-Pfarkoch C., Baldwin D.,
RA Baliew R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.X.,
RA Beeson K.Y., Bonos P.V., Berman B.P., Bhargava D., Bolshakov S.,
RA Borok D., Borczan W.R., Bock J., Brockstein P., Brocton P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry C.M., Cawley S., Danke C., Davernport L.B., Davies P.,
RA de Fabios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durkin K.C., Evangelista C.C., Ferrara C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Klip D., Lai Z.,
RA Lasko F., Lei Y., Levitsky A.A., Li C., Li Z., Liang Y., Lin X.,
RA Liu X., Martel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.X., Moy M., Murphy B., Murphy D., Nuzny D.X., Nelson J.L.,
RA Nelson J.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.V.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Slater E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Massaman D.A., Weinstein G.M., Weissbach C.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri U.S., Zhan Y., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith F.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RJ Science 287:2185-2195(2000).
CC - SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AE003625; AF52791.1; -.
DR HSSP: P37967; 1OE3.
DR Flybase: FBgn0032131; C33841.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
KM Hydroxylase.
SQ SEQUENCE 564 AA; 62785 MW; 9A6EAD2A9B7592C09 CRC64;

Query Match 1.1%; Score 9; DB 5; Length 564;
Best local similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 PVMVYIHGG 176
Db 120 PVMVYIHGG 128

RESULT 66
ID C8TD29 PRELIMINARY: PRT: 565 AA.
AC C8TD29:
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Brain carboxylesterase hbr2.
GN C8TD29.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Hosokawa M., Mori M., Ogasawara Y., Komori C., Tsukada E., Chiba K.;
RT "cDNA cloning and expression of carboxylesterase isozymes from human
brain.";
RJ Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Mori M., Hosokawa M., Tsukada E., Ogasawara Y., Chiba K.;
RT "cDNA cloning and stable expression of human brain carboxylesterase
isozymes.";
RJ Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC - SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.

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DR EMBL; AB025027; BAB5656.1;
DR InterPro: IPR002018; CarboxylaseB.
DR InterPro: IPR00379; Ser esters_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYL-ESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYL-ESTERASE_3_2; 1.
DR HydroLase.
SQ SEQUENCE 565 AA; 61962 MW; E255244C2CA9A1E CRC64;

Query Match 1.1%; Score 9; DB 4; Length 565;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYNLY 133
DE 114 EDCLYNLY 122

RESULT 67
Q23010 PRELIMINARY; PRT; 565 AA.
AC Q23010;
CT 01-NOV-1996 (TREMBLrel. 01, Created)
CT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
CT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE K11G9.1 protein.
GN K11G9.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodertinae; Caenorhabditis.
OX NCBI_TaxID=6219;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berts M.,
RA Bonfield C., Burton J., Connell X., Copsey T., Cooper J., Coulson A.,
RA Craxton K., Dear S., Du Z., Durbin R., Favello A., Fulton D.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan N.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Smailson N., Smith A., Sornhamer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sprat J., Wooldman P.;
RA "2.2 Mb of contiguous nucleotide sequence from chromosome I:: of C.
RT elegans.";
RT Nature 366:32-38(1994).
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Greco, T., Bradshaw H.;
RT "The sequence of C. elegans cosmid K1139.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3];
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
DR EMBL: U64853; AAB04976.-.-.
DR HSSP: P37967; 10E3.
DR WormPep: K11G9.1; CE07374.
DR InterPro: IPR002018; CarboxylaseB.
DR InterPro: IPR00379; Ser esters_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYL-ESTERASE_B_1; 1.
DR HydroLase.
SQ SEQUENCE 565 AA; 63560 MW; 38003941DF17503 CRC64;

Query Match 1.1%; Score 9; DB 5; Length 565;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 203 NYRLGILGF 211
DB 157 NYRLGILGF 165

RESULT 68
Q07540 PRELIMINARY; PRT; 565 AA.
AC Q07540;
CT 01-NOV-1998 (TREMBLrel. 08, Created)
CT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
CT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Liver carboxyl-esterase (EC 3.1.1.1).
DE Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98297515; PubMed=9635592;
RA Pottier P.M., Pawlik C.A., Morton C.L., Naeye C.W., Danks N.K.;
RT "Isolation and partial characterization of a cDNA encoding a rabbit
RT liver carboxyl-esterase that activates the prodrug rimotetan (CPT-
RT 221,000).";
RL Cancer Res. 58:2646-2651(1998).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
DR EMBL: AF036930; AAC39258.1; -.
DR HSSP: P21836; 1MAR.
DR InterPro: IPR002018; CarboxylaseB.
DR InterPro: IPR00379; Ser esters_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYL-ESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYL-ESTERASE_3_2; 1.
DR HydroLase.
SQ SEQUENCE 565 AA; 62291 MW; CAC61400CC81D2F CRC64;

Query Match 1.1%; Score 9; DB 6; Length 565;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYNLY 133
DB 114 EDCLYNLY 122

RESULT 69
Q095N05 PRELIMINARY; PRT; 565 AA.
AC Q095N05;
CT 01-DEC-2001 (TREMBLrel. 19, Created)
CT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
CT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Carboxyl-esterase D1.
GN CESD1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1];
RP SEQUENCE FROM N.A.
RC MEDLINE=21219511; PubMed=11339814;
RX Hosokawa M., Suzuki K., Takahashi D., Mori M., Satch T., Chiba K.;
RT "Purification, Molecular Cloning, and Functional Expression of Dog
RT Liver Microsomal acyl-CoA Hydroxylase: A Member of the Carboxyl-esterase
RT Multigene Family.";
RL Arch. Biochem. Biophys. 389:245-253(2001).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
DR EMBL: AB023629; BAB0696.1; -.
DR InterPro: IPR002018; CarboxylaseB.
DR InterPro: IPR00379; Ser esters_site.
DR Pfam: PF00135; Coesterase; 1.

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DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KM Hydrolase.
SQ SEQUENCE 565 AA; 62000 MW; 905AA4222FEF037H CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNIY 133
Db 114 EDCLYLNIY 122

RESULT 70
097582 PRELIMINARY; PRT; 565 AA.
AC 097582;
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE Carboxylesterase.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactylia; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestinal mucosa;
RX MEDLINE=99013456; Pubmed=799112;
RA David L., Guo X.G., Villard C., Moutin A., Puigserver A.;
RT "Purification and molecular cloning of porcine intestinal glycerol-
RT ester hydrolase--evidence for its identity with carboxylesterase.";
RL Eur. J. Biochem. 257:142-148(1998).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AF064741; AAC70613.1; -
DR HSPB: P21836; IMAA
DR InterPro: IPR000318; Carboxylesterase.
DR InterPro: IPR003379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KM Hydrolase.
SQ SEQUENCE 565 AA; 61712 MW; 77935CC0D93F00 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNIY 133
Db 114 EDCLYLNIY 122

RESULT 71
08VCC2 PRELIMINARY; PRT; 565 AA.
AC 08VCC2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Carboxylesterase 1.
GN CEB1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

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3F SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: BC021150; AAH2150.1; -
DR EMBL: BC026897; AAH26897.1; -
DR MGD: MG158378; Ceb1.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KM Hydrolase.
SQ SEQUENCE 565 AA; 62679 MW; 21F3B0184C2E881 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNIY 133
Db 114 EDCLYLNIY 122

RESULT 72
0924V8 PRELIMINARY; PRT; 565 AA.
AC 0924V8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Carboxylesterase MHI (EC 3.1.1.1).
GN CEB3 OR CEBMHI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL; TISSUE=Liver;
RA Hosokawa M., Nakamura T., Nakata F., Takahashi D., Sakae N., Satoh T.,
RA Chiba K.;
RT "Purification, molecular cloning and expression of cDNA encoding
RT peroxisome proliferator inducible carboxylesterase isozymes from
RT C57BL/6 mouse liver.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AB023631; BAB60698.1; -
DR MGD: MG1248202; Ceb3.
DR InterPro: IPR02018; Carboxylesterase.
DR InterPro: IPR003379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KM Hydrolase.
SQ SEQUENCE 565 AA; 61810 MW; AC122636F265D34C CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNIY 133
Db 114 EDCLYLNIY 122

RESULT 73
053136 PRELIMINARY; PRT; 565 AA.
AC 053136;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

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DT 01-OCT-2002 (TREMBlrel. 22, last annotation update)
DE Carboxylesterase precursor (EC 3.1.1.1).
CN CEST OR EX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090.
RN 1.
RP SEQUENCE FROM N.A.
RC STRAIN=B6/CBAF1J.
RX MEDLINE=98234306; PubMed=9565681.
RA Klinghaus P., Sector J., Assmann G.,
RT "Cloning and sequencing of a novel murine liver carboxylesterase
RT cDNA."
RL Biochim. Biophys. Acta 1397:175-179(1998).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DE EMBL: Y12887; CA97388.1; -.
DR HSP; P37967; I0E3.
DR MGD; MGI:88378; Cest1.
DR InterPro: IPR002018; CarbesteraseB.
DR InterPro: IPR003379; Ser_estr_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS0122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Signal.
FT SIGNAL.
FT SEQUENCE 565 AA; 62722 MW; B55A5A15C27B79 CRC64;

Query Match 1.1%; Score 9; DB 1; Length 565;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCCLYNTY 133
DB 114 EDCCLYNTY 122

RESULT 74
Q91ZV9 PRELIMINARY; PRT; 565 AA.
ID Q91ZV9;
AC Q91ZV9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Triacylglycerol hydrolase (EC 3.1.1.1).
GN CES3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090.
RN 1.
RP SEQUENCE FROM N.A.
RC STRAIN=129/J; TISSUE=Liver;
RX MEDLINE=21363045; PubMed=11470237;
RA Dolinsky V.W., Sidone S., Lehner R., Vance D.E.;
RT "The cloning and expression of a murine triacylglycerol hydrolase cDNA
RT and the structure of its corresponding gene."
RL Biochim. Biophys. Acta 1532:162-172(2001).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DE EMBL: AF378751; AAK5067.1; -.
DR MGD; MGI:2148202; Ces3.
DR InterPro: IPR002018; CarbesteraseB.
DR InterPro: IPR003379; Ser_estr_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS0122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
FT SEQUENCE 565 AA; 61887 MW; 2DAF9725721DF9A CRC64;

Query Match 1.1%; Score 9; DB 1; Length 565;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 125 EDCCLYNTY 133
DB 114 EDCCLYNTY 122

RESULT 75
Q35534 PRELIMINARY; PRT; 565 AA.
ID Q35534;
AC Q35534;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Carboxylesterase precursor (EC 3.1.1.1).
GN CARBOXYLESTERASE.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN 1.
RP SEQUENCE FROM N.A.
RC STRAIN=Syrian golden; TISSUE=Liver;
RA Sene T., Ishida Y., Takahatake E., Wang C., Isobe N.;
RT "Cloning and expression of a hamster liver cDNA encoding a novel
RT carboxylesterase which catalyzes the activation of carcinogenic
RT ary-hydroxamic acids."
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DE EMBL: D50578; BAA23604.1; -.
DR HSP; P21816; IMAH.
DR InterPro: IPR002018; CarbesteraseB.
DR InterPro: IPR003379; Ser_estr_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS0122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Signal.
FT SIGNAL.
FT SEQUENCE 565 AA; 62165 MW; 8273233A59DF1ED0 CRC64;

Query Match 1.1%; Score 9; DB 1; Length 565;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCCLYNTY 133
DB 114 EDCCLYNTY 122

Search completed: November 5, 2003, 15:25:15
Job time : 47 secs

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GenCore version 3.1.6
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OW protein - protein search, using sw tcode1

Run on: November 5, 2003, 15:22:08 ; Search time 17 Seconds

(without alignments)
2257.282 Million cell updates/sec

Title: US-09-978-423a-375

Perfect score: 816
Sequence: 1 MLNSVLMVLTALAKETLI.....TFSGGQNSTMLPRGHSTRV 816

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size: 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	538	65.9	816	1 NLG4_HUMAN	Q8NQW4 homo sapien
2	326	40.0	816	1 NLG4_HUMAN	Q8NQW4 homo sapien
3	213	26.1	816	1 NLG4_HUMAN	Q8NQW4 homo sapien
4	50	6.1	816	1 NLG4_HUMAN	Q8NQW4 homo sapien
5	50	6.1	816	1 NLG4_HUMAN	Q8NQW4 homo sapien
6	50	6.1	816	1 NLG4_HUMAN	Q8NQW4 homo sapien
7	48	5.9	816	1 NLG4_HUMAN	Q8NQW4 homo sapien
8	48	5.9	816	1 NLG4_HUMAN	Q8NQW4 homo sapien
9	35	4.3	816	1 NLG4_HUMAN	Q8NQW4 homo sapien
10	32	3.9	816	1 NLG4_HUMAN	Q8NQW4 homo sapien
11	32	3.9	816	1 NLG4_HUMAN	Q8NQW4 homo sapien
12	28	3.4	202	1 BAL_HUMAN	Q8NQW4 homo sapien
13	28	1.5	742	1 BAL_HUMAN	Q8NQW4 homo sapien
14	10	1.2	540	1 EST1_CULP1	Q8NQW4 homo sapien
15	9	1.1	532	1 EST2_RABIT	Q8NQW4 homo sapien
16	9	1.1	533	1 EST2_RABIT	Q8NQW4 homo sapien
17	9	1.1	549	1 EST2_RAT	Q8NQW4 homo sapien
18	9	1.1	554	1 EST2_RAT	Q8NQW4 homo sapien
19	9	1.1	554	1 EST2_RAT	Q8NQW4 homo sapien
20	9	1.1	556	1 EST1_MESAU	Q8NQW4 homo sapien
21	9	1.1	561	1 EST1_RAT	Q8NQW4 homo sapien
22	9	1.1	561	1 EST1_RAT	Q8NQW4 homo sapien
23	9	1.1	561	1 EST1_RAT	Q8NQW4 homo sapien
24	9	1.1	562	1 EST2_MOUSE	Q8NQW4 homo sapien
25	9	1.1	562	1 EST1_CAERR	Q8NQW4 homo sapien
26	9	1.1	566	1 EST1_PIG	Q8NQW4 homo sapien
27	9	1.1	567	1 EST1_HUMAN	Q8NQW4 homo sapien
28	9	1.1	597	1 BAL_BOVIN	Q8NQW4 homo sapien
29	9	1.1	620	1 ACE1_CAERR	Q8NQW4 homo sapien
30	9	1.1	620	1 ACE1_CAERR	Q8NQW4 homo sapien
31	8	1.0	382	1 GPIB_SCHPO	Q8NQW4 homo sapien
32	8	1.0	506	1 CYP1_PLVAN	Q8NQW4 homo sapien
33	8	1.0	563	1 LIP1_GEOCN	Q8NQW4 homo sapien

34	8	1.0	563	1 LIP2_GEOCN	P22394 geotrichum
35	8	1.0	581	1 ACES_BUNFA	Q22035 bungarus fa
36	8	1.0	586	1 ACES_TORCA	P04588 torpedo cal
37	8	1.0	590	1 ACES_TORMA	P07692 torpedo mar
38	8	1.0	599	1 BAL_MOUSE	Q64265 mus musculu
39	8	1.0	612	1 BAL_MOUSE	Q64265 mus musculu
40	8	1.0	629	1 ACES_LEPDE	Q27677 lepidoptera
41	8	1.0	664	1 ACES_ANOST	P56161 anopheles s
42	8	1.0	782	1 COSTA_HAEIN	P44646 haemophilus
43	8	1.0	837	1 YCOL_RAT	P98089 rattus norv
44	8	1.0	912	1 KECM_HUMAN	Q15137 homo sapien
45	8	1.0	918	1 KECM_MOUSE	Q62101 mus musculu
46	8	1.0	2144	1 GLUT_YEAST	Q12680 saccharomyc
47	8	1.0	2766	1 THYG_MOUSE	Q08710 mus musculu
48	8	0.9	52	1 LHA_RHOMA	P82259 rhodospheud
49	7	0.9	127	1 Y55B_MYCE	Q92481 mycoplasma
50	7	0.9	133	1 RAPA_ANASP	Q62068 arabidopsi
51	7	0.9	141	1 CHLE_BOVIN	P32749 bos taurus
52	7	0.9	141	1 CHLE_CANFA	P32750 canis famli
53	7	0.9	141	1 CHLE_MACMU	P32751 macaca mula
54	7	0.9	141	1 CHLE_PIG	P32752 sus scrofa
55	7	0.9	141	1 CHLE_SHEEP	P32753 ovis aries
56	7	0.9	156	1 CUS7_ARADI	P60518 araneus dia
57	7	0.9	159	1 CUS7_ARADI	P60518 araneus dia
58	7	0.9	198	1 EST1_SCHCA	P81428 schizopha:
59	7	0.9	199	1 SC21_RICCN	Q92475 rickettsia
60	7	0.9	204	1 GIDB_COXBU	P94614 coxiella bu
61	7	0.9	205	1 MAUD_METEX	Q49126 methylobact
62	7	0.9	208	1 YHNN_ECOLI	P37616 escherichia
63	7	0.9	234	1 TRAR_AGRVI	P13909 agrobacteri
64	7	0.9	262	1 MSA2_PLAFC	Q92317 plasmodium
65	7	0.9	270	1 TRPA_MYCE	Q92353 mycobacteri
66	7	0.9	270	1 TRPA_MYCTU	Q06130 mycobacteri
67	7	0.9	271	1 TRPA_MYCTU	Q06130 mycobacteri
68	7	0.9	272	1 ZUPR_XANAC	Q08493 xanthomonas
69	7	0.9	274	1 MSA2_PLAFC	P50497 plasmodium
70	7	0.9	274	1 YXG6_EUGER	P48318 euglena gra
71	7	0.9	282	1 Y265_MYCN	P75399 mycoplasma
72	7	0.9	295	1 UGPA_ECOLI	P10905 escherichia
73	7	0.9	307	1 UPK2_CLOAB	Q97416 clostridium
74	7	0.9	341	1 Y011_RICCN	Q92475 rickettsia
75	7	0.9	352	1 ABSC_MYCAV	Q52972 mycobacteri
76	7	0.9	357	1 CHLI_BRAIA	Q09000 branchiosco
77	7	0.9	357	1 PYRD_MYCTU	Q06216 mycobacteri
78	7	0.9	419	1 SHH_BRAE	Q92408 brachydanio
79	7	0.9	439	1 RCA_PRAAU	Q92497 phaseolus a
80	7	0.9	461	1 P55G_BOVIN	Q04404 bos taurus
81	7	0.9	461	1 P55G_HUMAN	Q92569 homo sapien
82	7	0.9	461	1 P55G_MOUSE	Q61413 mus musculu
83	7	0.9	489	1 PNEA_BACCU	P12647 bacillus su
84	7	0.9	505	1 SNM1_HUMAN	Q14424 homo sapien
85	7	0.9	505	1 SNM1_RABIT	Q28626 oryctolagus
86	7	0.9	505	1 TCMO_HELVN	Q04468 helianthus
87	7	0.9	526	1 YNDP_BACCU	Q03808 bacillus su
88	7	0.9	533	1 ARSB_HUMAN	Q18484 homo sapien
89	7	0.9	533	1 PUTY_EMENI	P12696 emericella
90	7	0.9	551	1 NCRP_PLAFA	P12696 human parai
91	7	0.9	554	1 ESTY_MOUSE	Q61880 mus musculu
92	7	0.9	557	1 SASB_ANAPL	Q63791 anas platyr
93	7	0.9	565	1 ES10_RAT	P181908 rattus norv
94	7	0.9	574	1 CHLE_HORSE	P219928 equus cabal
95	7	0.9	581	1 CHLE_RABIT	P219928 cuniculus
96	7	0.9	584	1 ACES_RABIT	Q28459 cuniculus
97	7	0.9	602	1 CHLE_HUMAN	P26226 homo sapien
98	7	0.9	603	1 CHLE_MOUSE	Q03311 mus musculu
99	7	0.9	607	1 YAZ7_SCHPO	Q06698 schizosacch
100	7	0.9	611	1 ACES_FELCA	Q62763 felis silve

ALIGNMENTS

RESULT 1

NLG4 HUMAN
 ID NLG4 HUMAN STANDARD: PRT: 8:6 AA.
 AC DBMCM4; C9ULG9;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Neuroigin 4 precursor (Neuroigin X) (HMLX).
 GN NLG4 OR KIAA26C.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OK NCBI_taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. AND DISBASE.
 RX PubMed=12669065;
 RA Jarrin S., Quach H., Betancur C., Rastam M., Colineaux C.,
 RA Gillberg J.C., Soderstrom H., Gatos B., Leboyer X., Gillberg C.,
 RA Bougeron T., Nyden A., Philippe A., Cohen D., Chabane N.,
 RA Moutereau S., Moutereau M.C., Bric A., Spohnheim E., Spuck and ...
 RA Skjeldal O.H., Coleman M., Pearl P.L., Cohen I.L., Tsouris C.,
 RA Zappella M., Menchetti G., Pampella A., Aschauer H., Van Milderger L.;
 RT "Mutations of the X-linked genes encoding neuroigin NGN3 and NLG4
 PT are associated with autism";
 PL Nat. Genet. 34:27-29(2003).
 RA [2]
 RE SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=2039619; PubMed=10574462;
 RA Nagase T., Ishikawa K.-I., Kikuno R., Hirosewa N., Nomura N.,
 RA Chana O.;
 RT "Prediction of the coding sequences of unidentified human genes. XV.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro";
 RN DNA Res. 6:337-345(1999).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=2239257; PubMed=7477932;
 RA Strussberg R.L., Feinsold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Schmeier C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong T.,
 RA Stalderon M., Soares M.B., Bonaldo M.F., Casavant T.L., Schreier T.E.,
 RA Brownstein M.J., Ustin T.S., Tomiyuki S., Carriani P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Kallaby S.C.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Yalok J.A., Garatracre P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Holyk S.W.,
 RA Villalón D.K., Muzny D.Y., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faley J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boultard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.V.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska M.,
 RA Scherch A., Schein J.E., Jones S.J.M., Matra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RN INTERACTION WITH DLG4.
 RP PubMed=9278515;
 RA Irie M., Hata Y., Takeuchi M., Ichchenko K., Toyoda A., Hirao K.,
 RA Takai Y., Rosahl T.W., Suedhof T.C.;
 RT "Binding of neuroigin to PSD-95";
 RL Science 277:1511-1515(1997).
 RN [5]
 RN INTERACTION WITH DLG4, AND TISSUE SPECIFICITY.
 RP PubMed=11368788;
 RA Bolliger M.F., Frei K., Winterhalter K.H., Gloor S.X.;
 RT "Identification of a novel neuroigin in humans which binds to PSD-95
 RL Blochem. J. 356:581-588(2001).
 CC -I- FUNCTION: Putative neuronal cell surface protein involved in cell-

CC cell-interactions.
 CC -I- SUBUNIT: Interacts through its C-terminus with DLG4/PSD-95 third
 CC P22 domain.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein. (Potential).
 CC TISSUE SPECIFICITY: Expressed at highest levels in heart.
 CC Expressed at lower levels in liver, skeletal muscle and pancreas
 CC and at very low levels in brain.
 CC -I- DISEASE: Defects in NLG4 may be the cause of X-linked autism
 CC [MIM:300425]; a pervasive developmental disorder (PDD),
 CC prototypically characterized by impairments in reciprocal social
 CC interaction and communication, restricted and stereotyped patterns
 CC of interests and activities, and the presence of developmental
 CC abnormalities by 3 years of age.
 CC -I- DISEASE: Defects in NLG4 may be the cause of Asperger syndrome
 CC (AS), a form of childhood autism.
 CC -I- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 CC
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: AF376803; AAA66112.1; -
 CC EMBL: AB031086; BAA66574.1; ALT_INT.
 CC EMBL: BC034018; AAA34018.1; -
 CC HSSP: P21816; IMAA.
 CC Genew: HGNC:14287; NLG4.
 CC XIM: J30427; -
 CC XIM: J30425; -
 CC Interpro: IPR002018; Carbestereab.
 CC Interpro: IPR000460; Neuroigin.
 CC Interpro: IPR000379; Ser_estr_site.
 CC Pfam: PF03135; Coesterase; -
 CC PRINTS: PR01090; NEUROIGIN.
 CC PROSITE: PS00941; CARBOXYLESTERASE_3_2; -
 CC Cell_adhesion; Glycoprotein; Signal; Transmembrane.
 CC FT SIGNAL 1 43
 CC FT CHAIN 44 816 NEUROIGIN 4.
 CC FT DOMAIN 44 675 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 677 697 POTENTIAL.
 CC FT DOMAIN 698 816 CYTOPLASMIC (POTENTIAL).
 CC FT DISULFID 110 446 BY SIMILARITY.
 CC FT DISULFID 306 317 BY SIMILARITY.
 CC FT DISULFID 476 510 BY SIMILARITY.
 CC FT CARBOHYD 182 102 N-LINKED (GLCNAc...) (POTENTIAL).
 CC FT CARBOHYD 511 511 N-LINKED (GLCNAc...) (POTENTIAL).
 CC SQ SEQUENCE 816 AA, 91915 MW, EA1320D690F76BBD CRC64;
 CC
 CC Query Match 65.9%; Score 538; DB 1; Length 816;
 CC Best Local Similarity 99.8%; Pred. No. 0;
 CC Matches 658; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 CC
 CC 155 DTHDQNSKRPVWYIHGGSSYEGGNMIDGSLASXGVYITINRGLIGFSTGDOA 218
 CC 158 DTHDQNSKRPVWYIHGGSSYEGGNMIDGSLASXGVYITINRGLIGFSTGDOA 217
 CC 219 AKGVYGLDQIALFWIEENWGAFGDQPKRTYIPSGSAGASCVSLTLTSHYSEGLFOKAI 278
 CC 218 AKGVYGLDQIALFWIEENWGAFGDQPKRTYIPSGSAGASCVSLTLTSHYSEGLFOKAI 277
 CC 279 IOSGALSSMAVWYOPAKYTRILADKVCNKLDTDMWECIRNXYKELIOCTTPAYH 337
 CC 279 IOSGALSSMAVWYOPAKYTRILADKVCNKLDTDMWECIRNXYKELIOCTTPAYH 338
 CC 339 IAFGVYIDGVYEDDQPOLMEGEPFLANDIMLVNQGSGLEFVGVINEDGVPNPDF 398
 CC 338 IAFGVYIDGVYEDDQPOLMEGEPFLANDIMLVNQGSGLEFVGVINEDGVPNPDF 397
 CC 399 SVSNFVDMLYGYPECKDRLRTIKMYITDMADKENPRTKRTVALFTDHWAPAVA-A 457

398 SVSNFVNDLVGYEGEGRCTLRETIKENYTDMAQXENPERBRKTVLALFTLHQVAFAPVAKTA 457

QY 458 DLAAYGSPPTVYAFATFHHCOSEKKEPMASASGDEVYVFGIMGTFELSCGSPKNDV 517

DQ 459 DLAAGSPPTVYAFATFHHCOSEKKEPMASASGDEVYVFGIMGTFELSCGSPKNDV 517

QY 518 MLSAVMTYTNNAKGGDPVQVPGCTKRIHKRNRFEEVNAASKNAPDQVYHIGKRF 577

DQ 519 XLSAVMTYTNNAKGGDPVQVPGCTKRIHKRNRFEEVNAASKNAPDQVYHIGKRF 577

QY 578 VRDHYRATKVAFLMLSEVPHLENLEIFGVYSTTAKVPEKMTSPFYGRSRPAKINPTK 637

DQ 578 VRDHYRATKVAFLMLSEVPHLENLEIFGVYSTTAKVPEKMTSPFYGRSRPAKINPTK 637

QY 638 RPAITTPANNKSGSKDPHKTGPEDTVLITKRDVSTELSVITAVGASLLFANILAPALY 697

DQ 638 RPAITTPANNKSGSKDPKGTGPEDTVLITKRDVSTELSVITAVGASLLFANILAPALY 697

QY 698 YKAKDKPRHEHRRSPQCRNTYNDIAIQNEELMSIQMQLIEHCESELSQHQJLRITCP 757

DQ 698 YKAKDKPRHEHRRSPQCRNTYNDIAIQNEELMSIQMQLIEHCESELSQHQJLRITCP 757

QY 758 PDVYGLTRFSGDDIPATNTFTITMILETGAQPHRTFSGGQNSYLNPHGSTRV 816

DQ 758 PDVYGLTRFSGDDIPATNTFTITMILETGAQPHRTFSGGQNSYLNPHGSTRV 816

RESULT 2			
ID	NLNGY_HUMAN	STANDARD:	PRT: 816 AA.
AC	Q8NFZ3, C9X2E8,		
DT	15-SEP-2003 (Rel. 42, Created)		
DT	15-SEP-2003 (Rel. 42, Last sequence update)		
DT	15-SEP-2003 (Rel. 42, Last annotation update)		
DE	Neurologin 4, Y-linked precursor (Neurologin Y).		
GN	NLGN4 OR KIA0395.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
CX	NCBI_TaxID=9606;		
KN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORM 1).		
RX	PubMed=12669065;		
RA	Jainin S., Quach H., Becanovic C., Rastam M., Colliniaux C.,		
RA	Gilberg I.C., Soderstrom H., Sjors B., Leboyer M., Gillberg C.,		
RA	Bourgeois T., Nyden A., Philippe A., Cohen D., Chabane N.,		
RA	Mourer-Stroem T., C.C., Brice A., Spohnheim E., Spunkling I.,		
RA	Skjeldal O.H., Coleman M., Pearl P.C., Cohen I.L., Isidoris J.,		
RA	Zappella X., Marchetti G., Pompella A., Aschauer H., Van Veldhoven J.,		
RT	"Mutations of the X-linked genes encoding neuro-logins NLGN3 and NLGN4		
RT	are associated with autism."		
RL	Nat. Genet. 34:27-29(2003).		
RN	?		
RP	SEQUENCE FROM N.A. (ISOFORM 2).		
RC	TISSUE=Brain;		
RX	MEDLINE=99246063; PubMed=10210032;		
RA	Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hiroseawa M.,		
RA	Miyajima K., Tanaka A., Kotani H., Nomura N., Ohara O.,		
RT	"Prediction of the coding sequences of unidentified human genes. XIII:		
RT	The complete sequences of 106 new cDNA clones from brain which code		
RT	for large proteins in vitro."		
RL	OMA Res. 6:63-70(1999).		
CC	-1 FUNCTION: Pirative: neuronal cell surface protein involved in cell-		
CC	cell-interactions.		
CC	-1 SUBUNIT: Interacts through its C-terminus with Dlg4/PSD-95 third		
CC	PDZ domain (by similarity).		
CC	-1 SUBCELLULAR LOCATION: Type I membrane protein (Potential).		
CC	-1 ALTERNATIVE PRODUCTS:		
CC	Event=Alternative splicing; Named isoforms=2;		
CC	Name=1;		
CC	Isoid=Q8NFZ3-1; Sequence=Displayed;		
CC	Name=2;		
CC	Isoid=Q8NFZ3-2; Sequence=VSP_007537;		

CC Note: No experimental confirmation available:
CC h- SIMILARITY: Belongs to the type-3 carboxylesterase/lyase family.
CC
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CC or send an email to license@sib-sib.ch).

Seq	SEQUENCES	816 AA:	92020 MM:	
DR	EMBL: AF376804; AAM46133.1; -			
DR	EMBL: AB023168; BAA76795.1; -			
DR	InterPro: IPR002018; Carboxylesterase.			
DR	InterPro: IPR009460; Neurotrophin			
DR	InterPro: IPR003379; Serine_esterase.			
DR	Plant: PFO0135; Coesterase; 1.			
DR	PRINTS; PRO1090; NEUROLIGIN.			
DR	PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.			
KM	Cell adhesion; Glycoprotein; Signal; Transmembrane;			
KM	Alternative splicing			
FT	SIGNAL	1	43	POTENTIAL.
FT	CHAIN	44	816	NEUROLIGIN 4, Y LINKED.
FT	DOMAIN	44	676	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	677	697	POTENTIAL.
FT	DOMAIN	698	816	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	110	146	BY SIMILARITY.
FT	DISULFID	306	317	BY SIMILARITY.
FT	D-SULFID	476	510	BY SIMILARITY.
FT	CARBOHYD	102	102	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	511	511	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPIC	1	168	Missing (in isoform 2).
Seq	SEQUENCES	816 AA:	92020 MM:	/FTId:VSP_037537
				/FB69310773BIHEB6 CRG64;

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Query Match: 40.0%; Score 326; DB 1; Length 816;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 546; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Cy 163 QNSKKPVMVYIHGGSYMEGTGMIDGSLASYNVIVITINRYLSIGLSTGDAKGN 222
Db 162 QNSKKPVMVYIHGGSYMEGTGMIDGSLASYNVIVITINRYLSIGLSTGDAKGN 221
Cy 223 YGLDIOIALKREBNVAGRGDPKATIGSSAGASCVSLTLHSYSGLFORKIIISG 282
Db 222 YGLDIOIALREBNVAGRGDPKATIGSSAGASCVSLTLHSYSGLFORKIIISG 281
Cy 283 TALSMAVNYCFPAKTRILADKVCNMJLTTDDVECCRFKNYKELIQCTITPAZYHAFG 342
Db 282 TALSMAVNYQPAKTRILADKVCNMLDITDVECLXKXKKEKLIQCTITPATVHZAFG 341
Cy 343 PVIDDDVVPDDEQCLIMEGGEFLAYDIMLSYNGCESLKFADJYVNDGCVTPMDPFSYSN 402
Db 342 PVIDDDVVPDDEQCLIMEGGEFLAYDIMLSYNGCESLKFADJYVNDGCVTPMDPFSYSN 401
Cy 403 FVNDGCVYPEGKDTLRETIKENYTDMAKDNKPESTRKTYVALFTDHWAPFAVAADJHA 461
Db 402 FVNDLVYGEPEGKDTLRETIKENYTDMAKDNKPESTRKTYVALFTDHWAPFAVAADJHA 461
Cy 462 QVGSPTVYAFYHHCQSEMKSWADSASGDEVYVFGIMIGTLELFCSESKNDVMJISA 521
Db 462 QVGSPTVYAFYHHCQSEMKSWADSASGDEVYVFGIMIGTLELFCSESKNDVMJISA 521
Cy 522 VVMTVATENAKGDNCPVQDRTFHTKTKNRFEEVAWSKYNKCDLYCHTLKRYVDH 581
Db 522 VVMTVATENAKGDNCPVQDRTFHTKTKNRFEEVAWSKYNKCDLYCHTLKRYVDH 581
Cy 582 YRAIKVAFWLELVPLHLNLNIEFQVYSTIKVPPDMTSPYGTRRSPAKIMPTTKRAI 641
Db 582 YRAIKVAFWLELVPLHLNLNIEFQVYSTIKVPPDMTSPYGTRRSPAKIMPTTKRAI 641
Cy 642 TPANNPKSKSDPKHKYGEDTTLVLETKRQDSTLSLSTIAVAGSFLNLILAAALYKDD 701
Db 642 TPANNPKSKSDPKHKYGEDTTLVLETKRQDSTLSLSTIAVAGSFLNLILAAALYKDD 701

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ID      642 IPANNPKHSPKNGICPDTIVLTIKADYSISVTVAVGASLFLNLAFAALYYKKD 70:
CY      702 KRRETHR 709
DB      702 KRRETHR 709

RESULT 3
NCBI_MACMU
ID      NCBI_MACMU      STANDARD:      FRT:      213 AA.
AC      Q9MMG7;
DT      15-SEP-2003 (rel. 42, Created);
DT      15-SEP-2003 (rel. 42, Last sequence update);
DT      15-SEP-2003 (rel. 42, Last annotation update);
DE      Neurologin 4 (Fragment).
CN      NCBI.
CS      Macaca mulatta (Rhesus macaque);
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecinae; Macaca.
OX      NCBI_TaxID=9544;
RN      1;
RP      SEQUENCE FROM N.A.
RC      TISSUE=Hypothalamus;
RA      Mungest A.E., Ojeda S.R.;
RL      Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
CC      - FUNCTION: Putative neuronal cell surface protein involved in cell-
CC      cell interactions (by similarity).
CC      - SUBMIT: Interacts through its C-terminus with Dlg4/PSD-95 third
CC      PDZ domain (by similarity).
CC      - SIMILAR: Belongs to the type I membrane protein (Potential).
CC      This SNIS-PRO entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
CC      or send an email to license@sib-sib.ch).
DR      EMBL: AF462636; AAL66382.1;
DR      PROSITE: PS00941; CARBOXYL-ESTERASE_B_2: PARTIAL.
KM      Cell adhesion; Transmembrane.
FT      NON_TER      1
FT      DOMAIN      <1 73      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      74 94      POTENTIAL.
FT      DOMAIN      95 213      CYTOPLASMIC (POTENTIAL).
SO      SEQUENCE 213 AA: 24036 KW; CAE21610035C660B CRC64;

Query Match      26.1%; Score 213; DB 1; Length 213;
Best Local Similarity 100.0%; Pred.No. 1.4e-212;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID      604 FOYVSTTKVPPPKDTSFPGYGRSPAKIMPTKSPATTPANNPGHSDPKPTDPTV 663
DB      1 FOYVSTTKVPPPKDTSFPGYGRSPAKIMPTKSPATTPANNPGHSDPKPTDPTV 60
CY      664 I-ETKADYSTELSVTVAVGASLFLNLAFAALYYKKDQRRSETHRRSPDQRTNDIAH 723
DB      61 I-ETKADYSTELSVTVAVGASLFLNLAFAALYYKKDQRRSETHRRSPDQRTNDIAH 120
CY      724 IONETKSLQKQLEHDECEGJAHDTIRLTCPEDTIVTIRSPEDIPKTPPTTMIIP 783
DB      121 IONETKSLQKQLEHDECEGJAHDTIRLTCPEDTIVTIRSPEDIPKTPPTTMIIP 183
CY      784 NTUTGVQPLATFTSSGGSNSTNLFPHGSTPRV 316
DB      161 NTUTGVQPLATFTSSGGSNSTNLFPHGSTPRV 213

RESULT 4
NCBI_HUMAN

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ID      NCBI_HUMAN      STANDARD:      FRT:      840 AA.
AC      Q9N07;
DT      15-SEP-2003 (rel. 42, Created);
DT      15-SEP-2003 (rel. 42, Last sequence update);
DT      15-SEP-2003 (rel. 42, Last annotation update);
DE      Neurologin 1 precursor.
CN      NCBI.
CS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      1;
RP      SEQUENCE FROM N.A. (ISOFORM 2).
RC      TISSUE=Brain;
RA      MEDLINE=99397452; PubMed=10470851;
RA      Kikuno R., Nagase T., Shikawa K.-I., Hirosawa Y., Miyajima N.,
RA      Tanaka A., Kotani H., Nomura N., Ohara O.;
RA      "Prediction of the coding sequences of unidentified human genes. XIV.
RA      The complete sequences of 100 new cDNA clones from brain which code
RA      for large proteins in vitro.";
RA      DNA Res. 6:197-205 (1999).
RN      12;
RP      SEQUENCE FROM N.A. (ISOFORM 2).
RC      TISSUE=Endothelium;
RA      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.L., Feilgenau E.A., Grosse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Xie S.I., Wang C., Hsieh F.,
RA      Batchenko L., Marusina K., Ramer A.A., Rudin G.K., Hong L.,
RA      Stapleton M., Soares M.B., Bonald M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ustun T.B., Toshynski S., Carrinzi P., Prange C.,
RA      Raha S.S., Loque-Jiang N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA      Bosak S.A., McEwan P.C., McKernan K.J., Malek C.A., Gunaratne P.H.,
RA      Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA      Villalón D.K., Muey D.M., Sodergren E.O., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kelleman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting Y., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Battefeld Y.S.N., Krzywinski M.T., Skalski U., Smalins J.E.,
RA      Schenker A., Schein C.E., Jones S.J.M., Marra M.A.;
RA      "Generation and initial analysis of more than 15,000 full-length human
RA      and mouse cDNA sequences.";
RA      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN      13;
RP      SEQUENCE OF 315-823 FROM N.A.
RC      TISSUE=Embryo;
RA      Itoigai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA      Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA      Yamamoto C., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA      Hattori Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA      Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RA      "XERO human cDNA sequencing project.";
RA      Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RN      14;
RP      CONCEPTUAL TRANSLATION (ISOFORM 1).
RA      Roehner B.;
RA      Unpublished observations (MAY-2003).
RN      15;
RP      INTERACTION WITH Dlg4.
RA      PubMed=9278515;
RA      Irie M., Hata Y., Takeuchi M., Ichtchenko K., Toyoda A., Hirao K.,
RA      Takai Y., Rosahl T.W., Suedhof T.C.;
RA      "Binding of neurologin to PSD-95.";
RA      Science 277:1511-1515 (1997).
RN      16;
RP      FUNCTION.
RA      PubMed=10892652;
RA      Scheiffele P., Fan J., Choich J., Fetter R., Serafini T.;
RA      "Neurologin expressed in nonneuronal cells triggers presynaptic
RA      development in contacting axons.";
RA      Cell 101:657-669 (2000).

```

CC -1- FUNCTION: Neuronal cell surface protein thought to be involved in
CC cell-cell interactions by forming intercellular junctions through
CC binding to beta-neurexins. Seems to play role in formation or
CC maintenance of synaptic junctions. In vitro, triggers de novo
CC formation of presynaptic structures. May be involved in
CC specification of excitatory synapses.
CC -1- SUBUNIT: Interacts with neuexin 1-beta, neuexin 2-beta and
CC neuexin 3-beta (By similarity). Interacts through its C-terminus
CC with DLG4/PSD-95 third PDZ domain.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Enriched in
CC synaptic plasma membranes and clustered in synaptic clefts and
CC postsynaptic densities (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9N2G7-1; Sequence=D:displayed;
CC Note=No experimental confirmation available;
CC Name=2;
CC IsoId=Q9N2G7-2; Sequence=VSP_007527;
CC -1- PTM: N- and O-glycosylated (By similarity).
CC -1- SIMILARITY: Belongs to the type-B carboxy-esterase/lipase family.
CC -----
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CC or send an email to license@ebi.ac.uk).

DR EMBL: AB028993; BAA33022.1;
DR EMBL: BC032555; AAH32555.1;
DR EMBL: AK074522; BAC11039.1; A21_NIT.
DR HSPB: P21836; 1MAA.
DR GeneW: HGNC:14291; NLGN1.
DR MIM: 600568;
DR InterPro: IPR002218; Carboxylesterase.
DR InterPro: IPR000460; Neurologin.
DR InterPro: IPR000379; Ser_esterase.
DR Pfam: PF00135; Coesterase; 1.
DR PRINTS: PR01080; NEUROLOGIN.
DR PROSITE: PS00941; CARBOXYESTERASE B 2; 1.
KM Cell adhesion; Glycoprotein; Signal; Transmembrane;
KM Alternative splicing.
FT SIGNAL 45
FT CHAIN 46
FT DOMAIN 46
FT TRANSMEM 695
FT DOMAIN 7-6
FT DISULFID 1-2
FT DISULFID 359
FT DISULFID 359
FT CARBOHYD 109
FT CARBOHYD 303
FT CARBOHYD 340
FT CARBOHYD 544
FT VARPPLIC 181
FT CONFILCT 711
SC SEQUENCE 940 AA; 93835 MW; A3FE21716F62DE29 CEC64;
Query Match 6.1%; Score 50; DB 1; Length 640;
Best Local Similarity 100.0%; Pred. No. 3.7e-43;
Matches 50; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 510 CNEKNDVYLSAVNTYWTNPAKTGCPQPVQDCTKTLTKNFEEVAV 558
DB 543 CNEKNDVYLSAVNTYWTNPAKTGCPQPVQDCTKTLTKNFEEVAV 592

RESULT 5
NGI_MOUSE STANDARD; PRT; 843 AA.

AC Q99XK0;
CC 15-SEP-2003 (Rel. 42, Created)
CC 15-SEP-2003 (Rel. 42, Last sequence update)
CC 15-SEP-2003 (Rel. 42, Last annotation update)
CC Neuroligin 1 precursor.
CC NLGN1 OR KIAA1370.
CC Mus musculus (mouse).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxId=10090;
CC (1)
CC SEQUENCE FROM N.A. (ISOPFORM 1).
CC TISSUE=Brain;
CC MEDLINE=22579291; PubMed=12693551;
CC Okazaki N., Kikuno R., Ohara R., Aizawa H., Yuasa S.,
CC Nakajima D., Nagase T., Ohara O., Koga H.,
CC Prediction of the coding sequences of 400 mouse KIAA-homologous
CC cDNAs identified by screening of terminal sequences of cDNA clones
CC randomly sampled from size-fractionated libraries.";
CC Random Res. 10:35-48(2003).
CC [2]
CC SEQUENCE FROM N.A. (ISOPFORM 2).
CC MEDLINE=22388257; PubMed=12477932;
CC Strussberg R., Feingold E.A., Grouse L.H., Derge J.G.,
CC Kjaer S.R., Collins F.S., Wagner L., Steinmetz C.M., Schuler G.D.,
CC Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
CC Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
CC Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
CC Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.J., Scheetz T.E.,
CC Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
CC Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
CC Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
CC Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
CC Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
CC Fahy J., Heltzer E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
CC Whitting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
CC Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
CC Rodriguez A.W., Grimwood J., Schmitz J., Myers R.M.,
CC Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
CC Scherch A., Schein J.F., Jones S.J.M., Marra M.A.,
CC "Generation and initial analysis of more than 15,000 full-length human
CC and mouse cDNA sequences.";
CC Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
CC [3]
CC TISSUE SPECIFICITY.
CC PubMed=11329178;
CC Gilbert M., Smith J., Roskams A.J., Auld V.J.,
CC "Neurologin 3 is a vertebrate gliotactin expressed in the olfactory
CC ensheathing glia: a growth-promoting class of macroglia.";
CC Glia 34:15-164(2001).
CC -1- FUNCTION: Neuronal cell surface protein thought to be involved in
CC cell-cell interactions by forming intercellular junctions through
CC binding to beta-neurexins. Seems to play role in formation or
CC maintenance of synaptic junctions. In vitro, triggers the de novo
CC formation of presynaptic structures (By similarity). May be
CC involved in specification of excitatory synapses.
CC -1- SUBUNIT: Interacts with neuexin 1-beta, neuexin 2-beta and
CC neuexin 3-beta, and through its C-terminus with DLG4/PSD-95 third
CC PDZ domain (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Enriched in
CC synaptic plasma membranes and clustered in synaptic clefts and
CC postsynaptic densities (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC Note=No experimental confirmation available;
CC IsoId=Q99XK0-1; Sequence=D:displayed;
CC Name=2;
CC IsoId=Q99XK0-2; Sequence=VSP_007528, VSP_007529, VSP_007530;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Expressed in olfactory bulb.
CC -1- PTM: N- and O-glycosylated (By similarity).


```

CC      [Ce:1 81:435-443(1995)].
CC
CC      RX      INTERACTION WITH NEUREXIN 1-BETA, AND FUNCTION.
CC      RX      MEDLINE=97467410; Pubmed=9325340;
CC      RA      Nguyen T., Suedhof T.C.;
CC      RT      "Binding properties of neuroligin 1 and neurexin 1beta reveal function
CC      RT      as heterophilic cell adhesion molecules."
CC      RL      J. Biol. Chem. 272:26032-26039(1997).
CC      RM      [3]
CC      RM      BLOCKAGE OF N-TERMINUS, AND INTERACTION WITH NEUREXIN 1-BETA; NEUREXIN
CC      RP      2-BETA AND NEUREXIN 3-BETA.
CC      RX      MEDLINE=96162010; Pubmed=8576240;
CC      RA      Ichtchenko K., Nguyen T., Suedhof T.C.;
CC      RT      "Structures, alternative splicing, and neurexin binding of multiple
CC      RT      neuroligins."
CC      RL      J. Biol. Chem. 271:2676-2682(1996).
CC      RN      [4]
CC      RP      TISSUE SPECIFICITY, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
CC      RX      Pubmed=99227700;
CC      RA      Song G.-Y., Ichtchenko K., Suedhof T.C., Brose N.;
CC      RT      "Neuroligin 1 is a postsynaptic cell-adhesion molecule of excitatory
CC      RT      synapses."
CC      RL      Proc. Natl. Acad. Sci. U.S.A. 96:1100-1105(1999).
CC      RN      [5]
CC      RP      TISSUE SPECIFICITY.
CC      RX      Pubmed=11329178;
CC      RA      Gilbert M., Smith J., Roskams A.J., Au-D V.J.;
CC      RT      "Neuroligin 3 is a vertebrate gliotactin expressed in the olfactory
CC      RT      ensheathing glia, a growth-promoting class of macroglia."
CC      RL      Glia 34:151-164(2001).
CC      RN      [-1]
CC      RP      FUNCTION: Neuronal cell surface protein thought to be involved in
CC      RP      cell-cell interactions by forming intercellular junctions through
CC      RP      binding to beta-neurexins. Seems to play role in formation or
CC      RP      maintenance of synaptic junctions. In vitro, triggers the de novo
CC      RP      formation of presynaptic structures (By similarity). May be
CC      RP      involved in specification of excitatory synapses.
CC      RN      [-1]
CC      RP      SUBUNIT: Interacts with neurexin 1-beta isoforms 3/Beta 4B5A and
CC      RP      4/Beta 4B5B. Interacts with neurexin 2-beta isoforms 3/Beta 4B5A,
CC      RP      4/Beta 4B5B, 7/Beta 4B5A6 and 8/Beta 4B5A6. Interacts with
CC      RP      corresponding neuexin 3-beta isoforms. Interacts through its C-
CC      RP      terminus with DLG4/PSD-95 third PDZ domain (By similarity).
CC      RN      [-1]
CC      RP      SUBCELLULAR LOCATION: Type I membrane protein. Enriched in
CC      RP      synaptic plasma membranes and clustered in synaptic clefts and
CC      RP      postsynaptic densities. Colocalized with DLG4/PSD-95 and
CC      RP      SHGAP1/glutamate (NMDA) receptor subunit zeta 1.
CC      RN      [-1]
CC      RP      ALTERNATIVE PRODUCTS:
CC      RP      Event=Alternative splicing; Named isoforms=4;
CC      CC      Name=:;
CC      CC      IsoId=Q62765-1; Sequence=Displayed;
CC      CC      Name=:;
CC      CC      IsoId=Q62765-2; Sequence=VSP_007531, VSP_007533;
CC      CC      Note=No experimental confirmation available;
CC      CC      Name=:;
CC      CC      IsoId=Q62765-3; Sequence=VSP_007532;
CC      CC      Name=:;
CC      CC      IsoId=Q62765-4; Sequence=VSP_007531;
CC      CC      [-1]
CC      RP      TISSUE SPECIFICITY: Expressed in brain, almost exclusively in
CC      CC      neurons, and spinal chord.
CC      RN      [-1]
CC      RP      DEVELOPMENTAL STAGE: Expression is low in embryonic brains (E12-
CC      CC      E16) and reaches dramatically after birth (postnatal days P0-P3)
CC      CC      and reaches a plateau during the period when most synapses are
CC      CC      formed (P5-P8).
CC      CC      [-1]
CC      RP      PTM: N- and O-glycosylated.
CC      CC      [-1]
CC      RP      PTM: The N-terminus is blocked.
CC      CC      [-1]
CC      RP      SIMILARITY: Belongs to the type-B carboxylesterase/1lipase family.
CC      CC      -----
CC      CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Neuroigin 2 precursor.
 GN NLGN2.
 CS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CX NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SEQUENCE OF N-TERMINUS, TISSUE
 RP SPECIFICITY, AND INTERACTION WITH NEUREXIN 1-BETA; NEUREXIN 2-BETA AND
 RP NEUREXIN 3-BETA.
 RC TISSUE=Forebrain;
 RX MEDLINE=96162010; PubMed=9576240;
 RA Ichtchenko K., Nguyen T., Suedhof T.C.,
 RT "Structures, alternative splicing, and neurexin binding of multiple
 RT neuroigins";
 RL J. Biol. Chem. 277:2676-2682(1996).
 RN (2)
 RP TISSUE SPECIFICITY.
 RX PubMed=11329178;
 RA Gilbert M., Smith J., Postkams A.O., Auld V.J.,
 RT "Neuroigin 3 is a vertebrate gliotactin expressed in the olfactory
 RT ensheathing glia, a growth-promoting class of "macroglia".
 RL Glia 34:151-164(2001).
 CC -1- FUNCTION: Neuronal cell surface protein thought to be involved in
 CC cell-cell interactions by forming intercellular junctions through
 CC binding to beta-neurexins. Seems to play role in formation or
 CC maintenance of synaptic structures. In vitro, triggers the de novo
 CC formation of presynaptic structures (By similarity).
 CC -1- SUBUNIT: Interacts with neurexin 1-beta isoforms 3/Beta 4B5A and
 CC 4/Beta 4B5B. 7/Beta 4B5A6 and 8/Beta 4B5B6. Interacts with
 CC neurexin 3-beta. Probably interacts through its C-terminus with
 CC DLG4/PSD-95 third PDZ domain (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (potential).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q62888-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q62888-2; Sequence=VSP 007533;
 CC -1- TISSUE SPECIFICITY: Expressed in brain, spinal chord and dorsal
 CC root ganglion.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL: U41662; AAA97870.1; -;
 DR HSPB: P37967; IOE3.
 DR InterPro: IPR002013; Carboxylesterase.
 DR InterPro: IPR000460; Neuroigin.
 DR InterPro: IPR003379; Ser_estr_site.
 DR Pfam: PF0135; Coesterase_1.
 DR PRINTS: PF01090; NEUROIGLIN.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; -;
 DR Cell adhesion; Glycoprotein; Signal; Transmembrane;
 KW Alternative splicing.
 FT SIGNAL 1 14
 FT CHAIN 15 836 PROBABLE.
 FT DOMAIN 15 678 NEUROIGLIN 2.
 FT TRANSMEM 679 699 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 700 836 POTENTIAL.
 FT DISULFID 106 142 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 317 328 BY SIMILARITY.
 FT DISULFID 487 522 BY SIMILARITY.
 FT CARBOHYD 98 98 N-LINKED (GLCNAC... (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC... (POTENTIAL).

FT CARBOHYD 522 522 N-LINKED (GLCNAC... (POTENTIAL).
 FT VARSPLIC 153 169 Missing (in isoform 2).
 FT /FTID=VSP_007533.
 SC SEQUENCE 836 AA; 90961 MW; 1AD51CB1BE4BF9CF CRC64;
 Query Match 5.9%; Score 48; DB 1; Length 836;
 Best Local Similarity 100.0%; Pred. No. 4,3e-41;
 Matches 48; Conservative 0; Indels 0; Gaps 0;
 QY 510 CNFSNDMLSAVMTYWTNFAKTGDPQOPQDPQKPRHTKPNRFEV 557
 DB 521 CNFSNDMLSAVMTYWTNFAKTGDPQOPQDPQKPRHTKPNRFEV 568
 RESCUT 9
 ID NLG3 HUMAN STANDARD; PRT; 846 AA.
 AC Q9NZ34; Q9NZC0; Q9NZ95; Q9NZ96; Q9NZ97; Q9NZ48;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Neuroigin 3 precursor (Gliotactin homolog).
 GN NLGN3 CR N13 OR KIAA1480.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=20231756; PubMed=10767552;
 RA Philibert R.A., Winfield S.L., Sandhu H.K., Martin P.Y., Gans E.I.,
 RT "The structure and expression of the human neuroigin-3 gene";
 RL Gene 246:303-310(2000).
 RN (2)
 RP SEQUENCE OF 12-848 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20277482; PubMed=10819333;
 RA Nagase T., Kikuno R., Ichikawa K., Hirosewa M., Ohara O.,
 RT "Prediction of the coding sequences of unidentified human genes. XVII.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RL for large proteins in vitro.";
 RL DNA Res. 7:143-150(2000).
 RN (3)
 RP SEQUENCE OF 410-848 FROM N.A.
 RA Itoigai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
 RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
 RA Yamamoto Y., Wakamatsu A., Nakamura Y., Kojima S., Nagabari K.,
 RA Kasuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
 RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.,
 RT "NEO human cDNA sequencing project.";
 RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
 RN (4)
 RP INTERACTION WITH DLG4.
 RX PubMed=9278515;
 RA Irie M., Hata Y., Takeuchi M., Ichtchenko K., Toyoda A., Hirao K.,
 RA Takai Y., Rosahl T.W., Suedhof T.C.,
 RT "Binding of neuroigins to PSD-95.";
 RL Science 277:1511-1515(1997).
 RN (5)
 RP VARIANT X-LINKED AUTISM CYS-451.
 RX PubMed=12669065;
 RA Jamain S., Quach H., Betancur C., Rastam M., Colonnaux C.,
 RA Gillberg I.C., Soderstrom H., Gires B., Leboyer M., Gillberg C.,
 RA Bourgeron T., Nyden A., Philippe A., Cohen D., Chabane N.,
 RA Mouren-Simeoni M.C., Brice A., Sponheim E., Spunkland L.,
 RA Skjeldal O.H., Coleman M., Pearl P.L., Cohen I.J., Tsiftouris J.,
 RA Zappella M., Menchetti G., Pompella A., Aschauer H., Van Maldergem T.,
 RT "Mutations of the X-linked genes encoding neuroigins NLGN3 and NLGN4
 RT are associated with autism.";
 RL Nat. Genet. 34:27-29(2003).
 CC -1- FUNCTION: Neuronal cell surface protein thought to be involved in
 CC cell-cell interactions by forming intercellular junctions through
 CC binding to beta-neurexins. May play a role in formation or

```

CC maintenance of synaptic junctions. May also play a role in glia-
CC glia or glia-neuron interactions in the developing peripheral
CC nervous system.
CC -1- SUBMIT: Interacts with neuexin 1-beta, neuexin 2-beta and
CC neuexin 3-beta (By similarity). Probably interacts through its C-
CC terminus with DLG4/PSD-95 third PDZ domain.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=HNL3;
CC IsoId=Q5N294-1; Sequence=Displayed;
CC Name=2; Synonyms=HNL3;
CC IsoId=Q5N294-2; Sequence=VSP_007534;
CC -1- DISEAS: Defects in NLGN3 may be the cause of X-linked autism
CC (NLM:300425); a pervasive developmental disorder, prototypically
CC characterized by impairments in reciprocal social interaction and
CC communication, restricted and stereotyped patterns of interests
CC and activities, and the presence of developmental abnormalities by
CC 3 years of age.
CC -1- DISEAS: Defects in NLGN3 may be the cause of Asperger syndrome
CC (AS), a form of childhood autism.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
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CC or send an email to license@sib-sib.ch).
CC
DR EMBL AF217411; AAF71230.1; ALT_TERM.
DR EMBL AF217412; AAF71231.1; ALT_TERM.
DR EMBL AF217413; AAF71232.1; .
DR EMBL AF217414; AAF71233.1; .
DR EMBL AB040913; BA976004.1; ALT_INT.
DR EMBL AK074814; BA011226.1; ALT_INT.
DR HSS2 P21836; 1MAA.
DR Genew; HGNC:14289; NLGN3.
DR MIM: 300336; .
DR InterPro: IPR002018; Carboxylase.
DR InterPro: IPR000460; NeuroLigin.
DR InterPro: IPR000379; Ser ester_ site.
DR Pfam: PF00135; Coesterase_1.
DR PRINTS: PR01390; NEURO_LGIN.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Cell adhesion; Glycoprotein; Signal; Transmembrane;
KW Alternative splicing; Disease mutation.
FT SIGNAL 1 37 POTENTIAL.
FT CHAIN 38 948 NEURO_LGIN 3.
FT DOMAIN 713 733 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 733 736 POTENTIAL.
FT DOMAIN 731 848 CYTOPLASMIC (POTENTIAL).
FT DISULFID 106 141 BY SIMILARITY.
FT DISULFID 340 351 BY SIMILARITY.
FT DISULFID 510 544 BY SIMILARITY.
FT CARBOHYD 98 98 N-LINKED (GLYCAN) (POTENTIAL).
FT CARBOHYD 545 545 N-LINKED (GLYCAN) (POTENTIAL).
FT VARSPLIC 153 172 Missing (in isoform 2).
FT VARSPLIC 153 172 /FTID=VSP_007534.
FT VARIANT 451 451 R -> C (in X-linked autism and AS).
FT CONFLICT 224 224 C -> P (in REF. 1; AAF71230).
FT SEQUENCE 846 AA; 53895 MW; BBE25AB7B427C68 CRC64;
SQ
Query Match 4.3%; Score 35; DB 1; Length 348;
Best Local Similarity 100.0%; Pred. No. 1,3e-27;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10
NCBI_MOUSE STANDARD; PRT; 825 AA.
AC Q8BXN5; Q8BXN4;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE NeuroLigin 3 precursor (Glycocalyx homolog).
GN NLGN3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
CX MCS_TaxID10990.
FN 11.
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus, and Retina;
RX MEDLINE=22354683; PubMed=1246851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamana K., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
RA Balazs L.M., Kaplin A., Matsuda H., Balazs S., Betzel K.N.,
RA Blake J.A., Brad D., Brusic V., Chochia C., Cortani L.E., Cousins S.,
RA Dalla E., Drogant T.A., Fletcher C.F., Forrest A., Fraser K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson J.D., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kongaya A., Kurochin T.V., Lee Y., Lenhard B., Lyons F.A.,
RA Magolda D.R., Maltats L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numa K., Okido T., Pavan W.J., Perlea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou Y., Shimada K.,
RA Sultana R., Takeuchi Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wanstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilting L.G., Wysshaw-Solis A., Yangisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Cernici P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura N., Sakazume N., Sato X.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imctani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.
RL Nature 420:563-573 (2002).
RK [2]
RP TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RX PubMed=1129178.
RA Gilbert W., Smith J., Roskams A.J., Auld V.J.;
RT "NeuroLigin 3 is a vertebrate gliotactin expressed in the olfactory
RT ensheathing glia, a growth-promoting class of macroglia."
RL Glia 34:15-164 (2001).
CC -1- FUNCTION: Neuronal cell surface protein thought to be involved in
CC binding to beta-neurexins. May play a role in formation or
CC maintenance of synaptic junctions. May also play a role in glia-
CC glia or glia-neuron interactions in the developing peripheral
CC nervous system.
CC -1- SUBMIT: Interacts with neuexin 1-beta, neuexin 2-beta and
CC neuexin 3-beta (By similarity). Probably interacts through its C-terminus with
CC DLG4/PSD-95 third PDZ domain (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: Expressed in olfactory bulb and olfactory
CC epithelium. Found in olfactory ensheathing glia but not in
CC olfactory neurons, and in developing peripheral glia.
CC -1- DEVELOPMENTAL STAGE: Detected at embryonic day E17 and postnatal
CC day P1 in retinal astrocytes, spinal chord astrocytes and Schwann
CC cells of the dorsal root ganglion.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.

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CC -----
DR EMBL AK035018; EAC0207.1; -
DR EMBL AK044438; EAC01918.1; -
DR MGI MG1:2444609; A23085M13R1K.
DR InterPro: IPR0020.8; Carboxylase.
DR Pfam: PF00135; Coesterase; 1; _site.
DR PROSITE: PS00941; CARBOXYL-ESTERASE B_2; 1.
DR Cell adhesion; Glycoprotein; Signal; Transmembrane.
KW CHAIN 1
FT SIGNAL 1
FT CHAIN 35
FT DOMAIN 35 686
FT TRANSMEM 687 707
FT DOMAIN 708 825
FT DISULFID 103 138
FT DISULFID 372 388
FT DISULFID 487 521
FT CARBOHYD 95
FT CARBOHYD 522
FT CONFLICT 459
SC SEQUENCE 825 AA; 21175 MW; 38F1758950A44CE CAC64;

Query Match: 3.9%; Score 32; DB 1; Length 825;
Best Local Similarity 100.0%; Pred. No. 17e-24;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 399 SVSNFVNLGYGPEGKDTLRITIKRYMTDMD 430
DB 409 SVSNFVNLGYGPEGKDTLRITIKRYMTDMD 440
|||||
AC 062859; STANDARD; PRT; 848 AA.
ID NLG3 RAT
DT 15-SEP-2003 (rel. 42, Created)
DT 15-SEP-2003 (rel. 42, Last sequence update)
DE 15-SEP-2003 (rel. 42, Last annotation update)
DE Neurotrophin 3 precursor (Glycocalyx homolog).
GN NLG3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4). BIOGRAPHY OF N-TERMINUS,
RP TISSUE SPECIFICITY, AND INTERACTION WITH NEUREXIN 1-BETA; NEUREXIN
RP 2-BETA AND NEUREXIN 3-BETA.
RC TISSUE-FOREBRAIN;
RX MEDLINE=96162010; PubMed=8576240;
RA Ichtchenko K., Nguyen T., Suedhof T.C.;
RT "Structures, alternative splicing, and neurexin binding of multiple
RT neurotrophins."
RL J. Biol. Chem. 271:2676-2682(1996).
RN (2)
RP TISSUE SPECIFICITY.
RX PubMed=11329178;
RA Gilbert M., Smith C., Roskams A.J., Auld V.J.;
RT "Neurotrophin 3 is a vertebrate gliotactin expressed in the olfactory
RT ensheathing glia, a growth-promoting class of macroglia."
RL Glia 34:151-164(2001).
SC -1- FUNCTION: Neuronal cell surface protein thought to be involved in
CC cell-cell-interactions by forming intercellular junctions through
CC binding to beta-neurexins. May play a role in formation or
CC maintenance of synaptic junctions. May also play a role in glia-
CC glia or glia-neuron interactions in the developing periphery.

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CC nervous system.
CC -1- SUBUNIT: Interacts with neurexin 1-beta isoforms 3/Beta 4B5A and
CC 4/Beta 4B5B. Interacts with neurexin 2-beta isoforms 3/Beta 4B5A,
CC 4/Beta 4B5B, 7/Beta 4B5A6 and 8/Beta 4B5B6. Interacts with
CC corresponding neurexin 1-beta isoforms. Probably interacts through
CC its C-terminus with DLG4/PSD-95 third PDZ domain (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1;
CC IsoId=C62889-1; Sequence=Displayed;
CC Name=2;
CC IsoId=C62889-2; Sequence=VSP_007535; VSP_007536;
CC Note=No experimental confirmation available;
CC Name=3;
CC IsoId=C62889-3; Sequence=VSP_007536;
CC Name=4;
CC IsoId=C62889-4; Sequence=VSP_007535;
CC -1- TISSUE SPECIFICITY: Expressed in brain, spinal chord and dorsal
CC root ganglion.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/-lipase family.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL U41663; AAA97871.1; -
DR HSSP: P21836; 1MAA.
DR InterPro: IPR002019; Carboxylase.
DR InterPro: IPR000460; Neurotrophin.
DR InterPro: IPR000379; Ser esterase.
DR Pfam: PF00135; Coesterase; 1.
DR PRINTS: PR01690; NEUROLOGIN.
DR PROSITE: PS00941; CARBOXYL-ESTERASE B_2; 1.
DR Cell adhesion; Glycoprotein; Signal; Transmembrane;
KW Alternative splicing.
FT CHAIN 1
FT SIGNAL 37
FT CHAIN 38 848
FT DOMAIN 38 709
FT TRANSMEM 710 730
FT DOMAIN 731 848
FT DISULFID 106 141
FT DISULFID 340 351
FT DISULFID 510 544
FT CARBOHYD 98
FT CARBOHYD 545
FT VARSP2C 153
FT VARSP2C 172
FT VARSP2C 192
SC SEQUENCE 848 AA; 93888 MW; 750653B25E3750 CAC64;

Query Match: 3.9%; Score 32; DB 1; Length 848;
Best Local Similarity 100.0%; Pred. No. 17e-24;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 399 SVSNFVNLGYGPEGKDTLRITIKRYMTDMD 430
DB 432 SVSNFVNLGYGPEGKDTLRITIKRYMTDMD 463
|||||
AC 062862; STANDARD; PRT; 202 AA.
ID NLG3 MACMU
DT 15-SEP-2003 (rel. 42, Created)
DT 15-SEP-2003 (rel. 42, Last sequence update)
DT 15-SEP-2003 (rel. 42, Last annotation update)

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DE  Neuroligin 3 (Glycocalyx homolog) (Fragment).
GN  NLGN3.
OS  Macaca mulatta (Rhesus macaque).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Corcolithectidae;
OC  Cercopitheciinae; Macaca.
CX  NCBI_TaxID=9544;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Hypothalamus;
RA  Mueneman A.E., Ojeda S.R.;
RL  Submitted (SEP-2001) to the EMBL/GenBank/DBS databases.
CC  -1- FUNCTION: Neuronal cell surface protein thought to be involved in
CC  cell-cell interactions by forming intercellular junctions through
CC  binding to beta-neurexins. May play a role in formation or
CC  maintenance of synaptic junctions. May also play a role in glia-
CC  glia or glia-neuron interactions in the developing periphery.
CC  nervous system.
CC  -1- SUBUNIT: Interacts with neuexin 1-beta, neuexin 2-beta and
CC  neuexin 3-beta, and probably through its C-terminus with
CC  DLG4/PSD-95 third PDZ domain (5% similarity).
CC  -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC  -1- SIMILARITY: Belongs to the type-B carboxylesterase/-lipase family.
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC  use by non-profit institutions as long as its content is in no way
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CC  entities requires a license agreement (see http://www.isb-sdb.ch/announce/
CC  or send an email to license@isb-sdb.ch).
CC  -----
DR  EMBL; AF424950; AAL40263.1; -
DR  InterPro; IPR002015; Carboxylesterases.
DR  InterPro; IPR000460; Neuroligin.
DR  Pfam; PF00135; Coesterase; 1.
DR  PRINTS; PR01090; NEUROLIGIN.
DR  PROSITE; PS00941; CARBOXYLESTERASE_B_2; PARTIAL.
KW  Cell adhesion; Glycoprotein.
FT  NON_TER 1
FT  DOMAIN <1> 202 EXTRACELLULAR (POTENTIAL).
FT  DISULFID 15 49 BY SIMILARITY.
FT  CARBOHYD 50 50 N-LINKED (GLCNAC... ) (POTENTIAL).
FT  NON_TER 202
SQ  SEQUENCE 202 AA; 22897 MW; 996C2C5B7C28E158 CRC64;

Query Match 3.4%; Score 28; DB 1; Length 202;
Best Local Similarity 100.0%; Pred. No. 6.8e-2;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY  510 CNEKQDVMLSAVMTYTNFAKTGDPN 537
DB  49 CNEKQDVMLSAVMTYTNFAKTGDPN 76

RESULT 13
BAL_HUMAN STANDARD; FRT; 742 AA.
AC  P19835;
CD  01-FEB-1991 (Rel. 17, Created;
DE  01-APR-1993 (Rel. 25, Last sequence update);
DE  15-SEP-2003 (Rel. 42, Last annotation update);
DE  Bile-salt-activated lipase precursor (EC 3.1.1.3) (EC 3.1.1.13) (SAL)
DE  (Bile-salt-activated lipase) (BSAL) (Carboxyl ester lipase) (Sterol
DE  esterase) (Cholesterol esterase) (Pancreatic lysophospholipase).
GN  CEL OR BAL.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC  TISSUE=Mammary gland;

```

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RX  MEDLINE=91062144; PubMed=1698625;
RA  Nilsson J., Blomberg U., Carlsson P., Enerbaeck S., Hennell O.,
RA  Bjursell G.;
RT  "cDNA Cloning of human-milk bile-salt-stimulated lipase and evidence
RT  for its identity to pancreatic carboxylic ester hydrolase.";
RL  Eur. J. Biochem. 192:543-550(1990).
EN  (2)
RP  SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC  TISSUE=Pancreas;
RA  MEDLINE=91092392; PubMed=2265692;
RA  Hul D.Y., Kiesel J.A.;
RT  "Sequence identity between human pancreatic cholesteryl esterase and
RT  bile salt-stimulated milk lipase.";
RL  FEBS Lett. 276:131-134(1990).
EN  (3)
RP  SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC  TISSUE=Mammary gland;
RA  MEDLINE=9105134; PubMed=1988041;
RA  Bala T., Downs D., Jackson K.W., Tang J., Wang C.-S.;
RT  "Structure of human milk bile salt activated lipase.";
RL  Biochemistry 30:500-510(1991).
EN  (4)
RP  SEQUENCE FROM N.A.
RA  MEDLINE=92347858; PubMed=1639390;
RA  Lidberg U., Nilsson J., Stromberg K., Stenman G., Sahlin P.,
RA  Enerbaeck S., Bjursell G.;
RT  "Genomic organization, sequence analysis, and chromosomal
RT  localization of the human carboxyl ester lipase (CEL) gene and a
RT  cell-like (CEL) gene.";
RL  Genomics 13:630-640(1992).
EN  (5)
RP  PARTIAL SEQUENCE, AND ACTIVE SITE.
RA  MEDLINE=9112282; PubMed=1991511;
RA  Christie D.L., Cleverly D.R., O'Connor C.J.C.;
RT  "Human milk bile-salt stimulated lipase. Sequence similarity with rat
RT  lysophospholipase and homology with the active site region of
RT  cholinesterases.";
RL  FEBS Lett. 276:190-194(1991).
EN  (6)
RP  CARBOHYDRATE-LINKAGE SITES.
RA  MEDLINE=9538331; PubMed=7654718;
RA  Wang C.S., Doshi A., Jackson K.W., Yeh J.C., Cummings R.D.,
RA  Tang J.;
RT  "Isolation and characterization of human milk bile salt-activated
RT  lipase C-cell fragment.";
RL  Biochemistry 34:10639-10644(1995).
EN  (7)
RP  STRUCTURE OF N-LINKED CARBOHYDRATES.
RA  MEDLINE=99150217; PubMed=10024650;
RA  Mechert Y., Chen P., Novotny M.V.;
RT  "Structural characterization of the N-linked oligosaccharides in bile
RT  salt-stimulated lipase originated from human breast milk.";
RL  Glycobiology 9:227-234(1999).
EN  (8)
RP  FUNCTION: CATALYZES FAT AND VITAMIN ABSORPTION. ACTS IN CONCERT
RP  WITH PANCREATIC LIPASE AND COLIPASE FOR THE COMPLETE DIGESTION OF
RP  DIETARY TRIGLYCERIDES.
CC  -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC  fatty acid anion.
CC  -1- CATALYTIC ACTIVITY: A sterol ester + H(2)O = a sterol + a fatty
CC  acid.
CC  -1- ENZYME REGULATION: ACTIVATED BY BILE SALTS CONTAINING A 7-HYDROXYL
CC  GROUP.
CC  -1- ALTERNATIVE PRODUCTS:
CC  Event=Alternative splicing; Named isoforms=2;
CC  Name=Long;
CC  isoId=P19835-1; Sequence=Displayed;
CC  Name=Short;
CC  isoId=P19835-2; Sequence=VSP_001463;
CC  TISSUE SPECIFICITY: MAMMARY GLAND, AND PANCREAS.
CC  -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL: X54457; CAA36325.1; ALT_INIT.
 DR EMBL: M85201; AAA52014.1; -
 DR EMBL: M54994; AAA53211.1; -
 DR EMBL: M94579; AAA51973.1; ALT_INIT.
 DR PDB: 1F6W; 18-OCT-00.
 DR GlycoSuiteDB; S19835; -
 DR Gene; HGN:1848; CEL.
 DR MIM: 114840; -
 DR InterPro: IPR032018; Carboxylesterases.
 DR InterPro: IPR003379; Ser_ester_site.
 DR Pfam: PF00135; Coesterase; 1; -
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1;
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1;
 KW Hydroxylase; Serine esterase; Lipid degradation; Glycoprotein; Repeat;
 KW Signal; Alternative splicing; 3D-structure.

FT SIGNAL 1 20
 FT CHAIN 1 20
 FT DOMAIN 21 742
 FT ACT_SITE 214 214
 FT ACT_SITE 340 340
 FT ACT_SITE 455 455
 FT DISULFID 84 100
 FT DISULFID 266 277
 FT CARBOHYD 207 207

N-LINKED (GLCNAC...) (COMPLEX).
 /FTG=CAR_000141.
 FT CARBOHYD 553 553
 FT CARBOHYD 563 563
 FT CARBOHYD 573 573
 FT CARBOHYD 596 596
 FT CARBOHYD 607 607
 FT CARBOHYD 618 618
 FT CARBOHYD 623 623
 FT CARBOHYD 643 643
 FT CARBOHYD 651 651
 FT CARBOHYD 662 662
 FT CARBOHYD 662 662
 FT DOMAIN 559 734

REPEAT 555 565
 FT REPEAT 570 580
 FT REPEAT 581 591
 FT REPEAT 592 602
 FT REPEAT 603 613
 FT REPEAT 613 624
 FT REPEAT 624 635
 FT REPEAT 635 646
 FT REPEAT 646 657
 FT REPEAT 657 668
 FT REPEAT 668 679
 FT REPEAT 679 690
 FT REPEAT 690 701
 FT REPEAT 701 712
 FT REPEAT 712 723
 FT REPEAT 723 734
 FT REPEAT 734 742
 FT VARSPLIC 430 435

Missing (in isoform short).
 /FTG=USP_001463.
 SQ SEQUENCE 742 AA; 78345 MW; 1A0C25FA0C8C2859 CRC64;

Query Match 1.5%; Score 12; DB 1; Length 742;
 Best Local Similarity 100.0%; Pred.No. 0.00079;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YMTNFAKGGDPN 537
 |||||
 Db 487 YMTNFAKGGDPN 498

RESULT 14

EST1_CUL2;
 ID EST1_CUL2; STANDARD; PRT; 540 AA.
 AC P16954;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Esterase B1 precursor (EC 3.1.1.1).
 GN CUL2
 OS Culex pipiens (House mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culex.
 OX NCBI_TaxID=7175;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TM-R;
 RX MEDLINE=90207238; PubMed=2320576;
 RA Moulos C., Fauglin Y., Agarwal M., Lemieux E., Herzog M.,
 RA Abadon M., Bessac-Arnaouty V., Hyten O., de Saint Vincent B.R.,
 RA Georgiou G.P., Pasteur N.;
 RT "Characterization of amplification core and esterase B1 gene
 RT responsible for insecticide resistance in Culex";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:2574-2578 (1990).
 CC -1- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON
 CC MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.
 CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
 CC -1- MISCELLANEOUS: THERE ARE TWO SUCH ESTERASES: A AND B. ALLELES OF
 CC -1- CATALYTIC ACTIVITY. BOTH A AND B ARE KNOWN.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 CC -----
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DR EMBL: M32328; AAA28189.1; -
 DR PIR: A35986; A35986.
 DR HSSD: P21836; IMAA.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR003379; Ser_ester_site.
 DR Pfam: PF00135; Coesterase; 1; -
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1;
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; FALSE NEG.
 KW Hydroxylase; Serine esterase; Glycoprotein; Multigene family; Signal.
 KW Signal
 FT CHAIN ? 540
 FT ACT_SITE 191 191
 FT ACT_SITE 442 442
 FT DISULFID 68 81
 FT CARBOHYD 452 452

N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 540 AA; 60806 MW; F73B25B3A757C95 CRC64;

Query Match 1.2%; Score 10; DB 1; Length 540;
 Best Local Similarity 100.0%; Pred.No. 0.071;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 AFGGPRKRV 250
 |||||
 DB 177 AFGGPRKRV 186

RESULT 15

EST2_RABIT
 ID EST2_RABIT; STANDARD; PRT; 532 AA.
 AC P14943;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Liver carboxylesterase 2 (EC 3.1.1.1).
 OS Oryctolagus cuniculus (Rabbit).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN (1)
RP SEQUENCE.
RX MEDLINE=8930866; PubMed=2745458;
RA Ozois J.;
RT "Isolation, properties, and the complete amino acid sequence of a
RT second form of 60-kDa glycoprotein esterase. Characterization of the
RT 60-kDa protein in the microsomal membrane."
RL J. Biol. Chem. 264:12533-12545(1989).
CC -1- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN
CC THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.
CC CATALYTIC ACTIVITY: A carboxylic ester + H₂O = an alcohol + a
CC carboxylic anion.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Mitochondrial membrane, lumen of endoplasmic
CC reticulum.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR PIR: A33329; A33329.
DR HSP: P37967; 1053.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000379; Ser_ests_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_2; 1.
KM Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
KM Pyroglutamate carboxylic acid. PYROGLUTAMATE CARBOXYLIC ACID.
FT ACT_SITE 201 201
FT ACT_SITE 430 430 BY SIMILARITY.
FT DISULFID 69 96 BY SIMILARITY.
FT DISULFID 254 264 BY SIMILARITY.
FT SITE 529 532 PREVENT SECRETION FROM ER (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC...).
SQ SEQUENCE 532 AA; 59058 MW; C57DD076A13A932 CRC64;

Query Match 1.1%; Score 9; DB 1; Length 532;
Best Local Similarity 100.0%; Pred. No. 0.76;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 125 EDCVLYNLY 133
DB 94 EDCVLYNLY 102

RESULT 16
EST1_RABIT STANDARD; PRT: 539 AA.
ID EST1_RABIT
AC P:2337;
DT 01-OCT-1999 (Rel. 12, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Liver carboxylesterase 2 (EC 3.1.1.1).
DE Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN (1)
RP SEQUENCE.
RX MEDLINE=8919431; PubMed=3343253;
RA Korza G., Ozois J.;
RT "Complete covalent structure of 60-kDa esterase isolated from
RT 2,3,7,8-tetrachlorodibenzo-p-dioxin-induced rabbit liver
RT microsomes."
RT J. Biol. Chem. 263:3486-3493(1988).
RN (2)
RP SEQUENCE OF 1-70 AND 532-539.
RX MEDLINE=88033124; PubMed=3567634;
RA Ozois J.;
RT "Isolation and characterization of a 60-kilodalton glycoprotein
RT esterase from liver microsomal membranes.";

EU J. Biol. Chem. 262:15316-15321(1987).
CC -1- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN
CC THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.
CC CATALYTIC ACTIVITY: A carboxylic ester + H₂O = an alcohol + a
CC carboxylic anion.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Mitochondrial membrane, lumen of endoplasmic
CC reticulum.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR PIR: A29923; A29923.
DR HSP: P21836; 1M4H.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000379; Ser_ests_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_2; 1.
KM Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum.
FT ACT_SITE 195 195 BY SIMILARITY.
FT ACT_SITE 441 441 BY SIMILARITY.
FT DISULFID 69 98 BY SIMILARITY.
FT DISULFID 247 258 BY SIMILARITY.
FT SITE 536 539 PREVENT SECRETION FROM ER (POTENTIAL).
FT CARBOHYD 61 61 N-LINKED (GLCNAC...).
FT CARBOHYD 363 363 N-LINKED (GLCNAC...).
SQ SEQUENCE 539 AA; 59539 MW; 98C72BC36A49B0BD CRC64;

Query Match 1.1%; Score 9; DB 1; Length 539;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 125 EDCVLYNLY 133
DB 96 EDCVLYNLY 104

RESULT 17
EST1_RAT STANDARD; PRT: 549 AA.
ID EST1_RAT
AC P10953; Q63106; Q64626;
DT 01-JUL-1999 (Rel. 11, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Liver carboxylesterase 1 precursor (EC 3.1.1.1) (Carboxylesterase ES-1)
DE (EU) (ES-THET)
DE Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A., AND SEQUENCE OF 19-48.
RP STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=89174514; PubMed=3235453;
RA Takagi Y., Kotohashi K., Kawabata S., Go M., Omura T.;
RT "Molecular cloning and nucleotide sequence of cDNA of microsomal
RT carboxylesterase B1 of rat liver."
RL J. Biochem. 104:801-806(1988).
RN (2)
RP SEQUENCE OF 10-549 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=8930119; PubMed=2973335;
RA Long R.M., Satch H., Martin B.M., Kimura S., Gonzalez F.J., Pohl L.R.;
RT "Rat liver carboxylesterase: cDNA cloning, sequencing, and evidence
RT for a multigene family."
RL Biochem. Biophys. Res. Commun. 156:866-873(1988).
RN (3)
RP SEQUENCE OF 13-549 FROM N.A.
RP STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=94274701; PubMed=8006016;
RA Alexson S.E.H., Finlay T.H., Helman U., Svensson L.T., Niczajus R.,
RA Eggertsen G.;
RT "Molecular cloning and identification of a rat serum carboxylesterase
RT expressed in the liver."
RL J. Biol. Chem. 269:17118-17124(1994).
CC -1- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN


```

CC THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -1- SUBCELLULAR LOCATION: Mitochondrial membrane, lumen of endoplasmic
CC reticulum.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
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CC -----
DR EMBL: M20623; AAA43871.1; -
DR EMBL: D36623; BAA6310.1; -
DR EMBL: D00362; BAA20565.1; -
DR EMBL: X78489; CAA5241.1; -
DR PIR: A31584; A31584.
DR HSSP: P21836; 1MAH.
DR InterPro: IPRO02018; Carboxylesterase.
DR Pfam: PF00315; Coesterase; 1; -
DR PROSITE: P500122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: P500941; CARBOXYLESTERASE_B_2; 1.
KW Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
KW Signal; Multigene family.
KM SIGNAL: 1
FT CHAIN: 19 549
FT ACT_SITE: 221 221
FT ACT_SITE: 453 453
FT DISULFID: 87 116
FT DISULFID: 273 284
FT SITE: 546 549
FT CARBOHYD: 79 79
FT CARBOHYD: 274 274
FT CARBOHYD: 275 275
FT CARBOHYD: 302 302
FT CARBOHYD: 375 375
FT CARBOHYD: 476 476
FT VARIANT: 372 372
FT CONFLICT: 48 48
FT CONFLICT: 174 175
FT CONFLICT: 250 250
FT CONFLICT: 399 399
FT CONFLICT: 504 504
FT CONFLICT: 512 513
SQ SEQUENCE: 549 AA; 60174 MW; 19D6A586DA50E662 CRC64;

Query Match: 1.1%; Score 9; DB 1; Length 549;
Best Local Similarity: 100.0%; Pred No. 0.78;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYNITY 133
DB 114 EDCLYNITY 122

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=9169540; PubMed=1840565;
RA Owen M., Tapperman K., Medda S., Elliott R.W., Stephenson D.A.,
RA Grant S.G., Garschow R.E.;
RT "Characterization of a murine cDNA encoding a member of the
RT carboxylesterase multigene family.";
RL Genomics 9:344-354(1991).
CC -1- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN
CC THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -1- SUBCELLULAR LOCATION: Mitochondrial membrane, lumen of endoplasmic
CC reticulum.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
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CC -----
DR EMBL: M57960; AAA63297.1; -
DR PIR: A39060; A39060.
DR HSSP: P37967; 1OZ3.
DR MGJ: MGI:95420; E51.
DR InterPro: IPRO02018; Carboxylesterase.
DR Pfam: PF00315; Coesterase; 1; -
DR PROSITE: P500122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: P500941; CARBOXYLESTERASE_B_2; 1.
KW Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
KW Signal; Multigene family.
KM SIGNAL: 1
FT CHAIN: 19 554
FT ACT_SITE: 221 221
FT ACT_SITE: 453 453
FT DISULFID: 87 116
FT DISULFID: 273 284
FT SITE: 551 554
FT CARBOHYD: 79 79
FT CARBOHYD: 274 274
FT CARBOHYD: 304 304
FT CARBOHYD: 377 377
FT CARBOHYD: 478 478
SQ SEQUENCE: 554 AA; 61140 MW; 8A8260553DC8F69 CRC64;

Query Match: 1.1%; Score 9; DB 1; Length 554;
Best Local Similarity: 100.0%; Pred No. 0.79;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYNITY 133
DB 114 EDCLYNITY 122

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RESULT 18
ESTN_MOUSE STANDARD; PRT; 554 AA.
AC P23953;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Liver carboxylesterase precursor (EC 3.1.1.1) (PES-N).
GN E51.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]

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RESULT 19
EST2 CAEEL STANDARD; PRT; 556 AA.
AC O07085; O16351;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Esterase OMO631 (EC 3.1.1.1).
GN F31H6.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodidae; Pelodidae; Pelodidae; Pelodidae; Pelodidae;
CX NCBI_TaxID=6239;
RN [1]

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BX MEDLINE=94033620; Pubmed=8219273;
RA Fecor X., Cousin X., Toulant J.-P., Thierry-Mieg D., Arpagaus N.;
RT "cDNA sequence, gene structure, and cholinesterase-like domains of an
AT esterase from Caenorhabditis elegans mapped to chromosome V";
RL DNA Seq. 3:347-356(1993).
RN [2]
R2 SEQUENCE FROM N.A.
R3 STRAIN=Bristol NZ;
R4 Jones K., Wohlmann P.;
RL Submitted (Aug-1997) to the EMBL/GenBank/DBS databases.
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -1- SUBCELLULAR LOCATION: CYTOSOLASMIC. ATTACHED TO THE INNER SIDE OF
CC THE MEMBRANE BY A LIPID ANCHOR.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EXBL: X66104; CAA46599.1; ..
CC EXBL: AFO:6437; AAB65887.1; ..
CC PIR: A56690; A56690.
CC PIR: T31783; T31783.
CC HSSP: P37967; 10E3.
CC WormPep: P13463; CE09375.
CC InterPro: IPR002018; Carboxylesterase.
CC InterPro: IPR00379; Ser_estrs_site.
CC Pfam: PF00135; Coesterase; 1.
CC PROSITE: PS00122; CARBOXYLESTERASE_3_1; 1.
CC PROSITE: PS00941; CARBOXYLESTERASE_3_2; FALSE NEG.
CC HydroLase: Serine esterase; Myristate; Membrane.
CC INT MET 0 POTENTIAL.
CC LIPID 1 MYRISTATE (POTENTIAL).
CC ACT_SITE 207 207 BY SIMILARITY.
CC ACT_SITE 330 330 BY SIMILARITY.
CC ACT_SITE 445 445 BY SIMILARITY.
CC DISULFID 75 97 BY SIMILARITY.
CC CONFLICT 542 556 NMSERRSRQRFNF -> ELYGKKKSAK (IN REF.
CC FT 2).
CC SQ SEQUENCE 556 AA; 62391 MW; 463E5B2428DB99B CRC64;

Query Match 1.1%; Score 9; DB 1; Length 556;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 PMVYIHGG 176
DB 117 PMVYIHGG 125

RESULT 20
EST1_MESAU STANDARD; PRT: 561 AA.
ID EST1_MESAU STANDARD; PRT: 561 AA.
AC 064419;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Liver carboxylesterase precursor (EC 3.1.1.1).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetidae;
OC Mesocricetus.
CX NCBI_TaxID=10336;
RN [1]
R2 SEQUENCE FROM N.A.
R3 STRAIN=Syrian golden; TISSUE=Liver;
R4 MEDLINE=94318665; Pubmed=8043605;
R5 Sore T., Isobe M., Takabatake E., Wang C.Y.;

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RT "Cloning and sequence analysis of a hamster liver cDNA encoding a
RT novel putative carboxylesterase";
RL Biochim. Biophys. Acta 1207:118-142(1994).
CC -1- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN
CC THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -1- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
CC reticulum.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EXBL: D28566; BAA05913.1; ..
CC PIR: S47655; S47655.
CC HSSP: P37967; 1CR3.
CC InterPro: IPR002018; Carboxylesterase.
CC InterPro: IPR00379; Ser_estrs_site.
CC Pfam: PF00135; Coesterase; 1.
CC PROSITE: PS00122; CARBOXYLESTERASE_3_1; 1.
CC PROSITE: PS00941; CARBOXYLESTERASE_3_2; 1.
CC Glycoprotein; HydroLase; Serine esterase; Endoplasmic reticulum;
CC Signal; Multigene family.
CC SIGNAL 1 27 POTENTIAL.
CC CHAIN 28 561 LIVER CARBOXYLESTERASE.
CC ACT_SITE 227 427 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC ACT_SITE 459 459 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC DISULFID 95 122 BY SIMILARITY.
CC DISULFID 280 291 BY SIMILARITY.
CC SITE 558 561 PREVENT SECRETION FROM ER (POTENTIAL).
CC CARBOHYD 276 276 N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOHYD 362 362 N-LINKED (GLCNAC...) (POTENTIAL).
CC SQ SEQUENCE 561 AA; 62330 MW; 46B11E422475321 CRC64;

Query Match 1.1%; Score 9; DB 1; Length 561;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCYLYNY 133
DB 120 EDCYLYNY 128

RESULT 21
EST3_RAT STANDARD; PRT: 561 AA.
ID EST3_RAT STANDARD; PRT: 561 AA.
AC 063108;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Liver carboxylesterase 3 precursor (EC 3.1.1.1) (Carboxylesterase ES-3)
DE (B2.5.5 esterase) (BS-HLE).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
R2 SEQUENCE FROM N.A.
R3 STRAIN=Sprague-Dawley; TISSUE=Liver;
R4 MEDLINE=95032008; Pubmed=7945287;
R5 Robbi M., Beaufay H.;
R6 "Cloning and sequencing of rat liver carboxylesterase ES-3 (egagyn).";
R7 Biochem. Biophys. Res. Commun. 203:1404-1411(1994).
CC -1- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN
CC THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.

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CC -1- SUBCELLULAR LOCATION: Mitochondrial membrane, lumen of endoplasmic
CC reticulum.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
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DR EMBL: X81395; CA57158.1; -

DR PIR: J02447; J02447.

DR HSSP: P21836; 1MAA.

DR InterPro: IPR002018; CarboxesteraseB.

DR InterPro: IPR003079; Ser_estrs_site.

DR Pfam: PF00135; Coesterase; 1.

DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.

DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.

KW Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;

KM Signal; Multigene family.

FT SIGNAL 1 18 BY SIMILARITY.

FT CHAIN 19 561 LIVER CARBOXYLESTERASE 3.

FT ACT_SITE 221 221 BY SIMILARITY.

FT ACT_SITE 466 466 BY SIMILARITY.

FT DISULFID 87 146 BY SIMILARITY.

FT DISULFID 273 284 BY SIMILARITY.

FT SITE 558 561 PREVENT SECRETION FROM ER (POTENTIAL).

FT CARBOHYD 79 79 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 107 107 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 489 489 N-LINKED (GLCNAC...) (POTENTIAL).

SQ SEQUENCE 561 AA; 61114 MW; 1E14D6EDF089B86F CRC64;

Query Match 1.1%; Score 9; DB 1; Length 561;

Best local Similarity 100.0%; Pred. No. 0.8;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCYLINLY 133

Db 114 EDCYLINLY 122

RESULT 22

EST4_RAT STANDARD; PRT; 561 AA.

AC Q64573; Q62679; (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Liver carboxylesterase 4 precursor (BC 3.1.1.1) (Carboxylesterase ES-4)

DE (Microsomal palmitoyl-CoA hydrolase) (Kidney microsomal

DE carboxylesterase).

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Liver;

RC MEDLINE=96190723; PubMed=8611161;

RA Robbi M., van Schaftingen E., Beaufay H.

RT "Cloning and sequencing of rat liver carboxylesterase ES-4

RT (microsomal palmitoyl-CoA hydrolase)."

RL Biochem. J. 313:821-826 (1996).

RN [2]

SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Kidney;

RC MEDLINE=95050819; PubMed=7961959;

RA Yan B., Yang D., Brady M., Parkinson A.

RT "Rat kidney carboxylesterase. Cloning, sequencing, cellular

RT localization, and relationship to rat liver hydrolase."

RL J. Biol. Chem. 269:29698-29696 (1994).

```
CC -1- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN THE
CC ACTIVATION OF ESTER AND AMIDE PRODRUGS. HYDROLYZES OMECRON-
CC NITROGENYLYL ACETATE AND ALPHA-NAPHTHYL ACETATE. IT ALSO
CC HYDROLYZES ACETANILIDE AND, DISTINGUISHIVELY, PALMITOYL-CoA.
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -1- SUBCELLULAR LOCATION: Mitochondrial membrane, lumen of endoplasmic
CC reticulum.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
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DR EMBL: X81825; CA57419.1; -

DR EMBL: U10697; AAA64638.1; -

DR PIR: S62788; S62788.

DR HSSP: P21836; 1MAA.

DR InterPro: IPR002018; CarboxesteraseB.

DR InterPro: IPR000866; ER_target.

DR InterPro: IPR003079; Ser_estrs_site.

DR Pfam: PF00135; Coesterase; 1.

DR PROSITE: PS00014; ER_TARGET; 1.

DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.

DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.

KW Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;

KM Signal; Multigene family.

FT SIGNAL 1 18 BY SIMILARITY.

FT CHAIN 19 561 LIVER CARBOXYLESTERASE 4.

FT ACT_SITE 221 221 BY SIMILARITY.

FT ACT_SITE 466 466 BY SIMILARITY.

FT DISULFID 87 116 BY SIMILARITY.

FT DISULFID 273 284 BY SIMILARITY.

FT SITE 558 561 PREVENT SECRETION FROM ER (POTENTIAL).

FT CARBOHYD 79 79 N-LINKED (GLCNAC...) (POTENTIAL).

FT CONFLICT 7 7 I -> F (IN REF. 2).

FT CONFLICT 60 60 L -> P (IN REF. 2).

FT CONFLICT 213 213 G -> A (IN REF. 2).

FT CONFLICT 253 253 P -> T (IN REF. 2).

FT CONFLICT 310 311 DN -> IT (IN REF. 2).

FT CONFLICT 342 342 T -> N (IN REF. 2).

FT CONFLICT 425 426 SI -> FY (IN REF. 2).

FT CONFLICT 426 426 G -> A (IN REF. 2).

FT CONFLICT 509 509 C -> E (IN REF. 2).

FT CONFLICT 553 553

SQ SEQUENCE 561 AA; 62274 MW; EDF48F3309521C79 CRC64;

Query Match 1.1%; Score 9; DB 1; Length 561;

Best local Similarity 100.0%; Pred. No. 0.8;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCYLINLY 133

Db 114 EDCYLINLY 122

RESULT 23

EST5_RAT STANDARD; PRT; 561 AA.

AC O63010; (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Liver carboxylesterase B-1 precursor (BC 3.1.1.1) (Liver microsomal

DE carboxylesterase).

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;

RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; Tissue=Liver;
RX MEDLINE=35350819; Pubmed=7961958;
RA Yang B., Yang D., Brady M., Parkinson A.;
RT "Rat kidney carboxylesterase. Cloning, sequencing, cellular
localization, and relationship to rat liver hydroxylase."
R. Biol. Chem. 269:29688-29696(1994)
CC -1- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN THE
ACTIVATION OF ESTER AND AMIDE PRODRUGS.
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
carboxylic anion.
CC -1- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
reticulum.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
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CC EMBL: J13698; AAA64633.1; -
CC HSSP: P21836; IMAH.
DR InterPro: IPR002318; Carboxylesterase.
DR InterPro: IPR003886; ER_target.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1. _site.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
KW signal; Multigene family.
FT CHAIN 19 561 BY SIMILARITY.
FT ACT_SITE 221 221 LIVER CARBOXYLESTERASE_B_1.
FT ACT_SITE 466 466 BY SIMILARITY.
FT DISULFID 87 116 BY SIMILARITY.
FT DISULFID 273 284 BY SIMILARITY.
FT SITE 558 561 PREVENT SECRETION FROM ER (POTENTIAL).
FT CARBOHYD 79 79 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 562 AA: 62494 MW: 61301336CB6C9 CAC64;

Query Match 1.1%; Score 9; DB 1; Length 561;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNTY 133
DB 114 EDCLYLNTY 122

RESULT 24
ES22 MOUSE STANDARD: PRT; 562 AA.
AC 064176;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Liver carboxylesterase 22 precursor (EC 3.1.1.1) (Eggsen; Esterase-
DE 22) (Es-22).
CN ES22.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10290;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE=9247141; Pubmed=1783403;
RA Ovnio M., Swank R.T., Fletcher C., Zhen L., Newak E.K., Baumann H.,
RA Heintz N., Ganschow R.E.;
RT "Characterization and functional expression of a cDNA encoding eggsen

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RT (esterase-22): the endoplasmic reticulum-targeting protein of beta-
guanylidase."
RL Genbank: U1956-967(1992).
CC -1- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN
THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
carboxylic anion.
CC -1- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
reticulum.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@sib-sib.ch).
CC EMBL: S80291; AA321335.1; -
CC PIR: A55281; A55281.
CC HSSP: P21836; IMAH.
CC MGD: MGI:95432; Es22.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1. _site.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
KW signal; Multigene family.
FT CHAIN 19 562 BY SIMILARITY.
FT ACT_SITE 220 222 LIVER CARBOXYLESTERASE 22.
FT ACT_SITE 467 467 BY SIMILARITY.
FT DISULFID 88 117 BY SIMILARITY.
FT DISULFID 274 285 BY SIMILARITY.
FT SITE 559 562 PREVENT SECRETION FROM ER (POTENTIAL).
FT CARBOHYD 80 80 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 490 490 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 562 AA: 61581 MW: F81A4367A0CC32E3 C8C64;

Query Match 1.1%; Score 9; DB 1; Length 562;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNTY 133
DB 115 EDCLYLNTY 123

RESULT 25
EST1 CAEBR STANDARD: PRT; 562 AA.
AC 004456;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gut esterase 1 precursor (EC 3.1.1.1) (Non-specific carboxylesterase).
DE GRS-1.
OS Caenorhabditis briggsae.
CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
CC Rhabditidae; Pelodermidae; Caenorhabditis.
CC NCBI_TaxID=6238;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93188021; Pubmed=8445654;
RA Kennedy B.P., Amodei E.O., Allen F.L., Chung M.A., Heschl M.F.P.,
RA McChes C.D.;
RT "The gut esterase gene (ges-1) from the nematode Caenorhabditis
elegans and Caenorhabditis briggsae."
R. Mol. Biol. 229:890-908(1993).
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a

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CC CARBOXYLIC ANION.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY IN THE INTACTIVE.
CC -1- DEVELOPMENTAL STAGE: APPEARS IN MID-PROLIFERATION PHASE WHEN
CC THE DEVELOPING GUT HAS FOUR TO EIGHT CELLS.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: M96144; AAA28056.1; -.
DR PIR: S27782; S27782.
DR HSP: P37967; 1Q63.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000886; ER target.
DR Pfam: PF00135; Coesterase; 1. _site.
DR PROSITE: PS00144; ER_TARGET; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
DR Hydroxylase; Serine esterase; Signal; Endoplasmic reticulum.
KW SIGNAL
FT CHAIN 1 16
FT ACT_SITE 17 566 GUT ESTERASE 1.
FT ACT_SITE 199 592 BY SIMILARITY.
FT ACT_SITE 451 451 BY SIMILARITY.
FT DISULFID 75 93 BY SIMILARITY.
FT DISULFID 251 259 BY SIMILARITY.
FT SITE 559 562 PREVENT SECRETION FROM ER.
SQ SEQUENCE 562 AA; 63819 MW; 7FA12F32587E53 CRC64;

Query Match 1.1%; Score 9; DB 1; Length 562;
Best Local Similarity 100.0%; Pred.No. 0.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 PYNVTVYXK 35
Db 19 PYNVTVYXK 26

RESULT 26
EST_HUMAN STANDARD; PRT; 566 AA.
AC Q29550;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Liver carboxylesterase precursor (EC 3.1.1.1) (Proline-beta-
DE naphthylamidase).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
CX NCBI_TaxID=96823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=92070571; PubMed=959668;
RA Matsushima M., Iroue H., Ichinohe M., Tsukada S., Miki K.,
RA Kurokawa K., Takahashi T., Takahashi K.;
RT "The nucleotide and deduced amino acid sequences of porcine liver
RT proline-beta-naphthylamidase. Evidence for the identity with
RT carboxylesterase."
RL FEBS Lett. 293:37-41 (1991).
CC -1- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN THE
CC ACTIVATION OF ESTER AND AMIDE PRODRUGS.
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.

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CC
DR EMBL: X63323; CAA4929.1; -.
DR PIR: S19307; S19307.
DR HSP: P21836; 1MAH.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000379; Ser esters _site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
DR Glycoprotein; Hydroxylase; Serine esterase; Endoplasmic reticulum;
KW Signal; Multigene family.
KW SIGNAL
FT CHAIN 1 18
FT ACT_SITE 19 566 LIVER CARBOXYLESTERASE.
FT ACT_SITE 222 222 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 467 467 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 88 117 BY SIMILARITY.
FT DISULFID 274 285 BY SIMILARITY.
FT SITE 563 566 PREVENT SECRETION FROM ER (POTENTIAL).
FT CARBOHYD 80 80 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 566 AA; 62016 MW; BE046545307DEDE5 CRC64;

Query Match 1.1%; Score 9; DB 1; Length 566;
Best Local Similarity 100.0%; Pred.No. 0.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLVNY 133
Db 115 EDCLYLVNY 123

RESULT 27
EST_HUMAN STANDARD; PRT; 567 AA.
AC P3141; G00015; Q3657; Q1462; Q6747; Q16788; Q07LX2;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Liver carboxylesterase precursor (EC 3.1.1.1) (Acyl coenzyme
DE A:cholesterol acyltransferase) (ACAT) (Monocyte/macrophage serine
DE esterase) (HME) (Serine esterase 1) (Brain carboxylesterase hBp1).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92011649; PubMed=1918003;
RA Wanger J.S., Shi G.P., Marx E.A., Chin D.T., Gerard C.,
RA Chapman H.A.;
RT "A serine esterase released by human alveolar macrophages is closely
RT related to liver microsomal carboxylesterases."
RL J. Biol. Chem. 266:18832-18838 (1991).
CC -1- FUNCTION:
CC -1- CATALYTIC ACTIVITY:
CC -1- SUBCELLULAR LOCATION:
CC -1- SIMILARITY:

```

RX MEDLINE=94310913; PubMed=8456473;
 RA Shibata F., Takagi Y., Kitajima M., Kuroda T., Gura T.;
 RT "Molecular cloning and characterization of a human carboxylesterase
 gene";
 RJ Genomics 17:76-82(1993).
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA MEDLINE=94325258; PubMed=8049197;
 RX Becker A., Botcher A., Jackner K.D., Fehring P., Nocka F.,
 RA Aslamidze C., Schmitz G.;
 RT "Purification, cloning, and expression of a human enzyme with acyl
 coenzyme A: cholesterol acyltransferase activity, which is identical
 to liver carboxylesterase";
 RL Arterioscler. Thromb. 14:1346-1355(1994).
 RN
 RP SEQUENCE OF 1-429 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99448370; PubMed=10548925;
 RA Mori M., Hosokawa M., Ogasawara Y., Tsukada E., Chiba K.;
 RT "CDNA cloning, characterization and stable expression of novel human
 brain carboxylesterase";
 RL FEBS Lett. 458:17-22(1999).
 RN
 RP SEQUENCE OF 61-567 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=91148424; PubMed=1997784;
 RA Long R.M., Calabrese M.R., Martin B.M., Pohl L.R.;
 RT "Cloning and sequencing of a human liver carboxylesterase isoenzyme";
 RL Life Sci. 48:PL43-PL49(1991).
 RN
 RP SEQUENCE OF 64-567 FROM N.A. AND PARTIAL SEQUENCE.
 RX MEDLINE=91300111; PubMed=2070086;
 RA Zechunke F., Salmassi A., Kreipe H., Buck F., Farwarsch M.R.,
 RA Radzun H.J.;
 RT "CDNA cloning and characterization of human monocyte/macrophage
 serine esterase-1";
 RL Blood 78:506-512(1991).
 RN
 RP SEQUENCE OF 114-567 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=92084150; PubMed=1740313;
 RA Riddels P.W., Richards L.J., Bowles M.R., Ford S.M.;
 RT "Cloning and analysis of a cDNA encoding a human liver
 carboxylesterase";
 RL Gene 163:289-292(1991).
 RN
 RP SEQUENCE OF 1-567 FROM N.A.
 CC -1- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN THE
 ACTIVATION OF ESTER AND AMIDE PRODRUGS. IS ABLE TO HYDROLYZE
 AROMATIC AND ALIPHATIC ESTERS BUT POSSESSED NO CATALYTIC ACTIVITY
 TOWARD AMIDES OR A FATTY ACYL COA ESTER.
 CC -1- CATALYTIC ACTIVITY: A carboxylester + H(2)O = an alcohol + a
 carboxylic anion.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 CC
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 CC
 DR EMBL: M73499; AAA35649.1; -;
 DR EMBL: U67764; AAA16036.1; -;
 DR EMBL: U67765; AAA35711.1; -;
 DR EMBL: D21088; BAA04650.1; -;
 DR EMBL: D21076; BAA04650.1; JOINED.
 DR EMBL: D21073; BAA04650.1; JOINED.
 DR EMBL: D21077; BAA04650.1; JOINED.
 DR EMBL: D21079; BAA04650.1; JOINED.
 DR EMBL: D21080; BAA04650.1; JOINED.
 DR EMBL: D21091; BAA04650.1; JOINED.

DR EMBL: D21092; BAA04650.1; JOINED.
 DR EMBL: D21083; BAA04650.1; JOINED.
 DR EMBL: D21084; BAA04650.1; JOINED.
 DR EMBL: D21085; BAA04650.1; JOINED.
 DR EMBL: D21086; BAA04650.1; JOINED.
 DR EMBL: D21087; BAA04650.1; JOINED.
 DR EMBL: ABC25026; BAA84995.1; -;
 DR EMBL: S73751; AAC60631.2; -;
 DR EMBL: M55509; AAA35650.1; -;
 DR EMBL: X52973; CAA37147.1; -;
 DR EMBL: M65261; AAA83932.1; -;
 DR PIR: A4010; A4010.
 DR HSSP: P21836; 10AH.
 DR Genew: HSC1863; CEST1.
 DR XIM: 114835; -;
 DR GC: G01004759; F:serine esterase activity; TAS.
 DR GC: G01008152; P:metabolism; TAS.
 DR GC: G01009636; P:response to toxin; TAS.
 DR InterPro: IPR002015; CarboxylesteraseB.
 DR InterPro: IPR000379; Ser_ester_site.
 DR Pfam: PF02135; Coesterase_1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 D3 GlycoProfile: Hydrolase; Serine esterase; Endoplasmic reticulum;
 KW Signal; Multigene family; Polymorphism.
 KN
 FT SIGNAL 1 18
 FT CHAIN 19 567
 FT ACT SITE 221 221
 FT ACT SITE 468 468
 FT DISULFID 87 116
 FT DISULFID 274 285
 FT SITE 564 567
 FT CARBOHYD 79 79
 FT VARIANT 18 18
 FT
 FT VARIANT 75 75
 FT
 FT VARIANT 199 199
 FT
 FT VARIANT 203 203
 FT
 FT VARIANT 362 362
 FT
 FT CONFLICT 4 7
 FT CONFLICT 12 12
 FT CONFLICT 17 17
 FT CONFLICT 56 56
 FT CONFLICT 64 64
 FT CONFLICT 115 115
 FT CONFLICT 186 186
 FT CONFLICT 281 281
 FT CONFLICT 301 317
 FT
 FT CONFLICT 337 337
 FT CONFLICT 383 390
 FT CONFLICT 417 417
 FT CONFLICT 512 512
 FT CONFLICT 536 536
 FT CONFLICT 563 563
 SQ SEQUENCE 567 AA; 62521 MW; DIA03DDCC755DFP CRC64;
 Query Match 1.1; Score 9; DB 1; Length 567;
 Best Local Similarity 100.0%; Pred. No. 0.81;
 Matches 9; Conservative C; Mismatches C; Indels C; Gaps 0;
 CQ 125 EDCGLYLVNY 133
 DB 114 EDCGLYLVNY 122
 RESULT 28
 BAL_BOVIN STANDARD; PRT; 597 AA.

FT TURN 447 448
 FT STRAND 452 452
 FT TURN 453 456
 FT HELIX 457 460
 FT TURN 461 462
 FT HELIX 463 466
 FT HELIX 468 470
 FT HELIX 473 492
 FT TURN 495 496
 FT TURN 511 513
 FT STRAND 515 519
 FT TURN 525 526
 FT STRAND 526 530
 FT TURN 532 533
 FT HELIX 534 541
 FT TURN 542 542
 FT HELIX 543 546
 SQ SEQUENCE 597 AA; 65161 MW; 823E37AED9CEBFD1 CRC64;

Query Match 1.1%; Score 9; DB 1; Length 597;
 Best Local Similarity 100.0%; Pred. No. 0.84;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 124 NEDCLINT 132
 Db 95 NEDCLINT 103

RESULT 29
 ACBI_CABR STANDARD; PRT; 620 AA.

AC Q27455;
 DT 01-NOV-1997 (Rel. 35, Created);
 DT 01-NOV-1997 (Rel. 35, Last sequence update);
 DT 28-FEB-2003 (Rel. 41, Last annotation update);
 DE Acetylcholinesterase 1 precursor (EC 3.1.1.7) (ACH1).
 GN ACH-1.
 OS Caenorhabditis briggsae.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6238;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9706944; PubMed=8912924;
 RA Graessle M., Colebatch B., Borge J.B., Toutant J.-P., Arpagaus X.;
 RT "Sequence comparison of ACH-1, the gene encoding acetylcholinesterase
 of class A, in the two nematodes *Caenorhabditis elegans* and
Caenorhabditis briggsae."
 RT DNA Seq. 6:217-227(1996).
 RL
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H₂O = choline + acetate.
 CC -1- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS (8;
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY).
 CC -1- SUBCELLULAR LOCATION: MAY BE SECRETED OR MEMBRANE ASSOCIATED VIA
 CC -1- A NON-CATALYTIC SUBUNIT (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 CC
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 CC
 CC EMBL: U41846; AB41269.1;
 CC HSSP: P21836; WMA.
 DR InterPro: IPR002018; Carboxylesterase3.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR003379; Ser esters_site.
 DR Pfam: PF00135; Coesterase_1.
 DR PRINTS: PR00872; CHOLINESTERASE.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.

DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolyase; Serine esterase; Synapse; Membrane; Signal; Glycoprotein;
 KN Neurotransmitter degradation; Multigene family.
 FT SIGNAL 1
 FT CHAIN 32 620
 FT ACT_SITE 216 216
 FT ACT_SITE 346 346
 FT ACT_SITE 468 468
 FT DISULFID 82 109
 FT DISULFID 270 286
 FT DISULFID 430 558
 FT DISULFID 618 618
 FT CARBOHYD 74 74
 FT CARBOHYD 272 272
 FT CARBOHYD 486 486
 FT CARBOHYD 536 536
 SQ SEQUENCE 620 AA; 71501 MW; 69D73CD3996E11FC CRC64;

Query Match 1.1%; Score 9; DB 1; Length 620;
 Best Local Similarity 100.0%; Pred. No. 0.87;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 529 NFAKTGDPN 537
 Db 504 NFAKTGDPN 512

RESULT 30
 ACBI_CABR STANDARD; PRT; 620 AA.

AC P38433;
 DT 01-OCT-1994 (Rel. 30, Created);
 DT 01-OCT-1994 (Rel. 30, Last sequence update);
 DT 16-OCT-2001 (Rel. 40, Last annotation update);
 DE Acetylcholinesterase 1 precursor (EC 3.1.1.7) (ACH1).
 GN ACH-1 OR W09812.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=84193691; PubMed=8144590;
 RA Arpagaus X., Pedon Y., Cousin X., Chatomet A., Borge J.-B.,
 RT "CDNA sequence, gene structure, and in vitro expression of ace-1, the
 gene encoding acetylcholinesterase of class A in the nematode
Caenorhabditis elegans."
 RT J. Biol. Chem. 269:9957-9965(1994).
 RL [2]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wu X., Le T.T.;
 RT Submitted (MAY-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H₂O = choline + acetate.
 CC -1- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS (BY
 CC -1- SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: MAY BE SECRETED OR MEMBRANE ASSOCIATED VIA
 CC -1- A NON-CATALYTIC SUBUNIT.
 CC -1- DEVELOPMENTAL STAGE: DETECTED AT ALL STAGES. FOUND TO BE MORE
 CC ABUNDANT IN LARVAL STAGES THAN IN EMBRYOS OR ADULTS.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 CC
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CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
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CC
CC -----
CC EMBL: J08500; NOT ANNOTATED_CDS.
CC PIR: S32561; S32561..
CC HSSP: P43335; IMEM.
CC MEROPS: C01.077; -.
CC InterPro: IPR000668; Peptidase_C1.
CC InterPro: IPR000169; SHprot_acstite.
CC Pfam: PF00112; Peptidase_C1; 1.
CC PRINTS: PR00705; PAPAIR.
CC ProDom: PD000158; Peptidase_C1; 2.
CC SMART: SY00645; Pept_C1; 1.
CC PROSITE: PS00139; THIOL_PROTEASE_CYS; 1.
CC PROSITE: PS00639; THIOL_PROTEASE_HIS; 1.
CC PROSITE: PS00640; THIOL_PROTEASE_ASN; 1.
CC Hydrolase: Hydrolase; Glycoprotein; Signal.
CC SIGNAL
CC PROPEP
CC CHAIN
CC ACT_SITE
CC ACT_SITE
CC ACT_SITE
CC ACT_SITE
CC DISULFID
CC CARBOHYD
CC CARBOHYD
CC CARBOHYD
CC CARBOHYD
CC SEQUENCE
Query Match 506 AA: 58255 MW: 74784944618617F CR664;
Best Local Similarity 100.0%; Score 8; DB 1; Length 506;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 677 VTAVGAS 664
DB 391 VTAVGAS 398

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RL Biochem. J. 269:279-280(1990).
RN (3)
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=91287805; PubMed=2062369;
RA Schrag J.D., Li Y., Wu S., Cyster M.;
RT "Ser-His-Glu triad forms the catalytic site of the lipase from
RL Geotrichum candidum."
RL Nature 351:761-765(1991).
CC -1- FUNCTION: THE EXTRACELLULAR LIPASE PRODUCED BY G. CANDIDUM
CC HYDROLYSES ALL ESTER BONDS IN TRIGLYCERIDE AND DISPLAYS A HIGH
CC AFFINITY FOR TRIOLEIN.
CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -1- SUBUNIT: Monomer.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC PIR: PN0492; AGU0QC.
CC PDB: 1THG; 3I-OC7-93.
CC InterPro: IPR002018; Carboxesterase.
CC InterPro: IPR000379; Ser_ester_site.
CC Pfam: PF00135; Coesterase; 1.
CC PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
CC PROSITE: PS00911; CARBOXYLESTERASE_B_2; 1.
CC Hydrolase: Lipid degradation; Glycoprotein; Signal; 3D-structure;
CC Pyroglutamate carboxylic acid.
CC SIGNAL
CC CHAIN
CC MOD_RES
CC ACT_SITE
CC ACT_SITE
CC ACT_SITE
CC DISULFID
CC DISULFID
CC CARBOHYD
CC CARBOHYD
CC SEQUENCE
FT STRAND 27 29
FT STRAND 30 33
FT STRAND 35 37
FT TURN 38 39
FT STRAND 40 47
FT STRAND 54 56
FT TURN 57 58
FT TURN 59 69
FT STRAND 71 72
FT STRAND 74 74
FT STRAND 79 79
FT HELIX 85 96
FT HELIX 98 101
FT HELIX 104 113
FT TURN 114 114
FT STRAND 120 120
FT STRAND 126 132
FT TURN 133 134
FT TURN 137 138
FT STRAND 141 147
FT TURN 151 152
FT HELIX 156 159
FT HELIX 163 171
FT TURN 172 173
FT STRAND 177 181
FT HELIX 186 190
FT HELIX 194 199
FT TURN 200 200
FT TURN 202 203
FT HELIX 204 219
FT HELIX 220 223
FT TURN 224 224
FT STRAND 225 235
FT TURN 236 236
FT HELIX 237 247
FT HELIX 248 250
FT TURN 251 251
FT STRAND 254 255

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FT TURN 256 257
FT STRAND 258 259
FT STRAND 263 267
FT HELIX 285 293
FT TURN 294 294
FT TURN 297 298
FT HELIX 301 310
FT HELIX 313 327
FT TURN 329 331
FT HELIX 334 336
FT TURN 337 337
FT HELIX 351 356
FT TURN 357 358
FT STRAND 365 370
FT TURN 371 371
FT STRAND 372 372
FT TURN 373 377
FT HELIX 378 381
FT TURN 383 383
FT HELIX 387 397
FT TURN 398 400
FT HELIX 403 412
FT HELIX 417 419
FT TURN 423 424
FT TURN 426 429
FT HELIX 435 445
FT TURN 447 447
FT HELIX 458 457
FT TURN 459 460
FT STRAND 463 468
FT TURN 473 474
FT TURN 476 478
FT STRAND 481 481
FT TURN 482 485
FT HELIX 486 490
FT TURN 491 491
FT TURN 495 496
FT HELIX 497 510
FT TURN 513 514
FT TURN 527 529
FT STRAND 531 535
FT STRAND 540 544
FT TURN 547 548
FT HELIX 549 557
FT HELIX 559 561
SQ SEQUENCE 563 AA: 61230 MW: 38132767ACB7BAAD CRC64:

```

Query Match 1.0%; Score 8; DB 1; Length 563;
 Best Local Similarity 100.0%; Pred. No. 8.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 124 NEDCLYN 131
 DB 121 NEDCLYN 128

```

RESULT 34
LIP2 GEOCN STANDARD; PRT; 563 AA.
AC P22394;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Lipase 2 precursor (EC 3.1.1.3).
CN LIP2.
OS Geotrichum candidum (Oospora lactis).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Gaiactomyces.
OX NCBI_TaxID=27317;
RN 1;
RS SEQUENCE FROM N.A.
RX MEDLINE=93380907; PubMed=8170674;
RA Nagao T., Shimada Y., Sugihara A., Tomimaga Y.;

```

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RT "Cloning and sequencing of two chromosomal lipase genes from
RT Geotrichum candidum.";
RL J. Biochem. 113:776-780(1993).
(2)
RP SEQUENCE OF 7-563 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=90375435; PubMed=2358037;
RA Shimada Y., Sugihara A., Tizumi T., Tomimaga Y.;
RT "cDNA cloning and characterization of Geotrichum candidum lipase II.";
RL J. Biochem. 107:703-707(1990).
(3)
RP SEQUENCE OF 20-26 AND 561-563.
RX MEDLINE=98256718; PubMed=2341377;
RA Sugihara A., Shimada Y., Tomimaga Y.;
RT "Separation and characterization of two molecular forms of Geotrichum
RT candidum lipase.";
RL J. Biochem. 107:426-430(1990).
CC -!- FUNCTION: THE EXTRACELLULAR LIPASE PRODUCED BY G. CANDIDUM
CC HYDROLYZES A.L. ESTER BONDS IN TRIGLYCERIDE AND DISPLAYS A HIGH
CC AFFINITY FOR TRIOLEIN.
CC -!- CATALYTIC ACTIVITY: triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
-----
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CC or send an email to license@sib-sib.ch).
-----
CC EMBL: D00697; BAA0603.1; -.
CC PIR: P04953; P04953.
CC PDB: 1THG; 3I-OCT-93.
CC InterPro: IPR002018; Carboxylesterase.
CC InterPro: IPR003079; Ser_esterase.
CC Pfam: PF00135; Coesterase.1.
CC PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
CC PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
CC Hydrolyase; Lipid degradation; Glycoprotein; Signal;
CC Pyridolone carboxylic acid; 3D-structure.
CC SIGNAL 1 19
CC CHAIN 20 563 LIPASE 2.
CC WCD RES 20 20 PYROLIDONE CARBOXYLIC ACID.
CC ACT_SITE 236 236
CC ACT_SITE 373 373
CC ACT_SITE 482 482
CC DISULFID 80 124
CC DISULFID 235 307
CC CARBOHYD 302 352
CC CARBOHYD 383 383
SQ SEQUENCE 563 AA: 61617 MW: 1284134A258C52F CRC64:

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Query Match 1.0%; Score 8; DB 1; Length 563;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 124 NEDCLYN 131
DB 121 NEDCLYN 128

RESULT 35
ACES_BUNFA STANDARD; PRT; 581 AA.
AC Q92035; Q10720;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
OS Bungarus fasciatus (Banded Krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

CC Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubridae;
 CC Eupidae; Bungarinae; Bungarus.
 CC NCBI_Taxid=8613;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RX MEDLINE=9627907; PubMed=8662867;
 RA Cousin X., Bon S., Duval N., Massoulié J., Bon C.;
 RT "Cloning and expression of acetylcholinesterase from Bungarus
 RT fasciatus venom. A new type of COOH-terminal domain: involvement of a
 RT positively charged residue in the peripheral site.";
 RL J. Biol. Chem. 271:15399-15108(1996).
 RN [2]
 RP SEQUENCE OF 206-220; 253-272; 321-340; 347-372 AND 503-511.
 RC TISSUE=Venom;
 RX MEDLINE=96244524; PubMed=8674543;
 RA Cousin X., Cremonini C., Grassi J., Meliah K., Cerini G., Sallou B.,
 RA Bon S., Massoulié J., Bon C.;
 RL "Acetylcholinesterase from Bungarus venom: a monomeric species.";
 RL FEBS Lett. 387:196-200(1996).
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
 CC -1- CATALYTIC ACTIVITY: Acetylcholine - H₂O = choline + acetate.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: THE N-TERMINUS IS BLOCKED.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-9 IS THE INTACTOR.
 CC -----
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 CC -----
 DR EMBL: U54591; AAC59905.1; -
 DR HSRP: P04058; ISCX.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser_esterase_site.
 DR Pfam: PF00135; Coesterase_1.
 DR PRINTS: PR00878; CHOLINESTRASE.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_2; 1.
 KM Hydrolyse; Serine esterase; Synapse; Membrane; Signal; Glycoprotein;
 KM Neurotransmitter degradation.
 KW SIGNAL.
 FT 1 28
 FT CHAIN 23 573
 FT PROPEP 574 581
 FT ACT_SITE 231 231
 FT ACT_SITE 358 358
 FT ACT_SITE 471 471
 FT DISULFID 98 125
 FT DISULFID 295 296
 FT DISULFID 433 552
 FT CARBOHYD 289 374
 FT CARBOHYD 374 374
 FT CARBOHYD 484 484
 FT CARBOHYD 564 564
 FT MUTAGEN 101 101
 FT MUTAGEN 316 316
 FT CONFLICT 268 268
 FT CONFLICT 350 350
 FT SEQUENCE 581 AA; 64722 MW; 436C3CB8457E199F CRC64;
 Query Match 100%; Score 9; DB 1; Length 581;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CY 125 EDCLYINI 132

DB 123 EDCLYINI 130
 RESULT 36
 ACES TORCA STANDARD; PRT; 586 AA.
 ID ACES TORCA
 RC P04058;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 21-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).
 OS Torpedo californica (Pacific electric ray).
 CC Euryarchia; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 CC Elasmobranchii; Squalea; Hynostomales; Pristigaster; Batoidae;
 CC Torpediniformes; Torpedinidae; Torpedo.
 CC NCBI_Taxid=77877;
 RN [1]
 RP SEQUENCE OF 10-586 FROM N.A.
 RX MEDLINE=86118676; PubMed=3753747;
 RA Schumacher M., Camp S., Maulet Y., Newton M., McPhee-Quigley K.,
 RA Taylor S.S., Friedmann T., Taylor P.;
 RT "Primary structure of Torpedo californica acetylcholinesterase
 RT deduced from its cDNA sequence.";
 RL Nature 319:407-409(1986).
 RN [2]
 RP SEQUENCE OF 1-9 FROM N.A.
 RX MEDLINE=89066695; PubMed=31980636;
 RA Schumacher M.;
 RT "Multiple messenger RNA species give rise to the structural diversity
 RT in acetylcholinesterase.";
 RL J. Biol. Chem. 263:18979-18987(1988).
 RN [3]
 RP SEQUENCE OF 552-558.
 RX MEDLINE=88087239; PubMed=3335534;
 RA Glibney G., McPhee-Quigley K., Thompson B., Vedvick T., Low M.G.,
 RA Taylor S.S., Taylor P., Thompson B., Vedvick T., Low M.G.,
 RT "Divergence in primary structure between the molecular forms of
 RT acetylcholinesterase.";
 RL J. Biol. Chem. 263:11440-11445(1988).
 RN [4]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=90166618; PubMed=2306366;
 RA Maulet Y., Camp S., Glibney G., Rachinsky T.L., Ekstrom T.J.,
 RA Taylor P.;
 RT "Sinye gene encodes glycopospholipid-anchored and asymmetric
 RT acetylcholinesterase forms: alternative coding exons contain inverted
 RT repeat sequences.";
 RL Neuron 4:289-301(1990).
 RN [5]
 RP DISULFIDE BONDS.
 RX MEDLINE=87006586; PubMed=3759980;
 RA McPhee-Quigley K., Vedvick T.S., Taylor P., Taylor S.S.;
 RT "Profile of the disulfide bonds in acetylcholinesterase.";
 RL J. Biol. Chem. 261:13565-13570(1986).
 RN [6]
 RP STRUCTURE OF THE GPI-ANCHOR.
 RX MEDLINE=94079692; PubMed=8257440;
 RA Mehler A., Vazou L., Silman I., Homans S.W., Ferguson M.A.;
 RT "Structure of the glycosyl-phosphatidylinositol membrane anchor of
 RT acetylcholinesterase from the electric organ of the electric fish,
 RT Torpedo californica.";
 RL Biochem. J. 296:473-479(1993).
 RN [7]
 RP GPI-ANCHOR.
 RX MEDLINE=96176849; PubMed=8597567;
 RA Buche G., Halmarsson K.;
 RT "Residues in Torpedo californica acetylcholinesterase necessary for
 RT processing to a glycosyl phosphatidylinositol-anchored form.";
 RL Biochim. Biophys. Acta 1292:223-232(1996).
 RN [8]
 RP MUTAGENESIS.
 RX MEDLINE=91017542; PubMed=2227195;

RA Glibrey G., Camp S., Dicome N., Meshee-Quigley K., Taylor P.,
 RT "Mutagenesis of essential functional residues in
 RL acetylcholinesterase.";
 RN Proc. Natl. Acad. Sci. U.S.A. 87:7546-7550(1990).
 RA X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE=9143928; PubMed=1678899;
 RA Sussman J.L., Harel M., Frolow F., Oefner C., Goldman A., Toket J.,
 RL Silman I.,
 RT "Atomic structure of acetylcholinesterase from Torpedo californica: a
 RL prototypic acetylcholine-binding protein.";
 RN Science 253:872-879(1991).
 RA X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF COMPLEX WITH FASCICULIN.
 RX MEDLINE=96363673; PubMed=8747462;
 RA Harel M., Kleywegt G.J., Ravelli R.B., Silman I., Sussman J.L.,
 RT "Crystal structure of an acetylcholinesterase-fasciculin complex:
 RT interaction of a three-fingered toxin from snake venom with its
 RL target.";
 RN Structure 3:1355-1366(1995).
 RA X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=97143314; PubMed=8893257;
 RA Harel M.L., Harel M., Pang Y.P., Silman I., Kozikowski A.P.,
 RA Sussman J.L.,
 RT "Structure of acetylcholinesterase complexed with the neurotoxic
 RL alkaloid, (-)-bupirazine A.";
 RN Nat. Struct. Biol. 4:57-63(1997).
 RA X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=99249780; PubMed=10231521;
 RA Bartolucci C., Perola E., Celai L., Brufani M., Jamba D.,
 RT "Back door" opening implied by the crystal structure of a
 RL cardamylated acetylcholinesterase.";
 RN Biochemistry 38:5714-5719(1999).
 RA X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=9928267; PubMed=10358614;
 RA Willard C.B., Kryger G., Gredelich A., Greenblatt H.M., Harel M.,
 RA Raves M.L., Segal Y., Sarak D., Shafferman A., Silman I.,
 RA Sussman J.L.,
 RT "Crystal structures of aged phosphorylated acetylcholinesterase:
 RT nerve agent reaction products at the atomic level.";
 RN Biochemistry 39:7032-7039(1999).
 RA X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=20074924; PubMed=10606746;
 RA Greenblatt H.M., Kryger G., Lewis T., Silman I., Sussman J.L.,
 RT "Structure of acetylcholinesterase complexed with (-)-galanthamine at
 RL 2.3-A resolution.";
 RN FEBS Lett. 463:321-326(1999).
 RA X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=99197295; PubMed=10368293;
 RA Kryger G., Silman I., Sussman J.L.,
 RT "Structure of acetylcholinesterase complexed with E2020 (Arixcept®):
 RL implications for the design of new anti-alzheimer drugs.";
 RN Structure 7:297-307(1999).
 RA FUNCTION: RAPIDLY HYDROLYSES CHOLINE RELEASED INTO THE SYNAPSE.
 CC MAY BE INVOLVED IN CELL-CELL INTERACTIONS.
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H2O = choline + acetate.
 CC -1- SUBUNIT: THE H FORM IS AN HOMODIMER; THE ASYMMETRIC FORM IS A
 CC DISULFIDE-BONDED OLIGOMER COMPOSED OF A COLLAGENIC SUBUNIT (Q) AND
 CC A VARIABLE NUMBER OF T CATALYTIC SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: THE H FORM IS ATTACHED TO THE MEMBRANE BY A
 CC GPI-ANCHOR.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=H; Synonyms=Globular;
 CC . IsoId=P04058-1; Sequence=Displayed;
 CC Name=T;
 CC IsoId=P04058-2; Sequence=VSP_001460;

CC -1- TISSUE SPECIFICITY: AChE IS FOUND IN THE SYNAPSES AND TO A LOWER
 CC EXTENT IN EXTRASYNAPTIC AREAS OF MUSCLE AND NERVE, AND ON
 CC ERYTHROCYTE MEMBRANES.
 CC -1- PTM: An interchain disulfide bond is present in what becomes
 CC position 593 of the T isoform.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lyase family.
 CC -----
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 CC -----
 DR EMBL; X03439; CAA27169.1; -;
 DR EMBL; X56516; -; NOT_ANNOTATED_CDS.
 DR EMBL; X56517; -; NOT_ANNOTATED_CDS.
 DR PDB; 2ACE; 08-NOV-96.
 DR PDB; 1ACJ; 31-AUG-94.
 DR PDB; 2ACX; 11-FEB-98.
 DR PDB; 1ACJ; 31-AUG-94.
 DR PDB; 1AMN; 03-APR-96.
 DR PDB; 1PSS; 03-SEP-97.
 DR PDB; 1VOT; 16-JUN-97.
 DR PDB; 1AX9; 11-FEB-98.
 DR PDB; 1EVE; 22-MAR-99.
 DR PDB; 1CFJ; 01-APR-99.
 DR PDB; 1OCF; 18-MAY-99.
 DR PDB; 2DFP; 28-JUN-99.
 DR PDB; 1BOM; 25-JUN-99.
 DR PDB; 1DX6; 02-JAN-00.
 DR PDB; 1EQQ; 01-OCT-02.
 DR PDB; 1E66; 08-MAR-02.
 DR PDB; 1EAS; 08-NOV-00.
 DR PDB; 1EAA; 12-JAN-00.
 DR PDB; 1GPN; 29-AUG-02.
 DR PDB; 1GCR; 15-MAR-02.
 DR PDB; 1GOS; 15-MAR-02.
 DR PDB; 1H23; 16-JAN-03.
 DR PDB; 1H5J; 05-OCT-01.
 DR PDB; 1JJB; 18-SEP-02.
 DR PDB; 1C1D; 28-JAN-00.
 DR PDB; 1D1E; 28-JAN-00.
 DR PDB; 1D1F; 28-JAN-00.
 DR PDB; 1D1G; 28-JAN-00.
 DR PDB; 1D1H; 28-JAN-00.
 DR PDB; 1Q11; 28-JAN-00.
 DR PDB; 1C1J; 28-JAN-00.
 DR PDB; 1D1K; 26-JAN-00.
 DR PDB; 1D1M; 28-JAN-00.
 DR PDB; 1D1N; 14-FEB-01.
 DR PDB; 1VXO; 26-SEP-01.
 DR PDB; 1VXR; 26-SEP-01.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR003379; Ser_estr_site.
 DR Pfam: PF00135; Coesterase; 1
 DR PRINTS: PRO0378; CHOLINESTERASE.
 Query Match 1.0%; Score 8; DB 1; Length 586;
 Best Local Similarity 100.0%; Pred. No. 9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 2Y 125 SDCLVLTNI 132
 2b 133 SDCLVLTNI 120
 RESULT 37
 ACES_TORMA
 ID ACES_TORMA STANDARD; PRT; 590 AA.

RT "Characterization of the mouse pancreatic/mammary gland cholesterol
 RT esterase encoding cDNA and gene.";
 RL Gene 155:255-259(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/c; TISSUE=lactating mammary gland;
 RX MEDLINE=96079099; PubMed=8510360;
 RA Uidmer A.S., Kannus M., Jundberg L., Bjurstedt G., Nilsson G.;
 RT "Molecular cloning and characterization of the mouse carboxyl ester
 RT lipase gene and evidence for expression in the lactating mammary
 RT gland.";
 RI Genomics 29:115-122(1995).
 CC -- FUNCTION: CATALYZES FAT AND VITAMIN A ABSORPTION. ACTS IN CONCERT
 CC WITH PANCREATIC LIPASE AND COLIPASE FOR THE COMPLETE DIGESTION
 CC OF DIETARY TRIGLYCERIDES (BY SIMILARITY).
 CC -- CATALYTIC ACTIVITY: triacylglycerol + H(2)O = diacylglycerol + a
 CC fatty acid anion.
 CC -- CATALYTIC ACTIVITY: A sterol + H(2)O = a sterol + a fatty
 CC acid.
 CC -- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 CC -----
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 CC -----
 DR EMBL: U33169; AAA92088.1; -
 DR EXBL: U37396; AAC52279.1; -
 DR PIR: A57701; A57701.
 DR HSSP: P30122; 2BC6.
 DR SWISS-2DPAGE: Q64285; MOUSE.
 DR MGD: MG1:88374; Cel.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000379; Ser esters_site.
 DR Pfam: PF00135; Coesterase; ..
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; ..
 DR PROSITE: PS00341; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolyase; Serine esterase; Lipid degradation; Glycoprotein;
 KW Repeat: Signal;
 FT SIGNAL 1 20
 FT CHAIN 21 599 BY SIMILARITY.
 FT ACT_SITE 214 214 BY SIMILARITY.
 FT ACT_SITE 343 343 BY SIMILARITY.
 FT ACT_SITE 455 455 BY SIMILARITY.
 FT DISULFID 84 100 BY SIMILARITY.
 FT DISULFID 266 277 BY SIMILARITY.
 FT DOMAIN 559 589 4 X 1: AA INDEX REPEATS, O-G-LYCOSYLATED
 FT REPEAT 559 569 REGION.
 FT REPEAT 570 580 2.
 FT REPEAT 581 588 3.
 FT CARBOXYD 207 207 N-LINKED (GLNAC...) (POTENTIAL);
 FT CARBOXYD 325 325 N-LINKED (GLNAC...) (POTENTIAL);
 SQ SECURE 599 AA; 65813 MW; 9E4428FDFCA86502E CDS64;
 Query Match: 1.0%; Score 8; DB 1; Length 599;
 Best Local Similarity 100.0%; Pred No: 3.2; Mismatches 0; Gaps 0;
 Matches 8; Conservative 0; Indels 0;
 OY 125 ECDLNLINI 132
 OY |||||
 OY 98 ECDLNLINI 105
 RESULT 39
 BAL_RAT STANDARD; PRT; 612 AA.
 AC P07882; P14722;
 RT 01-AUG-1988 (Rel. 08, Created)
 RT 01-APR-1990 (Rel. 14, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Bile-salt-activated lipase precursor (EC 3.1.1.3) (EC 3.1.1.13) (BAL
 DE Bile-salt-stimulated lipase) (BSL) (Carboxyl ester lipase) (sterol
 DE esterase) (Cholesterol esterase) (Pancreatic lipoprotein lipase).
 GN CEL.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Pancreas;
 RX MEDLINE=90089378; PubMed=2688744;
 RA Kessler J.A., Fontaine R.N., Turk C.W., Brockman H.L., Hui D.Y.;
 RT "Molecular cloning and expression of cDNA for rat pancreatic
 RT cholesterol esterase.";
 RL Biochim. Biophys. Acta 1036:227-237(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87242339; PubMed=3593682;
 RA Fan J.H., Stratawa C., Rutter W.J.;
 RT "Isolation of full-length putative rat lipophospholipase cDNA using
 RT improved methods for mRNA isolation and cDNA cloning.";
 RL Biochemistry 26:1617-1625(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91299758; PubMed=2069957;
 RA Fontaine R.N., Carter C.P., Hui D.Y.;
 RT "Structure of the rat pancreatic cholesterol esterase gene.";
 RL Biochemistry 30:7008-7014(1991).
 RN [4]
 RP ACTIVE SITE SER-214.
 RX MEDLINE=91009095; PubMed=2211955;
 RA Dipersio L.P., Fontaine R.N., Hui D.Y.;
 RT "Identification of the active site serine in pancreatic cholesterol
 RT esterase by chemical modification and site-specific mutagenesis.";
 RL J. Biol. Chem. 266:16801-16806(1990).
 RN [5]
 RP ACTIVE SITE HIS-455.
 RX MEDLINE=91154187; PubMed=1999399;
 RA Dipersio L.P., Fontaine R.N., Hui D.Y.;
 RT "Site-specific mutagenesis of an essential histidine residue in
 RT pancreatic cholesterol esterase.";
 RL J. Biol. Chem. 266:4033-4036(1991).
 CC -- FUNCTION: CATALYZES FAT AND VITAMIN A ABSORPTION. ACTS IN CONCERT
 CC WITH PANCREATIC LIPASE AND COLIPASE FOR THE COMPLETE DIGESTION
 CC OF DIETARY TRIGLYCERIDES.
 CC -- CATALYTIC ACTIVITY: triacylglycerol + H(2)O = diacylglycerol + a
 CC fatty acid anion.
 CC -- CATALYTIC ACTIVITY: A sterol + H(2)O = a sterol + a fatty
 CC acid.
 CC -- ENZYME REGULATION: ACTIVATED BY BILE SALTS CONTAINING A 7-HYDROXYL
 CC GROUP.
 CC -- TISSUE SPECIFICITY: SYNTHESIZED PRIMARILY IN THE PANCREAS AND THEN
 CC TRANSPORTED TO THE INTESTINE.
 CC -- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 CC -----
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 CC -----
 DR EMBL: X16054; CA134189.1; -
 DR EMBL: M15893; AA41540.1; -
 DR EMBL: M69157; AA846376.1; -
 DR PIR: A34967; A34967.
 DR HSSP: P30122; 2BC6.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000379; Ser esters_site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; ..
 DR PROSITE: PS00341; CARBOXYLESTERASE_B_2; 1.

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DR PROSITE: PS00122; CARBOXYLESTERASE_B_1;
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Serine esterase; Lipid degradation; Glycoprotein;
KW Repeat; Signal.
FT SIGNAL 1 20
FT CHAIN 21 612 BILE-SALT-ACTIVATED LIPASE.
FT ACT_SITE 214 214 BY SIMILARITY.
FT ACT_SITE 340 340 BY SIMILARITY.
FT ACT_SITE 455 455 BY SIMILARITY.
FT DISULFID 84 100 BY SIMILARITY.
FT DISULFID 256 277 N-LINKED (GLYCNC. . .) (POTENTIAL).
FT CARBOHYD 257 207 4 X 11 AA tandem repeats, O-Glycosylated
FT CARBOHYD 556 599 REGION.
FT REPEAT 556 566 1.
FT REPEAT 567 577 2.
FT REPEAT 578 588 3.
FT REPEAT 589 599 4.
FT MUTAGEN 440 440 H->Q, NO EFFECT ON ACTIVITY.
FT 455 455 H->Q,R,A,S,D: ABOXISH ACTIVITY.
FT CONFLICT 26 26 V->L (IN REF. 2).
FT CONFLICT 154 154 G->A (IN REF. 2).
FT CONFLICT 217 217 A->G (IN REF. 2).
FT CONFLICT 219 219 S->T (IN REF. 2).
FT CONFLICT 419 419 M->T (IN REF. 2) AND 31.
FT CONFLICT 513 513 T->W (IN REF. 3).
FT CONFLICT 576 577 GG->VV (IN REF. 3).
FT CONFLICT 608 609 GP->VA (IN REF. 3).
FT CONFLICT 611 611 G->A (IN REF. 3).
SQ SEQUENCE 612 AA; 67340 MW; 1569CE4EA71E02A CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 1; Length 612;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 EDCCYLNI 132
Db 98 EDCCYLNI 105

RESULT 40
ACES_LERPE
ID ACES_LERPE STANDARD; PRT; 629 AA.
AC 027677;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).
OS Lepidoptera decemlineata (Colorado potato beetle).
OC Zukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cuculiformia;
OC Physophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
OC Chrysomelini; Lepidoptera.
NCBI_TaxID=7539;
RX MEDLINE=9637747; Pubmed=8560913;
RA Zou K.Y., Clark J.X.;
RT "Cloning and sequencing of a cDNA encoding acetylcholinesterase in
R Colorado potato beetle, Lepidoptera decemlineata (Say)."
R Insect Biochem. Mol. Biol. 25:1129-1138(1995).
CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -1- SUBCELLULAR LOCATION: LINKED TO THE MEMBRANE OF THE NEURONAL
CC CHOLINERGIC SYNAPSES BY A GPI-ANCHOR (BY SIMILARITY).
CC -1- PTM: THE N-TERMINUS IS BLOCKED.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
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CC -----
DR EMBL: L41180; AAC0466.1; -.
DR HSSP: P21836; 1MAA.
DR InterPro: IPR002018; CarbesteraseB.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR000379; Ser ester_ssite.
DR Pfam: PF00135; Coesterase; 1.
DR PRINTS: PR00878; CHOLINESTRASE.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1;
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Signal;
KW Neurotransmitter degradation; Gpi-anchor; Glycoprotein.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 629 ACETYLCHOLINESTERASE.
FT ACT_SITE 253 253 BY SIMILARITY.
FT ACT_SITE 382 382 BY SIMILARITY.
FT ACT_SITE 496 496 BY SIMILARITY.
FT DISULFID 103 110 BY SIMILARITY.
FT DISULFID 307 322 BY SIMILARITY.
FT DISULFID 458 574 BY SIMILARITY.
FT DISULFID 595 595 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 125 125 N-LINKED (GLYCNC. . .) (POTENTIAL).
FT CARBOHYD 308 308 N-LINKED (GLYCNC. . .) (POTENTIAL).
FT CARBOHYD 418 419 N-LINKED (GLYCNC. . .) (POTENTIAL).
FT CARBOHYD 509 509 N-LINKED (GLYCNC. . .) (POTENTIAL).
SQ SEQUENCE 629 AA; 71142 MW; 06556F833EB16C72 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 1; Length 629;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 EDCCYLNI 132
Db 128 EDCCYLNI 135

RESULT 41
ACES_ANOCT
ID ACES_ANOCT STANDARD; PRT; 664 AA.
AC P56161;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).
OS Anopheles stephensi (Indo-Pakistani malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anophelinae.
NCBI_TaxID=30659;
RX MEDLINE=91191507; Pubmed=1901515;
RA Hall L.M.C., Malcolm C.A.;
RT "The acetylcholinesterase gene of Anopheles stephensi."
R Cell. Mol. Neurobiol. 11:131-141(1991).
CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
CC IF CAN HYDROLYZE BUTYRYLTHIOCHOLINE.
CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -1- SUBUNIT: THE ACTIVE ENZYME SEEMS TO BE COMPOSED OF THE NON-
CC COVALENT ASSOCIATION OF A 55 kDa AND A 16 kDa POLYPEPTIDE. TWO
CC ACTIVE UNITS ARE LINKED TOGETHER BY A DISULFIDE BOND AT THE C-
CC TERMINUS OF THE 55 kDa PEPTIDE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: LINKED TO THE MEMBRANE OF THE NEURONAL
CC CHOLINERGIC SYNAPSES BY A GPI-ANCHOR.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR HSSP: P21836; 1MAA.
DR InterPro: IPR002018; CarbesteraseB.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR000379; Ser ester_ssite.
DR Pfam: PF00135; Coesterase; 1.
DR PRINTS: PR00878; CHOLINESTRASE.

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AC 062101;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein kinase C, mu type (EC 2.7.1.1) (PKC_mu) (protein kinase D).
GN PKCM OR PKCM OR PKD.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAB/c; TISSUE=Lung;
RX MEDLINE=9435973; PubMed=8079325;
RA Velverde A.M., Simet-Smith J., Van Vint J., Rozengurt E.;
RT "Molecular cloning and characterization of protein kinase D: a target
RT for diacylglycerol and phorbol esters with a distinctive catalytic
RT domain."
RL Proc. Natl. Acad. Sci. U.S.A. 91:8572-8576(1994).
RN [2]
RP PHOSPHORYLATION OF SER-916.
RX MEDLINE=9940316; PubMed=104736-7;
RA Matthews S.A., Rozengurt E., Cantrell D.;
RT "Characterization of serine 916 as an in vivo autophosphorylation site
RT for protein kinase D/protein kinase Cmu."
RL J. Biol. Chem. 274:26543-26549(1999).
CC -1- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHO-PID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -1- ENZYME REGULATION: ACTIVATED BY DIACYLGLYCEROL AND PHORBOL ESTERS.
CC -1- PTM: Autophosphorylated.
CC -1- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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CC -----
DR EXBL: Z34524; CAA84283.1;
DR PIR: I48719; I48719.
DR HSSP: P28867; IPTQ.
DR MGD: MGI:99879; PKcm.
DR InterPro: IPR002219; DAG_FE-bind.
DR InterPro: IPR001849; PH.
DR InterPro: IPR000719; PKC-kinase.
DR InterPro: IPR002230; Ser_Thr_kinase.
DR Pfam: PF00133; DAG_PE-bind; 2.
DR Pfam: PF00163; PH; 1.
DR Pfam: PF00069; Kinase; 1.
DR PRINTS: PR00638; DAGPEDOMAIN.
DR PRODOM: PD00063; Prot_kinase; 1.
DR SMART: SM00109; C1; 2.
DR SMART: SMC0233; PH; 1.
DR SMART: SMC0220; S_TKc; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE: PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE: PSF0003; PH_DOMAIN_1; 1.
DR PROSITE: PS00137; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50013; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50014; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Transferase; Serine/threonine-protein kinase;
KM Phorbol-ester binding; Zinc; Repeat; Phosphorylation.
FT DOMAIN 145 194 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 277 326 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 428 547 PH.
FT DOMAIN 589 845 PROTEIN KINASE.
FT DOMAIN 16 26 POLY-ALA.

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FT DOMAIN 198 201 POLY-ARG.
FT NP_BIND 595 603 ATP (BY SIMILARITY).
FT BINDING 618 618 ATP (BY SIMILARITY).
FT ACT_SITE 712 712 BY SIMILARITY.
FT MOD_RES 916 916 PHOSPHORYLATION (ATTC-1).
SQ SEQUENCE 918 AA; 102067 MW; 234486186621BDDA CRC64;

Query Match 1.0%; Score 8; DB 1; Length 918;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 EDDIDHQ 163
DB 791 EDDIDHQ 798

RESULT 46
GUT1_YEAST STANDARD; PRT; 244 AA.
ID GUT1_YEAST
AC Q12680; Q12290;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 35, Last annotation update)
DE Glutamate synthase (NADPH precursor) (EC 1.4.1.13) (NADPH-GOGAT).
GN GUT1 OR YDL171C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC STRAIN=CN36;
RX MEDLINE=97082505; PubMed=8923741;
RA Flierici P., Martegani M.P., Valenzuela L., Gonzalez A., Ballario P.;
RT "Sequence of the GUT1 gene from Saccharomyces cerevisiae reveals the
RT domain structure of yeast glutamate synthase."
RL Yeast 12:1359-1366(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Pohl T.M.;
RT Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2 L-glutamate + NADP(+) = L-glutamine + 2-
CC -1- OXOGlutamate + NADPH.
CC -1- COFACTOR: BINDS A 3FE-4S CLUSTER; FAD AND FMN.
CC -1- SUBUNIT: Homotrimer.
CC -1- SIMILARITY: TO OTHER GLUTAMATE SYNTHASES.
CC -----
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CC -----
DR EXBL: X89221; CAA61505.1;
DR EMBL: Z67750; CAA91574.1;
DR EMBL: Z74219; CAA98745.1;
DR SGD: S0002330; GUT1.
DR GO: GO:0005623; C:cell; IDA.
DR GO: GO:0006537; P:glutamate biosynthesis; ISP.
DR InterPro: IPR000759; AGRdx_reductase.
DR InterPro: IPR002489; DCF1A.
DR InterPro: IPR001327; FAD pyr_redox.
DR InterPro: IPR006982; Glu_syn_central.
DR InterPro: IPR006991; Glu_syn_NTN.
DR InterPro: IPR002932; Glu_synthase.
DR InterPro: IPR006025; Glu_synth_sub1.
DR InterPro: IPR00103; Pyridine_redox_2.
DR Pfam: PF04898; Glu_syn_central; 1.
DR Pfam: PF04897; Glu_syn_NTN; 1.
DR Pfam: PF01645; Glu_synthase; 1.

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DR Pfam: PF01493; GXXGX; 1.
DR Pfam: PF06070; pyr_redox; 1.
DR PRINTS; PR00419; ADXR1BASE.
DR PRINTS; PR00368; FADPR.
DR PRINTS; PR00469; PNDPBASE1.
DR TIGRFamS; TIGR01317; GOGAT sm gam; 1.
KM Oxidoreductase: iron-sulfur [3Fe-4S]; Flavoprotein; FAD; FMN; NADP;
KM Glutamate biosynthesis; Zymogen.
FT PROPEP 1
FT CHAIN 54 2144 GUTAMATE SYNTHASE [NADPH].
FT METAL 1132 1183 FMN (BY SIMILARITY).
FT METAL_BIND 1184 1184 IRON-SULFUR (3FE-4S) (BY SIMILARITY).
FT METAL 1190 1190 IRON-SULFUR (3FE-4S) (BY SIMILARITY).
FT METAL 1195 1195 IRON-SULFUR (3FE-4S) (BY SIMILARITY).
FT CONFLICT 33 33 L -> D (IN REF. 2).
FT CONFLICT 168 172 TERRYRY -> NPEVSTT (IN REF. 2).
FT CONFLICT 449 451 ILS -> FLV (IN REF. 2).
FT CONFLICT 1752 1752 L -> V (IN REF. 2).
SQ SEQUENCE 2144 AA; 238220 KM; 5AA6A948EF995143 CRC64;

Query Match 1.0%; Score 8; DS 1; Length 2144;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 702 KRRETHR 709
Db :447 KRRETHR 1654

RESULT 47
THYG_MOUSE STANDARD; PRT; 2766 AA.
1D THYG_MOUSE
AC 008710; 093590; CDMWY;
ET 31-NOV-1997 (Ref. 35, Created)
ET 16-OCT-2001 (Ref. 40, Last sequence update)
ET 16-OCT-2001 (Ref. 40, Last annotation update)
DE Thyroglobulin precursor.
GN TG OR TGN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10093;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98008194; PubMed=9344706;
RA Cauregli P., Vidatain P.O., Vall M., Aguilera-Galaviz L.A.,
RA Rose N.R.;
RT "Cloning and characterization of murine thyroglobulin cDNA.";
RL Clin. Immunol. Immunopathol. 65:221-226(1997).
(2)
RN SEQUENCE FROM N.A. AND VARIANT GOITER PRO-2283.
RP SEQUENCE FROM N.A.
RC STRAIN=AKR/J; TISSUE=Thyroid;
RA Kim P.S., Hossain S.A., Park Y.-N., Lee I., Yoo S.-E., Arvan P.;
RA MEDLINE=98374279; PubMed=9707574;
RT "A single amino acid change in the acetylcholinesterase-like domain of
RT thyroglobulin causes congenital goiter with hypothyroidism in the
RT cogg/cogg mouse: a model of human endoplasmic reticulum storage
RT diseases.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:9909-9913(1998).
(3)
RN SEQUENCE FROM N.A.
RP STRAIN=AKR/J; TISSUE=Thyroid;
RA Hossain S.A., Yoo S.-E., Kim P.S.;
RT "Cloning, characterization, site-directed mutagenesis, and transient
RT expression of 830-nucleotide AKR/J mouse thyroglobulin cDNA:
RT defective secretion of mutant thyroglobulins.";
RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: PRECURSOR OF THE IODINATED THYROID HORMONES THYROXINE
CC (T4) AND TRIIODOTHYRONINE (T3).
CC -1- STRUITY: Homodimer (by similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: THYROID GLAND SPECIFIC (BY SIMILARITY).
CC -1- PTM: SULFATED (BY SIMILARITY)

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CC	-1-	DISEASE: SOME FORMS OF GOITER, AN ENLARGEMENT OF THE THYROID		
CC	GLAND, ARE PRODUCED BY DEFECTS IN TG. THE VARIANT P-2284 EXHIBIT A			
CC	DEFECT IN EXIT FROM THE ENDOPLASMIC RETICULON.			
CC	-1-	SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.		
CC	-1-	SIMILARITY: Contains 11 thyroglobulin type-I domains.		
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CC	or send an email to license@ebi.ac.uk).			
CC	-----			
DR	EMBL; J76389; AAB53204.1; -			
DR	EMBL; AF076186; AAC32268.1; -			
DR	EMBL; AF076187; AAC32269.1; -			
DR	HSSP; P21836; 1YAA.			
DR	MGD; MG1:98733; Tgm.			
DR	InterPro: IPR002018; Carboxylesterase.			
DR	InterPro: IPR006716; Thyroglobulin_1.			
DR	Pfam; PF00135; Coesterase; 1.			
DR	Pfam; PF00086; Thyroglobulin_1; 9.			
DR	SMART; SM00211; Ty; 10.			
DR	PROSITE; PS00584; THYROGLOBULIN 1; 9.			
DR	PROSITE; PS00594; CARBOXY-ESTERASE B_2; 1.			
KW	Glycoprotein; Repeat; Thyroid hormone; Iodination; Sulfation; Signal;			
KW	Disease mutation.			
FT	SIGNAL	1	20	
FT	CHAIN	21	2766	BY SIMILARITY.
FT	DOMAIN	32	93	THYROGLOBULIN TYPE IA 1.
FT	DOMAIN	94	161	THYROGLOBULIN TYPE IA 2.
FT	DOMAIN	162	298	THYROGLOBULIN TYPE IA 3.
FT	DOMAIN	299	359	THYROGLOBULIN TYPE IA 4.
FT	DOMAIN	605	658	THYROGLOBULIN TYPE IA 5.
FT	DOMAIN	659	726	THYROGLOBULIN TYPE IA 6.
FT	DOMAIN	727	922	THYROGLOBULIN TYPE IA 7.
FT	DOMAIN	923	1074	THYROGLOBULIN TYPE IA 8.
FT	DOMAIN	1075	1146	THYROGLOBULIN TYPE IB 1.
FT	DOMAIN	1147	1211	THYROGLOBULIN TYPE IA 9.
FT	REPEAT	1455	1468	TYPE II.
FT	REPEAT	1469	1485	TYPE II.
FT	REPEAT	1486	1502	TYPE II.
FT	DOMAIN	1511	1564	THYROGLOBULIN TYPE IB 2.
FT	REPEAT	1602	1722	TYPE IIA.
FT	REPEAT	1723	1889	TYPE IIB.
FT	REPEAT	1890	1992	TYPE IIA.
FT	REPEAT	1993	2125	TYPE IIB.
FT	REPEAT	2126	2183	TYPE IIA.
FT	DISULFID	2263	2280	POTENTIAL.
FT	MOD_RES	25	25	IODINATION (IN T4) (BY SIMILARITY).
FT	MOD_RES	25	25	SULFATION (POTENTIAL).
FT	MOD_RES	2572	2572	IODINATION (IN T4) (BY SIMILARITY).
FT	MOD_RES	2586	2586	IODINATION (IN T4) (BY SIMILARITY).
FT	MOD_RES	2764	2764	IODINATION (IN T3) (BY SIMILARITY).
FT	CARBOHYD	111	111	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	199	199	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	484	484	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	496	496	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	748	748	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	817	817	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	948	948	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1141	1141	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1349	1349	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1365	1365	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1715	1715	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1729	1729	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1773	1773	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1864	1864	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1935	1935	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	2010	2010	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	2120	2120	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	2249	2249	N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 2294 2294 N-LINKED GLUCONAC. (POTENTIAL).
FT CARBOHYD 2581 2581 N-LINKED GLUCONAC. (POTENTIAL).
FT VAR1ANT 2283 2283 E -> P (IN GOITER).
FT CONFLICT 80 80 E -> K (IN REF. 2 AND 3).
FT CONFLICT 92 92 V -> I (IN REF. 2 AND 3).
FT CONFLICT 1327 1327 T -> A (IN REF. 2 AND 3).
FT CONFLICT 1427 1427 N -> S (IN REF. 1).
FT CONFLICT 1436 1442 RTLOGM -> GLSLDYL (IN REF. 1).
FT CONFLICT 1721 1721 I -> T (IN REF. 2 AND 3).
FT CONFLICT 1813 1813 S -> T (IN REF. 1).
FT CONFLICT 1957 1959 RVK -> KVN (IN REF. 2 AND 3).
FT CONFLICT 2090 2092 S -> SS (IN REF. 2).
FT CONFLICT 2407 2407 R -> K (IN REF. 2 AND 3).
FT CONFLICT 2414 2414 G -> S (IN REF. 2 AND 3).
FT CONFLICT 2427 2427 R -> K (IN REF. 2 AND 3).
FT CONFLICT 2434 2434 A -> T (IN REF. 2 AND 3).
FT CONFLICT 2443 2453 TSSIGEVVSC -> NTHGSGTXYF (IN REF. 2 AND 3).
FT CONFLICT 2728 2728 D -> GN (IN REF. 1).
SQ SEQUENCE 2766 AA; 354512 MW; E195351DC5793A03 CRC64;

Query Match 1.0%; Score 8; DB 1; Length 2766;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 NEDCLYN 131
DB 2277 NEDCLYN 2284

RESULT 48
JHA RHOMA STANDARD; PRT; 52 AA.
ID LHA RHOMA
AC P80259;
BT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DB Light-harvesting protein B-860, alpha chain (Antenna pigment protein, alpha chain).
OS Rhodospirillum rubrum (Rhodospirillum rubrum).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OX NCBI_TaxID=1030;
RN [1]
RP SEQUENCE.
RC STRAIN=DSV 2693;
RA Brunisholz R.A., Bissig T., Wagner-Huber R., Frank G., Suter F.,
RA Niederer E., Zuber H.;
RT "The primary structures of the core antenna polypeptides from
RT Rhodospirillum rubrum."
RJ Z. Naturforsch. C 44:407-414(1989).
CC -1- FUNCTION: ANTENNA COMPLEXES ARE LIGHT-HARVESTING SYSTEMS, WHICH
CC TRANSFER THE EXCITATION ENERGY TO THE REACTION CENTERS.
CC -1- SUBUNIT: THE CORE COMPLEX IS FORMED BY DIFFERENT ALPHA AND BETA
CC CHAINS. BINDING BACTERIOCHLOROPHYLL MOLECULES, AND ARRANGED
CC MOST PROBABLY IN TETRAMERIC STRUCTURES DISPOSED AROUND THE
CC REACTION CENTER. THE NON-PIGMENTED GAMMA CHAINS MAY CONSTITUTE
CC ADDITIONAL COMPONENTS.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
CC InterPro: IPR000066; Antenna a/b.
DR InterPro: IPR002361; Antenna a.
DR Pfam: PF00556; LHC 1.
DR PRINTS: PR00673; LIGHTHARVSTA.
DR PROSITE: PS00968; ANTENNA_COMP_ALPHA.
KW Antenna complex; light-harvesting polypeptide; Transmembrane;
KW Macromolecular complex; Bacteriochlorophyll; inner membrane.
FT DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 13 33 POTENTIAL.
FT DOMAIN 34 52 PERIPLASMIC (POTENTIAL).
FT METAL 29 29 MAGNESIUM (BACTERIOCHLOROPHYLL AXIAL
FT LIGAND) (POTENTIAL).
SQ SEQUENCE 52 AA; 6095 MW; 5DBE633E3010C6B9 CRC64;

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Query Match 0.9%; Score 7; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 440 TLVAFT 446
DB 13 TLVAFT 19

RESULT 49
Y55B MYCGE STANDARD; PRT; 127 AA.
ID Y55B MYCGE
AC Q92B81;
BT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG055.2.
GN MG055.2.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischman J.L., Weidman J.F., Small K.V., Sandusky M., Fritchman J.L.,
RA Nguyen D.T., Uterback T.R., Sauder D.M., Phillips C.A., Merrick J.W.,
RA Tomb J.-F., Dougherty B.A., Boff K.F., Hu P.-C., Zuckers T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium."
RL Science 270:397-403(1995).
RN [2]
RP IDENTIFICATION.
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischman J.L., Weidman J.F., Small K.V., Sandusky M., Fritchman J.L.,
RA Nguyen D.T., Uterback T.R., Sauder D.M., Phillips C.A., Merrick J.W.,
RA Tomb J.-F., Dougherty B.A., Boff K.F., Hu P.-C., Zuckers T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.
CC -----
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CC -----
CC EMBL: U39695; AAC1281.1; -.
CC DR TIGR: MG055.2; -.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 13 35 POTENTIAL.
FT TRANSMEM 57 81 POTENTIAL.
SQ SEQUENCE 127 AA; 14631 MW; 4F00F3E6726D5ECF CRC64;

Query Match 0.9%; Score 7; DB 1; Length 127;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 597 LHNLEI 603
DB 7 LHNLEI 13

RESULT 50
REFA ANASP STANDARD; PRT; 133 AA.
ID REFA ANASP
AC Q820M8;
BT 28-FEB-2003 (Rel. 41, Created)

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ET 28-FEB-2003 (Rel. 41, Last sequence update)
LT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribosome-binding factor A.
GN BBFA OR ABR0063.
CS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
ON NCBI_TaxID=103690.
RX MEDLINE=21595285; PubMed=1759840;
RA Kaneo T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Katsube A., Itiguchi M., Shikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara Y., Matsumoto Y., Matsuo A., Kuraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT Cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
CC -!- FUNCTION: Associates with free 30S ribosomal subunits (but not
CC with 30S subunits that are part of 70S ribosomes or polyosomes).
CC Essential for efficient processing of 16S rRNA. May interact with
CC the 5' terminal helix region of 16S rRNA (by similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: BELONGS TO THE BBFA FAMILY.
CC -----
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CC -----
DR EMBL: AP003581; BAB7587.1; .
DR PIR: AG1814; AG1814.
DR HAMAP: MF_00003.1; .
DR InterPro: IPR000239; Rib_bind_factA.
DR Pfam: PF02333; BBFA; 1.
DR ProDom: PD020327; Rib_bind_factA; 1.
DR TrEMBL: TIGR00062; TbfA; 1.
DR PROSITE: PS01319; BBFA; 1.
KM rRNA processing; Complete proteome
SQ SEQUENCE 133 AA; 14665 MW; 68994937547BFC54 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 766 RSPDIP 772
Db 118 RSPDIP 124

RESULT 51
CHLE_BOVIN STANDARD; PRT; 141 AA.
ID CHLE_BOVIN
AC P32749;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cholinesterase (EC 3.1.1.8) (Acetylcholine acylhydrolase) (Choline
DE esterase II) (Butyrylcholine esterase) (Pseudocholinesterase)
DE (Fragment).
GN SCHE.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=91201348; PubMed=2016308;

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RA Atpagaus M., Chatornet A., Masson P., Newton M., Vaughan T.A.,
RA Batteis C.F., Nogueira C.P., La Du B.N., Lockridge O.;
RT "Use of the polymerase chain reaction for homology probing of
RT butyrylcholinesterase from several vertebrates."
RT J. Biol. Chem. 266:6966-6974(1991).
CC -!- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC carboxylic acid anion.
CC -!- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO DIMERS. THE
CC TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND.
CC -!- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
CC -!- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
CC ORGANOPHOSPHATE ESTERS.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M62410; AAA51412.1; .
DR PIR: F39768; F39768.
DR HSSP: P22303; 2CLC.
DR InterPro: IPR002018; Carbesterease.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR00379; Ser ests_site.
DR Pfam: PF00135; Coesterase; 1.
DR PRINTS: PR00878; CHOLNESTERASE.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_2; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KM Hydroxylase; Serine esterase; Glycoprotein.
FT NON_TER 1 1
FT ACCT_SITE 131 131 BY SIMILARITY.
FT CARBOHYD 33 39 N-LINKED (GLYCNA. . .) (POTENTIAL).
FT NON_TER 141 141
SO SEQUENCE 141 AA; 15234 MW; 5FDFA11730564D3 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCYLN 131
Db 23 EDCYLN 29

RESULT 52
CHLE_CANFA STANDARD; PRT; 141 AA.
ID CHLE_CANFA
AC P32750;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cholinesterase (EC 3.1.1.8) (Acetylcholine acylhydrolase) (Choline
DE esterase II) (Butyrylcholine esterase) (Pseudocholinesterase)
DE (Fragment).
GN BCHE.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91201348; PubMed=2016308;
RA Atpagaus M., Chatornet A., Masson P., Newton M., Vaughan T.A.,
RA Batteis C.F., Nogueira C.P., La Du B.N., Lockridge O.;
RT "Use of the polymerase chain reaction for homology probing of
RT butyrylcholinesterase from several vertebrates."
RT J. Biol. Chem. 266:6966-6974(1991).
CC -!- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a

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CC      carboxylic acid anion.
CC      -1- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO DIMERS. THE
CC      TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND.
CC      -1- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
CC      -1- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
CC      ORGANOPHOSPHATE ESTERS.
CC      -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: M62411; AAA5145.1; -.
CC      PIR: E39768; E39768.
CC      HSSP: P22303; 2CLD.
CC      InterPro: IPR002018; CarbesteraseB.
CC      InterPro: IPR000937; Cholinesterase.
CC      InterPro: IPR002379; Ser_estrs_site.
CC      Pfam: PF00135; Coesterase_1.
CC      PRINTS: PR00878; CHOLINESTERASE.
CC      PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
CC      PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
CC      KX Hydroxylase; Serine esterase; Glycoprotein.
CC      FT NON_TER 1 1
CC      FT ACT_SITE 131 131 BY SIMILARITY.
CC      FT CARBOHYD 39 39 N-LINKED (GLCNAC... ) (POTENTIAL).
CC      FT NON_TER 141 141
CC      SO SEQUENCE 141 AA; 15086 MW; 3581584590111FEB CRC64;

Query Match      0.9%; Score 7; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      125 EDCLYLN 131
DB      23 EDCLYLN 29

RESULT 53
CHLE_PIG      STANDARD; PRT; 141 AA.
ID      CHLE_PIG
AC      P32751;
DT      01-OCT-1993 (Rel. 27, Created)
DT      01-OCT-1993 (Rel. 27, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Cholinesterase (EC 3.1.1.8) (Acylcholine acylhydrolase) (Choline
DE      esterase 1) (Butyrylcholine esterase) (Pseudocholinesterase)
DE      (Fragment).
DE      BCHE.
GN      BCHE.
OS      Macaca mulatta (Rhesus macaque).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecinae; Macaca.
OX      NCB TaxID=9544;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Liver;
RX      MEDLINE=91201348; PubMed=2016308;
RA      Arpagaus M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,
RA      Barteis C.F., Nogueira C.P., La Du B.N., Lockridge O.;
RT      "Use of the polypeptide chain reaction for homology probing of
RT      butyrylcholinesterase from several vertebrates.";
RL      J. Biol. Chem. 266:6966-6974(1991).
CC      -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC      carboxylic acid anion.
CC      -1- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO DIMERS. THE
CC      TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND.
CC      -1- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
CC      -1- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH

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CC      ORGANOPHOSPHATE ESTERS.
CC      -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: M62777; AAA5636.1; -.
CC      PIR: G39768; G39768.
CC      HSSP: P22303; 2CLD.
CC      InterPro: IPR002018; CarbesteraseB.
CC      InterPro: IPR000937; Cholinesterase.
CC      InterPro: IPR002379; Ser_estrs_site.
CC      Pfam: PR00135; Coesterase_1.
CC      PRINTS: PR00878; CHOLINESTERASE.
CC      PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
CC      PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
CC      KX Hydroxylase; Serine esterase; Glycoprotein.
CC      FT NON_TER 1 1
CC      FT ACT_SITE 131 131 BY SIMILARITY.
CC      FT CARBOHYD 39 39 N-LINKED (GLCNAC... ) (POTENTIAL).
CC      FT NON_TER 141 141
CC      SO SEQUENCE 141 AA; 15224 MW; A3C1135E650D636 CRC64;

Query Match      0.9%; Score 7; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      125 EDCLYLN 131
DB      23 EDCLYLN 29

RESULT 54
CHLE_PIG      STANDARD; PRT; 141 AA.
ID      CHLE_PIG
AC      P32752;
DT      01-OCT-1993 (Rel. 27, Created)
DT      01-OCT-1993 (Rel. 27, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Cholinesterase (EC 3.1.1.8) (Acylcholine acylhydrolase) (Choline
DE      esterase 1) (Butyrylcholine esterase) (Pseudocholinesterase)
DE      (Fragment).
DE      BCHE.
GN      BCHE.
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX      NCB TaxID=9823;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Liver;
RX      MEDLINE=91201348; PubMed=2016308;
RA      Arpagaus M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,
RA      Barteis C.F., Nogueira C.P., La Du B.N., Lockridge O.;
RT      "Use of the polypeptide chain reaction for homology probing of
RT      butyrylcholinesterase from several vertebrates.";
RL      J. Biol. Chem. 266:6966-6974(1991).
CC      -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC      carboxylic acid anion.
CC      -1- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO DIMERS. THE
CC      TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND.
CC      -1- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
CC      -1- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
CC      ORGANOPHOSPHATE ESTERS.
CC      -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC      -----
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CC -----
DR EMBL: M62780; AAA31005.1; -.
DR PIR: D39768; D39768.
DR HSSP: P22303; ZCLJ.
DR InterPro: IPR002018; CarboxylaseB.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR00379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase_1.
DR PRINTS: PR00878; CHOLINESTRASE.
DR PROSITE: PS00122; CARBOXYL-ESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYL-ESTERASE_B_2; 1.
DR KMe Hydrolase; Serine esterase; Glycoprotein.
FT ACT_SITE 131 133 BY SIMILARITY.
FT CARBOHYD 39 39 N-LINKED (GLCNAC...) (POTENTIAL).
FT NON_TER 141 141
SQ SEQUENCE 141 AA; 15250 MW; 43D869C48D4164C CRC64;

Query Match 0.9%; Score 7; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLN 131
DB 23 EDCLYLN 29

RESULT 55
CHIEF_SHEEP
ID CHIEF_SHEEP STANDARD; PRT; 141 AA.
AC P32753;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 43, Last annotation update)
DE Cholinesterase (EC 3.1.1.8) (Acylcholine acetylhydrolase) (Choline
DE esterase II) (Butyrylcholine esterase) (Pseudocholinesterase)
DE [Fragment].
DE
OS Ovis aries (Sheep).
OS BCFE.
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC Bovidae; Caprinae; Ovis.
CC NCBI_TaxID=9940;
CC 11
CC SEQUENCE FROM N.A.
CC TISSUE=Liver;
RX MEDLINE=91201348; PubMed=2016308;
RA Arpagaus M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,
RA Batters C.F., Nogueira C.P., La Du B.N., Lockridge O.;
RT "Use of the polymerase chain reaction for homology probing of
RT butyrylcholinesterase from several vertebrates.";
RL J. Biol. Chem. 266:6966-6974(1991).
CC -1- CATALYTIC ACTIVITY: An acylcholine + H2O = choline + a
CC carboxylic acid anion.
CC -1- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO DIMERS. THE
CC TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND.
CC -1- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
CC -1- MISCELLANEOUS: CHOLINESTRASE IS HIGHLY REACTIVE WITH
CC ORGANOPHOSPHATE ESTERS.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
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DR EMBL: M62780; AAA31509.1; -.
DR PIR: B39768; B39768.
DR HSSP: P22303; ZCLJ.
DR InterPro: IPR002018; CarboxylaseB.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR00379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase_1.
DR PRINTS: PR00878; CHOLINESTRASE.
DR PROSITE: PS00122; CARBOXYL-ESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYL-ESTERASE_B_2; 1.
DR KMe Hydrolase; Serine esterase; Glycoprotein.
FT ACT_SITE 131 131 BY SIMILARITY.
FT CARBOHYD 39 39 N-LINKED (GLCNAC...) (POTENTIAL).
FT NON_TER 141 141
SQ SEQUENCE 141 AA; 15234 MW; 5FDFA11730564D3 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLN 131
DB 23 EDCLYLN 29

RESULT 56
CUS5_ARADI
ID CUS5_ARADI STANDARD; PRT; 156 AA.
AC PA0519;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Adult-specific rigid cuticular protein 15.5 (ACP 15.5).
DE Araneus diadematus (Spider).
CC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
CC Araneomorphae; Eutegynae; Araneoidae; Araneidae; Araneus.
CC NCBI_TaxID=45920;
CC 11
CC SEQUENCE.
CC TISSUE=Cuticle;
RX MEDLINE=9716616; PubMed=9014336;
RA Norup T., Berg T., Stenholm H., Andersen S.O., Hoggup P.;
RT "Purification and characterization of five cuticular proteins from
RT the spider Araneus diadematus.";
RL Insect Biochem. Mol. Biol. 26:907-915(1996).
CC -1- FUNCTION: COMPONENT OF THE RIGID CUTICLE OF THE SPIDER.
CC -1- MASS SPECTROMETRY: MM=15464.7; METHOD=Electrospray.
CC InterPro: IPR00618; Insect cuticle.
CC Pfam: PF00379; Chitin bind_4; 1.
CC PROSITE: PS00233; CUTICLE_1.
CC Structural protein; Cuticle.
SQ SEQUENCE 156 AA; 15463 MW; 89C7AD3DBA5107D CRC64;

Query Match 0.9%; Score 7; DB 1; Length 156;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 VAPAVVA 457
DB 104 VAPAVVA 110

RESULT 57
CUS7_ARADI
ID CUS7_ARADI STANDARD; PRT; 159 AA.
AC PA0519;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Adult-specific rigid cuticular protein 15.7 (ACP 15.7).
DE Araneus diadematus (Spider).
CC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
```


CC Araneomorphae; Entelegyidae; Araneidae; Araneidae; Araneus.
 CX NCBI_TaxID=45920;
 RN [1]
 RP SEQUENCE.
 RC Tissue=Cuticle;
 RX MEDLINE=9716616; PubMed=90:4336;
 RA Norp T., Berg T., Stenholm H., Andersen S.O., Hooprup P.;
 RT "Purification and characterization of five cuticular proteins from
 the spider Araneus diadematus";
 RL Insect Biochem. Mol. Biol. 26:907-915(1996).
 CC -1- FUNCTION: COMPONENT OF THE RIGID CUTICLE OF THE SPIDER.
 CC -1- MASS SPECTROMETRY: MW=15682.9; METHOD=Electrospray.
 DR InterPro: IPR00065; Insect-cuticle.
 DR Pfam: PF00373; Cuticle_king_4; 1.
 DR PRINTS: PR03947; CUTICLE.
 DR PROSITE: PS00233; CUTICLE; 1.
 KW Structural protein; Cuticle.
 FT DOMAIN 92 97
 FT SEQUENCE 159 AA; 15682 MW; 6FBA35E229EF598 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 159;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 451 VAPAVAA 457
 Db 109 VAPAVAA 115

RESULT 58
 EST1_SCHGA

ID EST1_SCHGA STANDARD; PRT: 198 AA.
 AC P81429;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Esterase SG1 precursor (EC 3.1.1.1) (Carboxylic-ester hydrolase)
 DE (Fragment).
 CK SGI

OS Schizaphis graminum (Aphid.).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
 CC Aphididae; Aphididae; Aphidini; Schizaphis.
 CX NCBI_TaxID=13362;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 22-41.
 RX MEDLINE=20078165; PubMed=10612041;
 RA Ono M., Swanson C.J., Field L.M., Devonshire A.L., Siegfried B.O.;
 RT "Amplification and methylation of an esterase gene associated with
 insecticide-resistance in greenbugs, Schizaphis graminum";
 RL Insect Biochem. Mol. Biol. 23:1065-1073(1998).
 CC -1- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON
 CC MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.
 CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
 CC carboxylic anion.
 CC -1- MISCELLANEOUS: THIS ESTERASE CONFERS ON INSECTICIDE RESISTANCE.
 CC -1- SIMILARITY: BELONGS TO THE type-B carboxylesterase/lipase family.
 CC -----
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 CC -----
 CC EMBL: Y17580; CAA75732.1; -
 DR HSSP: P37967; 10E3.
 DR InterPro: IPR02018; Carboxesterase.
 DR Pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; PARTIAL.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 KM Hydrolase; Serine esterase; Glycoprotein; Signal.

FT SIGNAL 1 21
 FT CHAIN 22 >198
 FT DISULFID 87 104
 FT CARBOHYD 79 79
 FT CONFLICT 24 24
 FT CONFLICT 28 28
 FT NON_TER 198 198
 FT SEQUENCE 198 AA; 21897 MW; EFFE43E6A5D5987 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 198;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 125 EDCVLYN 131
 Db 102 EDCVLYN 108

RESULT 59
 SC21_RICCN
 ID SC21_RICCN STANDARD; PRT: 199 AA.
 AC Q92JY5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE SC02-like protein RC0042.
 DE RC0042.
 GX RC0042.
 OS Rickettsia conorii.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 CX NCBI_TaxID=781;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Malish 7;
 RX MEDLINE=21442074; PubMed=11557893;
 RA Oeata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
 RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
 RA Raoult D.;
 RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii";
 RL Science 293:2093-2098(2001).
 CC -1- SIMILARITY: BELONGS TO THE SC01/2 FAMILY.
 CC -----
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 CC -----
 CC EMBL: AE008572; AA02580.1; -
 DR PIR: B97705; B97705.
 DR InterPro: IPR03782; SC01_Senc.
 DR Pfam: PF02610; SC01-Senc; 1.
 KM Hypothetical protein; Complete proteome.
 SO SEQUENCE 199 AA; 23101 MW; 80CACBDD4DF0CB4 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 199;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 15 IKFTLID 21
 Db 53 IKFTLID 59

RESULT 60
 G1DR_COXBU
 ID G1DR_COXBU STANDARD; PRT: 204 AA.
 AC P94614;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)

```

DE Methyltransferase gids (EC 2.1.1.-) (Glucose inhibited division
DE protein 3).
GN GIDB OR C301925.
OS Coxella burnetii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Coxiellaceae; Coxiella.
OX NCBI_Taxid=777;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Nine Mile Phase I;
RA Willems H., Jaeger C.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Nine Mile Phase I / RSA 493;
RX MEDLINE=94292425; PubMed=8021167;
RA Chistoseedov A.Y., Chistoseedova L.V., McIntire W.S., Lidstrom M.E.;
RT "Genetic organization of the mau gene cluster in Methylobacterium
RT extorquens AM1: complete nucleotide sequence and generation and
RT characteristics of mau mutants.";
RL Bacteriol. 176:4052-4065(1994).
CC
CC -1- FUNCTION: MAY BE SPECIFICALLY INVOLVED IN THE PROCESSING,
CC TRANSPORT, AND/OR MATURATION OF THE MAHA BETA-SUBUNIT.
CC -1- PATHWAY: Methylamine utilization.
CC
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CC
CC EMBL: Y10436; CAA71460.1;
DR EMBL; AEC:6966; AA01416.1;
DR TIGR; CB01925;
DR HAXAP; MF_00074;
DR InterPro; IPR003682; GIDB.
DR InterPro; IPR000051; SAM_bind.
DR Pfam; PF02527; GIDB; 1.
DR Pfam; PF004441; GIDB; 1.
DR TIGRFAMs; TIGR00338; gids; 1.
DR Transferase; Methyltransferase.
SQ SEQUENCE 204 AA; 22617 MW; EFTGBD16C18F445E CRC64;

Query Match 0.9%; Score 7; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RC STRAIN=AM1 / NCIMB 9133;
RX MEDLINE=94292425; PubMed=8021167;
RA Chistoseedov A.Y., Chistoseedova L.V., McIntire W.S., Lidstrom M.E.;
RT "Genetic organization of the mau gene cluster in Methylobacterium
RT extorquens AM1: complete nucleotide sequence and generation and
RT characteristics of mau mutants.";
RL Bacteriol. 176:4052-4065(1994).
CC
CC -1- FUNCTION: MAY BE SPECIFICALLY INVOLVED IN THE PROCESSING,
CC TRANSPORT, AND/OR MATURATION OF THE MAHA BETA-SUBUNIT.
CC -1- PATHWAY: Methylamine utilization.
CC
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CC
CC EMBL: Z26406; AAB46935.1;
DR EMBL; A38123; A38123.
DR InterPro; IPR006663; ThioRedox_dom2.
FM TRANSMEMBRANE.
FT TRANSMEM 5 25 POTENTIAL.
SQ SEQUENCE 205 AA; 22233 MW; 78364F3DA07C1104 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 205;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DE Methyltransferase gids (EC 2.1.1.-) (Glucose inhibited division
DE protein 3).
GN GIDB OR C301925.
OS Coxella burnetii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Coxiellaceae; Coxiella.
OX NCBI_Taxid=777;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Nine Mile Phase I;
RA Willems H., Jaeger C.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Nine Mile Phase I / RSA 493;
RX MEDLINE=94292425; PubMed=8021167;
RA Chistoseedov A.Y., Chistoseedova L.V., McIntire W.S., Lidstrom M.E.;
RT "Genetic organization of the mau gene cluster in Methylobacterium
RT extorquens AM1: complete nucleotide sequence and generation and
RT characteristics of mau mutants.";
RL Bacteriol. 176:4052-4065(1994).
CC
CC -1- FUNCTION: MAY BE SPECIFICALLY INVOLVED IN THE PROCESSING,
CC TRANSPORT, AND/OR MATURATION OF THE MAHA BETA-SUBUNIT.
CC -1- PATHWAY: Methylamine utilization.
CC
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CC
CC EMBL: Y10436; CAA71460.1;
DR EMBL; AEC:6966; AA01416.1;
DR TIGR; CB01925;
DR HAXAP; MF_00074;
DR InterPro; IPR003682; GIDB.
DR InterPro; IPR000051; SAM_bind.
DR Pfam; PF02527; GIDB; 1.
DR Pfam; PF004441; GIDB; 1.
DR TIGRFAMs; TIGR00338; gids; 1.
DR Transferase; Methyltransferase.
SQ SEQUENCE 204 AA; 22617 MW; EFTGBD16C18F445E CRC64;

Query Match 0.9%; Score 7; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RA MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Pankett G. III, Burling V., Mau R., Claesner J.C.,
RA Rose D.C., Maynew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackett C., Klink S., Boutin A., Shao Y., Miller B.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamocis K.,
RA Apodaca J., Anantharaman T.S., Lin T., Yen G., Schwartz D.C.,
RA Welch R.A., Balthner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).
RN
RC SPECIES=Es. coli; STRAIN=O157:H7 / RIMD 0503952;
RC MEDLINE=2156233; PubMed=11258756;
RA Hayash T., Makino K., Chishiro M., Kirokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka Y., Tobe T.,
RA Iida T., Takari H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kihara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 9:11-22(2002).
RN
RP SEQUENCE FROM N.A.
RP SPECIES=Es. flexneri; STRAIN=301 / Serotype 2a;
RC MEDLINE=2272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu C., Wang Y., Shen Y., Lu M., Wang T., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun Y., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang J., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157:H7."
RL Nucleic Acids Res. 30:4432-4441(2002).
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CC
DR EMBL; U00039; AAB18443.1; -
DR EMBL; AE000422; AAC76493.1; -
DR EMBL; AE016768; AAN82697.1; -
DR EMBL; AE005570; AAG58577.1; -
DR EMBL; AE002565; BAB37740.1; -
DR EMBL; AE015356; AAN44945.1; -
DR F1R; E86014; E86014; -
DR F1R; E86014; E86014; -
DR F1R; E91168; E91168; -
DR F1R; S47687; S47687; -
DR EColGene; ECol2214; ynfN.
KM Hypothetical protein; Complete proteome.
FT CONFLICT 56 L -> Q (IN REF. 3).
SQ SEQUENCE 208 AA; 23790 MW; 9409944326CECB9E CRC64;

Query Match 0.9%; Score 7; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 681 VGASLLEF 687
DB 163 VGASLLEF 169

RESULT 63
TRAR AGRVI STANDARD; PRT; 234 AA.
AC P33959;
CT 01-FEB-1994 (Rel. 28, Created)
CT 01-FEB-1994 (Rel. 28, Last sequence update)
CT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transcriptional activator protein trar.
GN TRAR.
```

```

OS Agrobacterium vitis (Rhizobium vitis).
CC Plasmid pT1638.
CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
CC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
CC NCBI_TaxID=373;
RN [1]_TaxID=373;
RP SEQUENCE FROM N.A.
RC STRAIN=2608;
RX MEDLINE=94281667; PubMed=8012036;
RA Fournier P., de Ruffray P., Otten L.;
RT "Natural instability of Agrobacterium vitis T1 plasmid due to unusual
RT duplication of a 2.3-kb DNA fragment."
RL Mol. Plant Microbe Interact. 7:164-172(1994).
CC
CC -1- FUNCTION: POSITIVE REGULATION OF CONJUGAL TRANSFER OF T1
CC PLASMIDS.
CC -1- SIMILARITY: BELONGS TO THE LUXE/UMPA FAMILY OF TRANSCRIPTIONAL
CC REGULATORS. AUTOINDUCER REGULATED SUBFAMILY.
CC
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CC
DR EMBL; Z22732; CA80423.1; -
DR EMBL; Z22733; CA80425.1; -
DR EMBL; Z22734; CA80427.1; -
DR F1R; S37463; S37463; -
DR InterPro; IPR005143; Autoind. bind.
DR InterPro; IPR005792; HTH_LuxR.
DR Pfam; PF03472; Autoind. bind. 1.
DR Pfam; PF00196; GntR_1.
DR PRODOM; PD0030307; HTH_LuxR; 1.
DR SMART; SM0042; HTH_LuxR; 1.
DR PROSITE; PS00622; HTH_LuxR_FAMILY; FALSE_NEG.
KM Transcription regulation; DNA-binding; Activator; Quorum sensing;
KM Conjugation; Plasmid.
FT DNA BIND 191 210 H-T-H MOTIF (BY SIMILARITY).
FT VARIANT 230 230 K -> R.
SQ SEQUENCE 234 AA; 26528 MW; 33997F03B284B859 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 LTLALAK 16
DB 224 LTLALAK 230

RESULT 64
MSA2_PLAFC STANDARD; PRT; 262 AA.
ID MSA2_PLAFC
AC 099317;
CT 01-OCT-1996 (Rel. 34, Created)
CT 01-OCT-1996 (Rel. 34, Last sequence update)
CT 01-OCT-1996 (Rel. 34, Last annotation update)
CT Merozoite surface antigen 2 precursor (MSA-2) (Allelic form 1).
GN MSA2.
OS Plasmodium falciparum (Isolate Camp / Malaysia).
CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
CC NCBI_TaxID=5835;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91218803; PubMed=2090943;
RA Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.;
RT "Sequence comparison of allelic forms of the Plasmodium falciparum
RT merozoite surface antigen MSA2."
RL Mol. Biochem. Parasitol. 43:211-220(1990).
CC
CC -1- FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT TO THE
CC EPITHELIAL CELL.
```

```
CC -1- SEQUENCE LOCATION: Attached to the membrane by a GPI-anchor
CC (potential)
CC -1- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.
CC -----
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CC -----
CC EMBL: M60186; AAA29687.1;
CC InterPro: IPR001136; NSA_2.
CC DR Pfam; PF00985; NSA_2.
CC KW Malattia; Membrane; Glycoprotein; Antigen; Signal; Repeat;
CC GPI-anchor; Mercotile.
CC FT SIGNAL 1 20 POTENTIAL.
CC FT SIGNAL 21 238 MEROZOITE SURFACE ANTIGEN 2
CC FT PROPEP 239 262 HYDROPHOBIC, REMOVED DURING MATURATION
CC (BY SIMILARITY).
CC FT DOMAIN 44 188 POLYMORPHIC REGION.
CC FT DOMAIN 91 93 POLY-TIR.
CC FT CARBOHYD 22 22 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 35 35 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 139 133 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 211 211 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 235 235 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 235 235 N-LINKED (GLCNAC...) (POTENTIAL).
CC SQ SEQUENCE 262 AA; 27374 MW; 72E0B3A3;5E9D164 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 262;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 GSGAGAS 259
DQ 59 GSGAGAS 65

RESULT 65
TRPA_MYCLE STANDARD; PRT; 270 AA.
ID TRPA_MYCLE STANDARD; PRT; 270 AA.
AC 09CC53;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Tyrocyphar synthase alpha chain (EC 4.2.1.20).
GN TRPA OR ML1273.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RA MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Sigleifer K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungai K., Basam D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Duthoy S., Fellwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagers K., Lacroix C., Mclennan C., Meule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream N.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
CC -1- FUNCTION: The alpha subunit is responsible for the acid cleavage
CC of indoleglycerol phosphate to indole and glyceraldehyde 3-
CC phosphate.
CC -1- CATALYTIC ACTIVITY: L-serine + 1-(indol-3-yl)glycerol 3-phosphate
CC = L-tryptophan + glyceraldehyde 3-phosphate.
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CC -1- PATHWAY: Tryptophan biosynthesis; fifth (last) step.
CC -1- SUBUNIT: Tetramer of two alpha and two beta chains (By
CC similarity).
CC -1- SIMILARITY: BELONGS TO THE TRPA FAMILY.
CC -----
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CC -----
CC EMBL: A583921; CAC31654.1;
CC DR PIR; C87068; C87068.
CC DR Lepisma; ML1273;
CC DR HAMAD; MF 00131;
CC DR InterPro: IPR003009; PFM enzyme.
CC DR InterPro: IPR002028; TRP synthase.
CC DR Pfam; PF00290; trp_synA; 1.
CC DR ProDom; PD001535; trp_synA; 1.
CC DR CIGRAME; TIGR00262; trpA; 1.
CC DR PROSITE; PS00167; TRP SYNTHASE ALPHA; 1.
CC KW Tyrocyphar biosynthesis; Lyase; Complete proteome.
CC SQ SEQUENCE 270 AA; 26330 MW; D5D3D9815D4CBAC CRC64;

Query Match 0.9%; Score 7; DB 1; Length 270;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 521 AYVMTYW 527
DQ 103 AYVMTYW 109

RESULT 65
TRPA_MYCTU STANDARD; PRT; 270 AA.
ID TRPA_MYCTU STANDARD; PRT; 270 AA.
AC 006130;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tyrocyphar synthase alpha chain (EC 4.2.1.20).
GN TRPA OR RV1613 OR M1648 OR MTCY01B2.05.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RA MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Sigleifer K., Gas S., Barry C.E. III, Tekela F.,
RA Adcock K., Basam D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagers K., Krogh A., Mclennan C., Meule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream N.A., Rogers J.,
RA Rutter S., Seeger K., Skelton J., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
CC -1- FUNCTION: The alpha subunit is responsible for the acid cleavage
CC of indoleglycerol phosphate to indole and glyceraldehyde 3-
CC phosphate.
CC -1- CATALYTIC ACTIVITY: L-serine + 1-(indol-3-yl)glycerol 3-phosphate
CC = L-tryptophan + glyceraldehyde 3-phosphate.
CC -1- whole genome comparison of Mycobacterium tuberculosis clinical and
CC laboratory strains.";
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RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: The alpha subunit is responsible for the aldol cleavage
CC of indoleglycerol phosphate to indole and glyceraldehyde 3-
CC phosphate.
CC -!- CATALYTIC ACTIVITY: D-serine + L-(indol-3-yl)-glycerol 3-phosphate
CC = D-tryptophan + glyceraldehyde 3-phosphate.
CC -!- PATHWAY: Tryptophan biosynthesis; fifth (last) step.
CC -!- SUBUNIT: Tetramer of two alpha and two beta chains (by
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE TRPA FAMILY.
CC -----
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CC -----
DR EMBL; Z55554; CAGC8990.1; -
DR EMBL; AE307028; AAK45917.1; -
DR PIR; C70557; C70557.
DR TIGR; M1648; -
DR Truncullist; Rv1613; -
DR HAMAP; MF_C0311; -
DR InterPro; IPR003303; FMN enzyme.
DR InterPro; IPR002028; Trp synthaseA.
DR Pfam; PF00290; trp_synA; 1.
DR ProDom; PD001535; trp_synthaseA; 1.
DR TIGRFAMs; TIGR00262; trpA; 1.
DR PROSITE; PS00167; TRP SYNTHASE ALPHA; 1.
DR TrpTophan_biosynthesis; Lysase; Complete proteome.
DR KW TrpTophan_biosynthesis; Lysase; Complete proteome.
DR SEQUENCE 270 AA; 27727 MW; 9855994F704A0C76 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 270;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 521 AVMWTY 527
Db 103 AVMWTY 109

RESULT 67
TRPA_MYCIT STANDARD; PRT; 271 AA.
AC 068906;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tryptophan synthase alpha chain (EC 4.2.1.20).
OS TRPA.
SN Mycobacterium intracellulare.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1767;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=atcc;
RA Alavi M.R.; Rouse D.A.; Morris S.L.;
RT "Nucleotide sequence and functional analysis of the tryptophan
RT synthase genes of Mycobacterium intracellulare."
RL Submitted (APR-1998) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: The alpha subunit is responsible for the aldol cleavage
CC of indoleglycerol phosphate to indole and glyceraldehyde 3-
CC phosphate.
CC -!- CATALYTIC ACTIVITY: D-serine + L-(indol-3-yl)-glycerol 3-phosphate
CC = L-tryptophan + glyceraldehyde 3-phosphate.
CC -!- PATHWAY: Tryptophan biosynthesis; fifth (last) step.
CC -!- SUBUNIT: Tetramer of two alpha and two beta chains (by
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE TRPA FAMILY.
CC -----

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CC -----
DR EMBL; AF057042; AAC11735.1; -
DR HSSP; P00929; ZTYS.
DR HAMAP; MF_C0131; -
DR InterPro; IPR003009; FMN enzyme.
DR InterPro; IPR002028; Trp synthaseA.
DR Pfam; PF00290; trp_synA; 1.
DR ProDom; PD001535; trp_synthaseA; 1.
DR TIGRFAMs; TIGR00262; trpA; 1.
DR PROSITE; PS00167; TRP SYNTHASE ALPHA; 1.
DR TrpTophan_biosynthesis; Lysase.
DR KW TrpTophan_biosynthesis; Lysase.
DR SEQUENCE 271 AA; 27804 MW; BA0E0C5C0786318 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 271;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 521 AVMWTY 527
Db 102 AVMWTY 108

RESULT 68
ZUPT_XANAC STANDARD; PRT; 272 AA.
AC 086R05;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Zinc transporter zupt.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
NCBI_TaxID=92829;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R.; Ferro J.A.; Reinach F.C.; Farah C.S.; Furlan L.R.;
RA Quaggio R.B.; Monteiro-Vitorello C.B.; Van Sluys M.A.; Almeida N.F.;
RA Alves L.M.C.; do Amaral A.M.; Bertolini M.C.; Camargo L.B.A.;
RA Camarotte G.; Camavar F.; Cardozo J.; Chamberg F.; Ciapina L.P.;
RA Cicarelli R.M.B.; Coutinho L.L.; Cursino-Santos J.R.; El-Dorri H.;
RA Faria J.B.; Ferreira A.J.S.; Ferreira R.C.C.; Ferro X.I.T.;
RA Fortighieri E.F.; Franco M.C.; Greggio C.C.; Gruber A.;
RA Katsuyama A.M.; Kishi L.T.; Leite R.P.; Lemos E.G.W.; Lemos M.V.P.;
RA Locali E.C.; Machado Y.A.; Madeira A.M.B.N.; Martinez-Rossi N.M.;
RA Martins E.C.; Meidanis J.; Menck C.F.M.; Miyaki C.Y.; Moon D.H.;
RA Moreira L.M.; Novo M.T.K.; Okura V.K.; Oliveira M.C.; Oliveira V.R.;
RA Pereira H.A.; Rossi A.; Seta C.A.D.; Silva C.; de Souza R.F.;
RA Spindola L.A.F.; Takita M.A.; Tamura R.E.; Teixeira E.C.; Tezza R.I.D.;
RA Trindade dos Santos M.; Truffi D.; Tsai S.M.; White F.F.;
RA Secual J.C.; Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nucleotide sequence and functional analysis of the tryptophan
RL synthase genes of Mycobacterium intracellulare."
CC -!- FUNCTION: Mediates zinc uptake. May also transport other divalent
CC cations (by similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE ZIP FAMILY. ZUPT SUBFAMILY.
CC -----
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CC -----

DR EMBL: AE011847; AAM36967.1; -

DR HAMAP: MF_00548; -

DR InterPro: IPR003689; Zn_transp.zip.

KW Pfam: PF02335; Zip_1.

FT TRANSPORT; Zinc transport; Transmembrane; Complete proteome.

FT TRANSMEM 10 32 POTENTIAL.

FT TRANSMEM 39 6 POTENTIAL.

FT TRANSMEM 76 35 POTENTIAL.

FT TRANSMEM 124 146 POTENTIAL.

FT TRANSMEM 186 178 POTENTIAL.

FT TRANSMEM 185 237 POTENTIAL.

FT TRANSMEM 211 233 POTENTIAL.

FT TRANSMEM 249 271 POTENTIAL.

SO SEQUENCE 272 AA; 28664 MW; 69FC1117470BFC87 CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 51;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 683 AVGASL 686

Pb 186 AVGASL 192

RESULT 69

MSA2_PLAF6 STANDARD; PRT; 274 AA.

ID MSA2_PLAF6

AC P50497;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Merozoite surface antigen 2 precursor (MSA-2).

GN MSA2.

OS Plasmodium falciparum (isolate K1316).

CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI_TaxID=57269;

RN (1)

RA MEDLINE=92178286; PubMed=1542312;

RT "Two novel alleles within subfamilies of the merozoite surface antigen 2 (MSA-2) of Plasmodium falciparum."

RL Mol. Biochem. Parasitol. 50:181-184(1992).

CC -1- FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT TO THE ERYTHROCYTE.

CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (potential).

CC -1- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.

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CC -----

DR EMBL: M73810; AAA29696.1; -

DR PIR: A45632; A45632.

DR InterPro: IPR001136; MSA_2.

KW Malaria; Merozoite; Glycoprotein; Antigen; Signal; Repeat;

KM GPI-anchor; Merozoite.

FT CHAIN 1 20 POTENTIAL.

FT CHAIN 21 250 MEROZOITE SURFACE ANTIGEN 2.

FT PROPEP 251 274 HYDROPHOBIC; REMOVED DURING MATURATION.

FT DOMAIN 44 200 POLYMORPHIC REGION.

FT DOMAIN 97 110 POLY-THR.

FT CARBOHYD 22 22 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 36 36 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 151 151 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 223 223 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 248 248 N-LINKED (GLCNAC...) (POTENTIAL).

SO SEQUENCE 274 AA; 28367 MW; 63C4CD1F07425D53 CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 51;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 253 GSGAGAS 259

Pb 59 GSGAGAS 65

RESULT 70

VCX6_EUGGR STANDARD; PRT; 274 AA.

ID VCX6_EUGGR

AC P48336;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical 32.3 kDa protein in RECL-ATPE intergenic region (ORF274).

CS Euglena gracilis.

OS Chloroplast.

CC Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.

OX NCBI_TaxID=3039;

FN (1)

RC SEQUENCE FROM N.A.

RP STRAIN=Z / UTEX 753;

RA MEDLINE=9347989; PubMed=8346031;

RA Hallick R.B., Hong L., Diager R.G., Favreau M.R., Montfort A., Orsat B., Spielmann A., Stutz E.;

RT "Complete sequence of Euglena gracilis chloroplast DNA."

RL Nucleic Acids Res. 21:3537-3544(1993).

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CC -----

DR EMBL: Z11874; -; NOT ANNOTATED; CDS.

DR EXBL: X70810; CA50124.1; -

DR PIR: S34543; S34543.

KW Chloroplast; Hypothetical protein.

SO SEQUENCE 274 AA; 32317 MW; 63C4CD1F07425D53 CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 51;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 128 LYUNIV 134

Pb 159 LYUNIV 165

RESULT 71

Y265_MYCPN STANDARD; PRT; 282 AA.

ID Y265_MYCPN

AC P75399;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein MG265 homolog (Al9_orf282).

GN MPN383 OR MP454.

CS Mycoplasma pneumoniae.

CC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.

OX NCBI_TaxID=2104;

FN (1)

RP SEQUENCE FROM N.A.
 SC STRAIN=ATCC 29342 / M129;
 RX MEDLINE=97105885; PubMed=6948633;
 RA Heremans R.;
 RA Heremans R.;
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 pneumoniae";
 RL Nucleic Acids Res. 24:4420-4449 (1996).
 CC -1- SIMILARITY: BELONGS TO THE COF/YHHA/YIDA/YIGL (E.COLI) / YGSE/YXEH
 (B.SUBTILIS) FAMILY.
 CC -----
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 CC -----
 CC EMBL: AEC00044; AAB96132.1;
 DR PIR: S33780; S33780.
 DR InterPro: IPR006179; HAD_SF_1TB.
 DR InterPro: IPR006179; HAD_SF_1TB.
 DR InterPro: IPR006179; HAD_SF_1TB.
 DR Pfam: PF00702; Hydrolase_1.
 DR TIGRfam: TIGR00059; COF-subfamily_1.
 DR TIGRfam: TIGR01484; HAD_SF_1TB; 1.
 DR PROSITE: PS01228; COF_1; 1.
 DR PROSITE: PS01229; COF_2; 1.
 DR PROSITE: PS01229; COF_2; 1.
 KM Hypothetical protein: Complete proteome.
 SQ SEQUENCE 282 AA; 3193 MW; 0095F9131B1B04D CRC64;
 Query Match 0.9%; Score 7; DB 1; Length 282;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 81 IRTTQF 87
 DB 52 -RTTQF 58
 RESULT 72
 ID UPGA_ECOLI STANDARD; PRT; 295 AA.
 AC P10905;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE SN-glycerol-3-phosphate transport system permease protein ugpA.
 GN UPGA OR B3452.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN (1)
 RF SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=88996498; PubMed=3062313;
 RA Overduin P.; Boos W.; Tomaszewski J.;
 RA "Nucleotide sequence of the ugp genes of Escherichia coli K-12;
 RA homology to the talose system";
 RL Mol. Microbiol. 2:767-775 (1988).
 CC [2]
 CC SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=94316500; PubMed=8041620;
 RA Sofia H.J.; Sorland V.; Daniels D.L.; Plunkett G. III; Blatter F.P.;
 RA "Analysis of the Escherichia coli genome. V. DNA sequence of the
 RA region from 76.0 to 81.5 minutes";
 RL Nucleic Acids Res. 22:2576-2586 (1994).
 CC -1- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
 CC FOR SN-GLYCEROL-3-PHOSPHATE; PROBABLY RESPONSIBLE FOR THE
 CC TRANSLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC (potential).
 CC -1- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT
 CC SYSTEM PERMEASE FAMILY, MALFG SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: X13141; CA3:532.1;
 DR EMBL: U00032; AAB18427.1;
 DR EMBL: AEC00421; AAC76477.1;
 DR PIR: S03781; WMECQA.
 DR EcoGene: EG-1046; UPGA.
 DR InterPro: IPR000515; BPD_transp.
 DR Pfam: PF00528; BPD_transp_1.
 DR PROSITE: PS00432; BPD_TRANSF_INN_MEMB_1.
 DR Transmembrane: Inner membrane; Transport; Complete proteome.
 DR TRANSMEM 12 32
 FT TRANSMEM 10 130 POTENTIAL.
 FT TRANSMEM 157 177 POTENTIAL.
 FT TRANSMEM 208 228 POTENTIAL.
 FT TRANSMEM 263 283 POTENTIAL.
 SQ SEQUENCE 295 AA; 33264 MW; C08765DE0FB647A9 CRC64;
 Query Match 0.9%; Score 7; DB 1; Length 295;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 451 VAPVAA 457
 DB 117 VAPVAA 123
 RESULT 73
 ID UPK2_CLOAB STANDARD; PRT; 307 AA.
 AC O97X66;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Putative undecaprenol kinase 2 (EC 2.7.1.66) (Bactiracin resistance
 DE protein 2).
 GN UPK2 OR BACAZ OR CAC0963.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1488;
 RN (1)
 RF SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RA Noelling U.; Breton G.; Omelchenko M.V.; Makarova K.S.; Zeng C.;
 RA Gibson R.; Lee H.K.; Dubois O.; Qiu D.; Hittner W.; Wolf Y.I.;
 RA Tatusov R.; Sabathe F.; Doucette-Stamm L.; Socacile P.; Daly M.J.;
 RA Bennett G.N.; Koonin E.V.; Smith D.R.;
 RA "Genome sequence and comparative analysis of the solvent-producing
 RA bacterium Clostridium acetobutylicum";
 RL J. Bacteriol. 183:4823-4838 (2001).
 CC -1- FUNCTION: Probably phosphorylates undecaprenol to undecaprenyl
 CC phosphate. Confers resistance to bacteriicin (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + undecaprenyl = ADP + undecaprenyl
 CC phosphate.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- MISCELLANEOUS: Bactiracin is thought to be involved in inhibition
 CC of peptidoglycan synthesis by sequestering undecaprenyl
 CC disphosphate reducing the pool of lipid carrier available.
 CC -1- SIMILARITY: BELONGS TO THE UPK FAMILY.

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CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: A500761; AAK78939.1; -
DR PIR: H97018; H97018.
DR HAVAP: MF_01006; - 1.
DR InterPro: IPR003824; BACA.
DR Pfam: PF02673; BACA. 1.
DR TIGRfam: TIGR00753; under kin back: 1.
KW Transferase; Kinase; Antibiotic resistance; Transmembrane;
KW Complete proteome.
FT TRANSMEM 19 41 POTENTIAL.
FT TRANSMEM 36 75 POTENTIAL.
FT TRANSMEM 116 135 POTENTIAL.
FT TRANSMEM 145 164 POTENTIAL.
FT TRANSMEM 212 234 POTENTIAL.
FT TRANSMEM 249 271 POTENTIAL.
FT TRANSMEM 254 335 POTENTIAL.
SC SEQUENCE 307 AA; 33640 MW; 32FF21C78024F34D CRC64;

Query Match 0.9%; Score 7; DB 1; Length 307;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 652 GASLIF 688
Db 235 GASLIF 241

RESULT 74
Y011_RICPR STANDARD; PRT: 341 AA.
ID Y011_RICPR
AC CEZED;
DT 30-MAY-2000 (Rel. 39, Last sequence update);
DT 30-MAY-2000 (Rel. 39, Last sequence update);
DT 16-OCT-2001 (Rel. 40, Last annotation update);
DE Hypothetical 37.5 kDa protein P011..
GN P011.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
CX NCBI_TaxID=782;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=Madrid B;
RX MEDLINE=99039493; PubMed=9821893;
RA Anderson S.G.E., Zorrodipour A., Anderson C.O.,
RA Sicheit-Ponten T., Alsmark U.C.K., Podowski R.M., Meslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria."
RL Nature 396:133-140(1998).
CC -1- SIMILARITY: BELONGS TO THE UPF034 (NIFR3/SXM) FAMILY.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: A0235270; CA14483.1; -
DR PIR: D71708; D71708.
DR InterPro: IPR003009; FMN enzyme.
DR InterPro: IPR004652; NIFR3 YhdG.
DR InterPro: IPR001269; UPF0034.
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DR Pfam: PF01267; Dns: 1.
DR TIGRfam: TIGR00737; NIFR3 YhdG: 1.
DR EPOSITE: PS01136; UPF0034; 1.
KW Hypothetical protein; Complete proteome.
SC SEQUENCE 341 AA; 37519 MW; F7E8B77436C34D3 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 342;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 LNYDML 370
Db 2 LNYDML 8

RESULT 75
A85C_MYCAV STANDARD; PRT: 352 AA.
ID A85C_MYCAV
AC 052972;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 85-C precursor (85C) (Antigen 85 complex C) (Ag85C) (Mycobyl)
DE transferase 85C) (EC 2.3.1.-) (Fibronectin-binding protein C).
GN FBPC.
OS Mycobacterium avium.
OC Bacteria; Actinobacteria; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
CX NCBI_TaxID=1764;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15769;
RX MEDLINE=97427949; PubMed=9284137;
RA Ohara N., Ohara-Wada N., Kitaoka H., Nishiyama T., Matsumoto S.,
RA Yamada T.;
RT "Analysis of the gene encoding the antigen 85 complex and MPT51 from
RT Mycobacterium avium."
RL Infect. Immun. 65:3680-3685(1997).
CC -1- FUNCTION: PROTEINS OF THE ANTIGEN 85 COMPLEX ARE RESPONSIBLE FOR
CC THE HIGH AFFINITY OF MYCOBACTERIA TO FIBRONECTIN. POSSESSES A
CC MYCOBACTERIAL TRANSFERASE ACTIVITY REQUIRED FOR THE BIOSYNTHESIS OF
CC TREHALOSE DIMYCOLATE (CORD FACTOR), A DOMINANT STRUCTURE NECESSARY
CC FOR MAINTAINING CELL WALL INTEGRITY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: TO OTHER MYCOBACTERIUM A85 ANTIGENS AND TO THE
CC N-TERMINAL OF C.GLUTAMINUM PSI PROTEIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: D87323; BAA24161.1; -
DR HSSP: P11953; IDOY.
DR InterPro: IPR000801; Esterase_Put.
DR Pfam: PF00756; Esterase; 1.
KW Transferase; Acyltransferase; Antigen; Signal.
FT CHAIN 1 46 POTENTIAL.
FT ACT SITE 170 352 ANTIGEN 85-C.
FT ACT SITE 170 170 BY SIMILARITY.
FT ACT SITE 274 274 BY SIMILARITY.
FT ACT_SITE 306 306 BY SIMILARITY.
SC SEQUENCE 352 AA; 37756 MW; A29277C8550D6C4A CRC64;

Query Match 0.9%; Score 7; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 680 AVGASL 686
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D5 25 AVGASLU 31

Search completed: November 5, 2003, 15:25:42
Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2003, 15:23:18 ; Search time 21 Seconds

(without alignments)
1644,079 Million cell updates/sec

File: US-09-978-423a-375

Percent score: 816
Sequence: 1 MLNSVLLMTALAIFKFTL.....TSGGQNSITNLPKHSITRV 816Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 328727 seqs, 4230858 residues

Word size: 0

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database:

1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/5A-COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/5B-COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCITUS-COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	6.1	843	4	US-09-431-356C-20 Sequence 27, Appl
2	48	5.3	836	4	US-09-431-356C-21 Sequence 21, Appl
3	35	4.3	553	4	US-09-431-356C-24 Sequence 24, Appl
4	32	3.9	823	4	US-09-431-356C-22 Sequence 22, Appl
5	32	3.9	848	4	US-09-431-356C-22 Sequence 22, Appl
6	12	1.5	535	1	US-08-445-050-4 Sequence 4, Appl
7	12	1.5	535	2	US-08-445-050-5 Sequence 4, Appl
8	12	1.5	546	1	US-08-445-050-5 Sequence 5, Appl
9	12	1.5	546	2	US-08-445-050-5 Sequence 5, Appl
10	12	1.5	568	1	US-08-445-050-6 Sequence 6, Appl
11	12	1.5	568	2	US-08-445-050-6 Sequence 6, Appl
12	12	1.5	571	6	5200183-17 Parent No. 5200183
13	12	1.5	668	1	US-08-445-050-9 Sequence 9, Appl
14	12	1.5	668	2	US-08-445-050-9 Sequence 9, Appl
15	12	1.5	722	1	US-08-347-718B-1 Sequence 1, Appl
16	12	1.5	722	1	US-08-445-050-3 Sequence 3, Appl
17	12	1.5	722	1	US-08-445-050-3 Sequence 7, Appl
18	12	1.5	722	2	US-08-482-262-1 Sequence 1, Appl
19	12	1.5	722	2	US-08-204-691-3 Sequence 3, Appl
20	12	1.5	722	2	US-08-204-691-3 Sequence 7, Appl
21	12	1.5	722	4	US-09-355-295B-4 Sequence 4, Appl
22	12	1.5	722	6	5200183-3 Parent No. 5200183
23	12	1.5	742	1	US-08-347-718B-2 Sequence 2, Appl
24	12	1.5	742	2	US-08-482-262-2 Sequence 2, Appl
25	12	1.5	745	6	5200183-2 Parent No. 5200183
26	12	1.5	745	1	US-08-445-050-2 Sequence 2, Appl
27	12	1.5	745	2	US-08-204-691-2 Sequence 2, Appl

28	12	1.5	745	3	US-08-370-223-13 Sequence 13, Appl
29	12	1.5	745	4	US-09-355-295B-3 Sequence 3, Appl
30	12	1.5	747	4	US-09-347-878B-32 Sequence 32, Appl
31	9	1.1	539	3	US-09-264-737-1 Sequence 1, Appl
32	9	1.1	566	3	US-09-264-737-2 Sequence 2, Appl
33	9	1.1	584	2	US-08-845-295A-2 Sequence 2, Appl
34	9	1.1	584	3	US-09-140-931-2 Sequence 2, Appl
35	9	1.1	584	3	US-09-146-661-2 Sequence 2, Appl
36	9	1.1	584	3	US-09-150-515-2 Sequence 2, Appl
37	9	1.1	597	1	US-08-462-884A-1 Sequence 1, Appl
38	9	1.1	597	2	US-08-461-881B-1 Sequence 1, Appl
39	9	1.1	605	1	US-09-123-960-1 Sequence 1, Appl
40	9	1.1	605	1	US-08-462-884A-3 Sequence 3, Appl
41	9	1.1	605	2	US-08-461-881B-3 Sequence 3, Appl
42	9	1.1	605	2	US-09-123-960-3 Sequence 3, Appl
43	9	1.1	637	4	US-09-347-878B-34 Sequence 34, Appl
44	8	1.0	137	3	US-08-747-221B-11 Sequence 11, Appl
45	8	1.0	137	3	US-09-005-051-11 Sequence 11, Appl
46	8	1.0	244	3	US-08-827-171B-8 Sequence 8, Appl
47	8	1.0	528	3	US-08-747-221B-37 Sequence 37, Appl
48	8	1.0	528	3	US-09-005-051-37 Sequence 37, Appl
49	8	1.0	563	3	US-08-362-525-12 Sequence 12, Appl
50	8	1.0	570	3	US-08-747-221B-54 Sequence 54, Appl
51	8	1.0	570	3	US-08-747-221B-55 Sequence 55, Appl
52	8	1.0	570	3	US-09-005-051-54 Sequence 54, Appl
53	8	1.0	575	3	US-09-003-051-55 Sequence 55, Appl
54	8	1.0	575	3	US-08-348-920-1 Sequence 1, Appl
55	8	1.0	595	3	US-08-348-920-2 Sequence 2, Appl
56	8	1.0	595	3	US-08-747-221B-31 Sequence 31, Appl
57	8	1.0	595	3	US-09-005-051-31 Sequence 31, Appl
58	8	1.0	596	3	US-08-747-221B-25 Sequence 25, Appl
59	8	1.0	596	3	US-09-005-051-25 Sequence 25, Appl
60	8	1.0	723	6	5200183-4 Parent No. 5200183
61	8	1.0	767	4	US-09-252-991A-28373 Sequence 28373, A
62	8	1.0	894	4	US-10-060-333-4 Sequence 4, Appl
63	8	1.0	951	1	US-08-308-086-8 Sequence 8, Appl
64	7	0.9	96	1	US-08-167-035-17 Sequence 17, Appl
65	7	0.9	96	1	US-08-208-887A-17 Sequence 17, Appl
66	7	0.9	96	2	US-08-479-078-20 Sequence 20, Appl
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68	7	0.9	96	4	US-09-280-598-19 Sequence 19, Appl
69	7	0.9	96	4	US-09-820-754-25 Sequence 25, Appl
70	7	0.9	99	3	US-08-956-652-25 Sequence 25, Appl
71	7	0.9	99	3	US-08-956-652-25 Sequence 25, Appl
72	7	0.9	99	3	US-08-956-652-25 Sequence 25, Appl
73	7	0.9	99	3	US-08-956-652-25 Sequence 25, Appl
74	7	0.9	103	3	US-08-948-547-25 Sequence 25, Appl
75	7	0.9	103	3	US-08-747-221B-8 Sequence 8, Appl
76	7	0.9	117	4	US-08-976-063E-12 Sequence 12, Appl
77	7	0.9	147	4	US-09-482-273-209 Sequence 209, Appl
78	7	0.9	163	4	US-09-252-991A-22533 Sequence 22533, A
79	7	0.9	178	3	US-08-478-316-24 Sequence 24, Appl
80	7	0.9	178	4	US-09-019-793A-24 Sequence 24, Appl
81	7	0.9	178	5	PCR-US95-10904-71 Sequence 71, Appl
82	7	0.9	198	4	US-09-252-991A-19680 Sequence 19680, A
83	7	0.9	207	3	US-09-068-960-15 Sequence 15, Appl
84	7	0.9	255	6	52-5908-9 Parent No. 5215909
85	7	0.9	334	4	US-09-252-991A-18795 Sequence 18795, A
86	7	0.9	339	4	US-09-328-1952-7424 Sequence 7424, A
87	7	0.9	388	4	US-09-596-196-4 Sequence 4, Appl
88	7	0.9	418	1	US-08-176-427B-10 Sequence 10, Appl
89	7	0.9	418	1	US-08-356-060A-12 Sequence 12, Appl
90	7	0.9	418	3	US-08-946-329A-18 Sequence 18, Appl
91	7	0.9	418	3	US-08-967-357A-18 Sequence 18, Appl
92	7	0.9	418	3	US-08-460-900C-12 Sequence 12, Appl
93	7	0.9	418	3	US-08-729-743A-18 Sequence 18, Appl
94	7	0.9	418	3	US-08-757-230A-7 Sequence 7, Appl
95	7	0.9	418	3	US-08-674-509B-12 Sequence 12, Appl
96	7	0.9	418	3	US-08-954-698-12 Sequence 12, Appl
97	7	0.9	418	3	US-08-349-498-18 Sequence 18, Appl
98	7	0.9	418	4	US-08-957-874-12 Sequence 12, Appl
99	7	0.9	418	4	US-09-325-256-21 Sequence 21, Appl
100	7	0.9	418	4	US-08-700-393-7 Sequence 7, Appl

ALIGNMENTS

RESULT 1

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US-09-491-356C-20
; Sequence 22, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Gims, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491.356C
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 943
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-491-356C-20

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Query Match

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Best Local Similarity 5.1%; Score 50; DB 4; Length 843;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY

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DB

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RESULT 2
US-09-491-356C-21
; Sequence 21, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Gims, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491.356C
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 836
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-491-356C-21

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Query Match

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QY

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DB

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RESULT 3
US-09-491-356C-24

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; Sequence 24, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Gims, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491.356C
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; NUMBER OF SEQ ID NOS: 24
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; SEQ ID NO 24
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-491-356C-24

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Query Match

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Best Local Similarity 4.3%; Score 35; DB 4; Length 553;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY

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DB

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RESULT 4
US-09-491-356C-23
; Sequence 23, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Gims, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491.356C
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 823
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-491-356C-23

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Query Match

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Best Local Similarity 3.9%; Score 32; DB 4; Length 823;
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QY

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412 SVSNFVDNLVGYPEGCKTJRETIKXYVTWAD 443
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DB

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RESULT 5
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; Sequence 22, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Gims, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13

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US-09-491-356C-24

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FILE REFERENCE: 9465.6US1;
CURRENT APPLICATION NUMBER: US/09/491.356C
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: PCT/US99/09365
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 60/093,465
PRIOR FILING DATE: 1998-04-29
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patent version 3.1
SEQ ID NO: 22
LENGTH: 848
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-491-356C-22

Query Match
Best Local Similarity 100.0%; Score 32; DB 4; Length 848;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 399 SVSNFVDNLGYGEECKDILREIKRYTDMAD 430
DB 432 SVSNFVDNLGYGEECKDILREIKRYTDMAD 463

RESULT 6
US-08-445-050-4
Sequence 4, Application US/08445050
Patent No. 5763739
GENERAL INFORMATION:
APPLICANT: Blaeckberg, Lars
APPLICANT: Edlund, Michael
APPLICANT: Hansson, Lennart
APPLICANT: Herneil, Olie
APPLICANT: Lundberg, Lennart
APPLICANT: Stromqvist, Mats
APPLICANT: Toerneil, Jan
TITLE OF INVENTION: No. 5763739el Polypeptides
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445.050
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/204.691
FILING DATE:
APPLICATION NUMBER: SE 930686-4
FILING DATE: 01-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300722-7
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Steerner Ph.D., Richard J
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-850
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)354-813
TELEFAX: (212)354-813
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Mammary gland
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..535
OTHER INFORMATION: /label= Variant_A
US-08-445-050-4

Query Match
Best Local Similarity 100.0%; Score 12; DB 1; Length 535;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YMTNFAKTGDPN 537
DB 467 YMTNFAKTGDPN 478

RESULT 7
US-08-204-691-4
Sequence 4, Application US/08204691
Patent No. 5827683
GENERAL INFORMATION:
APPLICANT: Blaeckberg, Lars
APPLICANT: Edlund, Michael
APPLICANT: Hansson, Lennart
APPLICANT: Herneil, Olie
APPLICANT: Lundberg, Lennart
APPLICANT: Stromqvist, Mats
APPLICANT: Toerneil, Jan
TITLE OF INVENTION: No. 5827683el Polypeptides
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204.691
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 930686-4
FILING DATE: 01-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300722-7
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Steerner Ph.D., Richard J
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-850
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)819-8783
TELEFAX: (212)354-8113
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens

TISSUE TYPE: Mammary gland
FEATURE: Peptide
NAME/KEY: Peptide
LOCATION: 1..535
OTHER INFORMATION: /label= Variant_A
US-08-204-691-4

Query Match 1.5%; Score 12; DB 2; Length 535;
Best Local Similarity 100.0%; Pred. No. 3,0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 WMTNFAKTGDPN 537
DB 467 WMTNFAKTGDPN 478

RESULT 8
US-08-445-050-5
Sequence 5, Application US/08445050
Patent No. 5763729
GENERAL INFORMATION:
APPLICANT: Blackberg, Lars
APPLICANT: Edlund, Michael
APPLICANT: Hansson, Lennart
APPLICANT: Herrell, Olle
APPLICANT: Lundberg, Lennart
APPLICANT: Stromqvist, Mats
APPLICANT: Toerrell, Jan
TITLE OF INVENTION: No. 5763739el Polypeptides
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,050
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/204,691
FILING DATE:
APPLICATION NUMBER: SE 9300686-4
FILING DATE: 01-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300722-7
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sterner Ph.D., Richard J
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-850
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)8-9-8783
TELEFAX: (212)354-8113
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORGANISM: Homo sapiens
TISSUE TYPE: Mammary gland
FEATURE:
NAME/KEY: Peptide

LOCATION: 1..546
OTHER INFORMATION: /label= Variant_B
US-08-445-050-5

Query Match 1.5%; Score 12; DB 1; Length 546;
Best Local Similarity 100.0%; Pred. No. C.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 WMTNFAKTGDPN 537
DB 467 WMTNFAKTGDPN 478

RESULT 9
US-08-204-691-5
Sequence 5, Application US/08204691
Patent No. 5827683
GENERAL INFORMATION:
APPLICANT: Blackberg, Lars
APPLICANT: Edlund, Michael
APPLICANT: Hansson, Lennart
APPLICANT: Herrell, Olle
APPLICANT: Lundberg, Lennart
APPLICANT: Stromqvist, Mats
APPLICANT: Toerrell, Jan
TITLE OF INVENTION: No. 5827683el Polypeptides
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,691
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300686-4
FILING DATE: 01-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300722-7
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sterner Ph.D., Richard J
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-850
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)819-8783
TELEFAX: (212)354-8113
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Mammary gland
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..546
OTHER INFORMATION: /label= Variant_B
US-08-204-691-5

Query Match 1.5%; Score 12; DB 2; Length 546;

Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 526 YMTNPAKTGDPN 537
|||||
DB 467 YMTNPAKTGDPN 478

RESULT 10

US-08-445-050-6
Sequence 6, Application US/08445056
Patent No. 5763739
GENERAL INFORMATION:
APPLICANT: Blacberg, Lars
APPLICANT: Edlund, Michael
APPLICANT: Hansson, Lennart
APPLICANT: Herneil, Oile
APPLICANT: Lundberg, Jemart
APPLICANT: Stromqvist, Mats
APPLICANT: Toernell, Jan
TITLE OF INVENTION: No. 5763739el Polypeptides
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/445,050
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/204,691
FILING DATE:
FILING DATE: 04-MAR-1993
APPLICATION NUMBER: SE 9300686-4
FILING DATE: 01-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300722-7
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Steiner Ph.D., Richard J
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1:03326-850
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)819-8783
TELEFAX: (212)354-8113
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHECAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSE TYPE: Mammary gland
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..568
OTHER INFORMATION: /label= Variant_C
US-08-445-050-6

Query Match 1.5%; Score 12; DB 1; Length 568;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 526 YMTNPAKTGDPN 537
|||||
DB 467 YMTNPAKTGDPN 478

RESULT 11

US-08-204-691-6
Sequence 6, Application US/08204691
Patent No. 5827683
GENERAL INFORMATION:
APPLICANT: Blacberg, Lars
APPLICANT: Edlund, Michael
APPLICANT: Hansson, Lennart
APPLICANT: Herneil, Oile
APPLICANT: Lundberg, Jemart
APPLICANT: Stromqvist, Mats
APPLICANT: Toernell, Jan
TITLE OF INVENTION: No. 5827683el Polypeptides
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,691
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300686-4
FILING DATE: 01-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300722-7
FILING DATE: 04-MAR-1993
APPLICATION NUMBER: SE 9300686-4
FILING DATE: 01-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Steiner Ph.D., Richard J
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1:03326-850
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)819-8783
TELEFAX: (212)354-8113
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHECAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSE TYPE: Mammary gland
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..568
OTHER INFORMATION: /label= Variant_C
US-08-204-691-6

Query Match 1.5%; Score 12; DB 2; Length 568;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 526 YMTNPAKTGDPN 537
|||||
DB 467 YMTNPAKTGDPN 478

RESULT 12
52c0183-17
PATENT No. 5200183
APPLICANT: TANG, JORDAN J.N.; WANG, CHI-SUN
TITLE OF INVENTION: RECOMBINANT BILE SALT ACTIVATED LIPASES
NUMBER OF SEQUENCES: 22
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/537,426
FILING DATE: 12-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 564,635
FILING DATE: 04-MAR-1990
APPLICATION NUMBER: 122,410
FILING DATE: 19-NOV-1987
SEQ ID NO: 17
LENGTH: 571
52c0183-17

Query Match 1.5%; Score 12; DB 6; Length 571;
Best Local Similarity 100.0%; Pred. No. 3,0029;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 526 YWTFNFAKTGDPN 537
DB 467 YWTFNFAKTGDPN 478

RESULT 13
US-08-445-050-9
Sequence 9, Application US/08445050
PATENT No. 5763738
GENERAL INFORMATION:
APPLICANT: Blaeckberg, Lars
APPLICANT: Edlund, Michael
APPLICANT: Hansson, Lennart
APPLICANT: Hernell, Oile
APPLICANT: Lundberg, Lennart
APPLICANT: Stromqvist, Mats
APPLICANT: Toernell, Jan
TITLE OF INVENTION: No. 5763739e1 Polypeptides
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,050
FILING DATE:
CLASSIFICATION: 83C
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/204,691
FILING DATE:
APPLICATION NUMBER: SE 9300686-4
FILING DATE: 01-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300722-7
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Steiner Ph.D., Richard J
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-850
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)819-8783
TELEFAX: (212)354-8113
INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 668 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-445-050-9

Query Match 1.5%; Score 12; DB 1; Length 668;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 526 YWTFNFAKTGDPN 537
DB 490 YWTFNFAKTGDPN 501

RESULT 14
US-08-204-691-9
Sequence 9, Application US/08204691
PATENT No. 5827683
GENERAL INFORMATION:
APPLICANT: Blaeckberg, Lars
APPLICANT: Edlund, Michael
APPLICANT: Hansson, Lennart
APPLICANT: Hernell, Oile
APPLICANT: Lundberg, Lennart
APPLICANT: Stromqvist, Mats
APPLICANT: Toernell, Jan
TITLE OF INVENTION: No. 5827683e1 Polypeptides
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,691
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300686-4
FILING DATE: 01-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300722-7
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Steiner Ph.D., Richard J
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-850
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)819-8783
TELEFAX: (212)354-8113
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 668 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-204-691-9

Query Match 1.5%; Score 12; DB 2; Length 668;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 526 YWTFNFAKTGDPN 537
DB 467 YWTFNFAKTGDPN 478

DB 493 YWTNFAKTGDPN 501

RESULT 15

US-08-347-718B-1

Sequence 1, Application US/09347718B

Patent No. 5696087

GENERAL INFORMATION:

APPLICANT: Wang, Chu-San

APPLICANT: Tang, Jordan J.N

TITLE OF INVENTION: METHOD FOR REDUCING INTESTINAL ABSORPTION OF CHOLESTEROL

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrea L. Fabsi

STREET: 2800 One Atlantic Center

STREET: 1201 West Peachtree Street

CITY: Atlanta

STATE: Georgia

COUNTRY: USA

ZIP: 30309-3450

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/347,718B

FILING DATE: December 1, 1994

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Patrea, Patrea L.

REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: OMR-F50

TELECOMMUNICATION INFORMATION:

TELEPHONE: (404) 873-8794

TELEFAX: (404) 873-8795

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 722 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Protein

HYPOTHETICAL: NO

FRAGMENT TYPE: Internal

US-08-347-718B-1

Query Match 1.5% Score 12; EB 1; Length 722;

Best Local Similarity 100.0%; Pred. No. 0.0037;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTNFAKTGDPN 537

DB 467 YWTNFAKTGDPN 478

RESULT 16

US-08-445-050-3

Sequence 3, Application US/08445050

Patent No. 5763739

GENERAL INFORMATION:

APPLICANT: Blaeckberg, Lars

APPLICANT: Edlund, Michael

APPLICANT: Hansson, Lennart

APPLICANT: Hernell, Olle

APPLICANT: Lundberg, Lennart

APPLICANT: Stromqvist, Mats

APPLICANT: Toernell, Jan

TITLE OF INVENTION: No. 5763739e1 Polypeptides

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: White & Case

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: United States

ZIP: 10036-2787

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/445,050

FILING DATE:

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/204,691

FILING DATE:

APPLICATION NUMBER: SE 9300686-4

FILING DATE: 01-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE 9300722-7

FILING DATE: 04-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Steiner Ph.D., Richard J

REGISTRATION NUMBER: 35,372

REFERENCE/DOCKET NUMBER: 1103326-850

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 819-8783

TELEFAX: (212) 354-8113

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 722 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

TISSUE TYPE: Mammary gland

US-08-445-050-3

Query Match 1.5% Score 12; DB 1; Length 722;

Best Local Similarity 100.0%; Pred. No. 0.0037;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTNFAKTGDPN 537

DB 467 YWTNFAKTGDPN 478

RESULT 17

US-08-445-050-7

Sequence 7, Application US/08445050

Patent No. 5763739

GENERAL INFORMATION:

APPLICANT: Blaeckberg, Lars

APPLICANT: Edlund, Michael

APPLICANT: Hansson, Lennart

APPLICANT: Hernell, Olle

APPLICANT: Lundberg, Lennart

APPLICANT: Stromqvist, Mats

APPLICANT: Toernell, Jan

TITLE OF INVENTION: No. 5763739e1 Polypeptides

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: White & Case

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: United States

ZIP: 10036-2787

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible


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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/445,053
/ FILING DATE:
/ CLASSIFICATION: 80C
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/204,691
/ FILING DATE:
/ APPLICATION NUMBER: SE 9300686-4
/ FILING DATE: 01-MAR-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: SE 9300722-7
/ FILING DATE: 04-MAR-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Steiner Ph.D., Richard J
/ REGISTRATION NUMBER: 35,372
/ REFERENCE/DOCKET NUMBER: 1103326-850
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)8-9-8783
/ TELEFAX: (212)354-8113
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 722 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHEICAL: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
/ TISSUE TYPE: Mammary gland
/ FEATURE:
/ NAME/KEY: Peptide
/ LOCATION: 1..722
/ OTHER INFORMATION: /label= Variant_N
/
/ US-08-445-050-7
/
Query Match 1.5%; Score 12; DB 1; Length 722;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
QY 526 YWTFNFAKTGDPN 537
DB 467 YWTFNFAKTGDPN 478
/
RESULT 18
/ US-08-482-262-1
/ Sequence 1, Application US/08482262
/ Patent No. 5821226
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Chu-Sar
/ APPLICANT: Tang, Jordan C.N
/ TITLE OF INVENTION: BAL C-TAIL DRUG DELIVERY MOLECULES
/ NUMBER OF SEQUENCES: 3
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Patrea L., Pabst
/ STREET: 2800 One Atlantic Center
/ STREET: 1201 West Peachtree Street
/ CITY: Atlanta
/ STATE: Georgia
/ COUNTRY: USA
/ ZIP: 30309-3450
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/482,262
/ FILING DATE: June 7, 1993
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:

```

```

/ NAME: Pabst, Patrea L.
/ REGISTRATION NUMBER: 31,284
/ REFERENCE/DOCKET NUMBER: OMRF:51
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (404) 873-8794
/ TELEFAX: (404) 873-8795
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 722 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHEICAL: NO
/ FRAGMENT TYPE: Internal
/
/ US-08-482-262-1
/
Query Match 1.5%; Score 12; DB 2; Length 722;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
QY 526 YWTFNFAKTGDPN 537
DB 467 YWTFNFAKTGDPN 478
/
RESULT 19
/ US-08-204-691-3
/ Sequence 3, Application US/08204691
/ Patent No. 5827683
/ GENERAL INFORMATION:
/ APPLICANT: Blaeckberg, Lars
/ APPLICANT: Edlund, Michael
/ APPLICANT: Hansson, Lemnart
/ APPLICANT: Hennell, Olle
/ APPLICANT: Lundberg, Lennart
/ APPLICANT: Stromqvist, Mats
/ APPLICANT: Toernell, Jan
/ TITLE OF INVENTION: No. 5827683el Polypeptides
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: White & Case
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: United States
/ ZIP: 10036-2787
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/204,691
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: SE 9300686-4
/ FILING DATE: 01-MAR-1993
/ APPLICATION NUMBER: SE 9300722-7
/ FILING DATE: 04-MAR-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Steiner Ph.D., Richard J
/ REGISTRATION NUMBER: 35,372
/ REFERENCE/DOCKET NUMBER: 1103326-850
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)819-8783
/ TELEFAX: (212)354-8113
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 722 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear

```

MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Mammary Gland
US-08-204-691-3

Query Match 1.5%; Score 12; DB 2; Length 722;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 526 YWTFNFAKTGDPN 537
|||||
DB 467 YWTFNFAKTGDPN 478

RESULT 20

US-08-204-691-7
Sequence 7, Application US/08204691
Patent No. 5827683

GENERAL INFORMATION:
APPLICANT: Backeberg, Lars
APPLICANT: Edlund, Michael
APPLICANT: Hansson, Lennart
APPLICANT: Herrel, Olle
APPLICANT: Lundberg, Lennart
APPLICANT: Stromqvist, Mats
APPLICANT: Toernell, Jan
TITLE OF INVENTION: No. 5827683el Polypeptides
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,691

FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 930686-4
FILING DATE: 31-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9306722-7
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Steiner Ph.D., Richard J
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-850
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)819-8783
TELEFAX: (212)354-8113

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 722 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:

ORGANISM: Homo sapiens
TISSUE TYPE: Mammary gland

FEATURE:
NAME/KEY: Peptide
LOCATION: 1..722
OTHER INFORMATION: /label= Variant_N

US-08-204-691-7

Query Match 1.5%; Score 12; DB 2; Length 722;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 526 YWTFNFAKTGDPN 537
|||||
DB 467 YWTFNFAKTGDPN 478

RESULT 21

US-09-355-295B-4
Sequence 4, Application US/09355295B
Patent No. 6525241

GENERAL INFORMATION:
APPLICANT: Dattipam, M.
APPLICANT: Lundberg, J.
APPLICANT: Stromqvist, M.
TITLE OF INVENTION: Expression Methods
FILE REFERENCE: 1754 SEQUENCE LISTING v2a.txt
CURRENT APPLICATION NUMBER: US/09/355,295B
CURRENT FILING DATE: 1999-07-18
PRIOR APPLICATION NUMBER: PCT/SE99/00648
PRIOR FILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 4
LENGTH: 722
TYPE: PRT
ORGANISM: Homo sapiens
US-09-355-295B-4

Query Match 1.5%; Score 12; DB 4; Length 722;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 526 YWTFNFAKTGDPN 537
|||||
DB 467 YWTFNFAKTGDPN 478

RESULT 22

US-08-204-691-7
Patent No. 5820183

APPLICANT: WANG, JORDAN J.N.; WANG, CHI-SUN
TITLE OF INVENTION: RECOMBINANT BILE SALT ACTIVATED LIPASES
NUMBER OF SEQUENCES: 22
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,426
FILING DATE: 12-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 504,635
FILING DATE: 04-APR-1990
APPLICATION NUMBER: 122,410
FILING DATE: 19-NOV-1987
SEQ ID NO: 3
LENGTH: 722
5260183-3

Query Match 1.5%; Score 12; DB 6; Length 722;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 526 YWTFNFAKTGDPN 537
|||||
DB 467 YWTFNFAKTGDPN 478

RESULT 23

US-08-347-718B-2
Sequence 2, Application US/08347718B
Patent No. 5696087
GENERAL INFORMATION:

APPLICANT: Wang, Chu-San
APPLICANT: Tang, Jordan J.N
TITLE OF INVENTION: METHOD FOR REDUCING INTESTINAL ABSORPTION OF
TITLE OF INVENTION: CHOLESTERO.
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Patrea U. Pabst
STREET: 2800 One Atlantic Center
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDICAL TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347,7198
FILING DATE: December 1, 1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea U.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRP151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8795
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 742 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Modified-site
LOCATION: 186..187
OTHER INFORMATION: /note= "Position 187 represents a
OTHER INFORMATION: potential N-linked glycosylation site."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 193..194
OTHER INFORMATION: /note= "The serine at position 194
OTHER INFORMATION: represents an active site serine."
FEATURE:
NAME/KEY: misc. feature
LOCATION: 1..742
OTHER INFORMATION: /Function = "Amino acid sequence for
OTHER INFORMATION: the Human Milk Bile Salt-activated Lipase."
US-09-347-7198-2
Query Match 1.5%; Score 12; DB 1; Length 742;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 526 YWTFNPAKTGDPN 537
DB 487 YWTFNPAKTGDPN 498
RESULT 24
US-08-482-262-2
Sequence 2, Application US/0842262
Patent No. 5821226
GENERAL INFORMATION:
APPLICANT: Wang, Chu-San
APPLICANT: Tang, Jordan J.N
TITLE OF INVENTION: BIL C-TAIL DRUG DELIVERY MOLECULES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:

ADDRESS: Patrea U. Pabst
STREET: 2800 One Atlantic Center
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDICAL TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,262
FILING DATE: June 7, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea U.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRP151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8795
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 742 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Modified-site
LOCATION: 186..187
OTHER INFORMATION: /note= "Position 187 represents a
OTHER INFORMATION: potential N-linked glycosylation site."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 193..194
OTHER INFORMATION: /note= "The serine at position 194
OTHER INFORMATION: represents an active site serine."
FEATURE:
NAME/KEY: misc. feature
LOCATION: 1..742
OTHER INFORMATION: /Function = "Amino acid sequence for
OTHER INFORMATION: the Human Milk Bile Salt-activated Lipase."
US-08-482-262-2
Query Match 1.5%; Score 12; DB 2; Length 742;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 526 YWTFNPAKTGDPN 537
DB 487 YWTFNPAKTGDPN 498
RESULT 25
5200183-2
Patent No. 5200193
APPLICANT: TANG, JORDAN J.N.; WANG, CHI-SUN
TITLE OF INVENTION: RECOMBINANT BILE SALT ACTIVATED LIPASES
NUMBER OF SEQUENCES: 22
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,426
FILING DATE: 12-JUN-1990
FIRM APPLICATION NUMBER:
APPLICATION NUMBER: 504,635
FILING DATE: 04-APR-1990
APPLICATION NUMBER: 122,410
FILING DATE: 19-NOV-1987
SEQ ID NO: 2
LENGTH: 742

5200193-2

Query Match 1.5%; Score 12; DB 6; Length 745;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTFNFAKTGDPN 537
DB 487 YWTFNFAKTGDPN 498

RESULT 26

US-08-445-050-2
Sequence 2, Application US/08445050
Patent No. 5763739

GENERAL INFORMATION:

APPLICANT: Blackberg, Lars

APPLICANT: Edlund, Michael

APPLICANT: Hansson, Lemnart

APPLICANT: Herneil, Oile

APPLICANT: Lundberg, Lemnart

APPLICANT: Stromqvist, Mats

APPLICANT: Toernell, Jan

TITLE OF INVENTION: No. 5763739el Polypeptides

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESS: White & Case

CITY: New York

STATE: New York

COUNTRY: United States

ZIP: 10036-2787

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/06/445-050

FILING DATE:

CLASSIFICATION: 803

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/204-691

FILING DATE:

APPLICATION NUMBER: SE 930686-4

FILING DATE: 01-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE 9300722-7

FILING DATE: 04-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Sterner Ph.D., Richard J

REGISTRATION NUMBER: 35,372

REFERENCE/DOCKET NUMBER: 1103326-850

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)819-8783

TELEFAX: (212)354-8113

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-445-050-2

Query Match 1.5%; Score 12; DB 1; Length 745;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTFNFAKTGDPN 537
DB 490 YWTFNFAKTGDPN 501

RESULT 27

US-08-204-691-2
Sequence 2, Application US/08204691
Patent No. 5827693

GENERAL INFORMATION:

APPLICANT: Blackberg, Lars

APPLICANT: Edlund, Michael

APPLICANT: Hansson, Lemnart

APPLICANT: Herneil, Oile

APPLICANT: Lundberg, Lemnart

APPLICANT: Stromqvist, Mats

APPLICANT: Toernell, Jan

TITLE OF INVENTION: No. 5827693el Polypeptides

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESS: White & Case

CITY: New York

STATE: New York

COUNTRY: United States

ZIP: 10036-2787

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/204-691

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE 9300686-4

FILING DATE: 01-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE 9300722-7

FILING DATE: 04-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Sterner Ph.D., Richard J

REGISTRATION NUMBER: 35,372

REFERENCE/DOCKET NUMBER: 1103326-850

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)819-8783

TELEFAX: (212)354-8113

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-204-691-2

Query Match 1.5%; Score 12; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTFNFAKTGDPN 537
DB 490 YWTFNFAKTGDPN 501

RESULT 28

US-08-370-223-13
Sequence 13, Application US/08370223
Patent No. 6,07026

GENERAL INFORMATION:

APPLICANT: Lange, Lili, Louis G.

APPLICANT: Kumar, B. Vijaya

TITLE OF INVENTION: Methods and Reagents for RFLP Analysis

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESS: Allegretti & Witcoff, Ltd.

STREET: 10 South Wacker, Suite 3000

```
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDICAL TYPE: floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/370.223
/ FILING DATE:
/ CLASSIFICATION: 357
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/28/053.308
/ FILING DATE:
/ APPLICATION NUMBER: 07/730.224
/ FILING DATE: July 15, 1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McDonnell, John J.
/ REGISTRATION NUMBER: 26,949
/ REFERENCE/DOCKET NUMBER: 91,441
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-715-1000
/ TELEFAX: 312-715-1234
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 745 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-370-223-13

Query Match 1.5% Score 12; DB 3; Length 745;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 526 YWTFNPAKTGDPN 537
DB 490 YWTFNPAKTGDPN 501

RESULT 29
US-09-355-295B-3
/ Sequence 3, Application US/09355295B
/ Patent No. 6525241
/ GENERAL INFORMATION:
/ APPLICANT: Dairyple, M.
/ APPLICANT: Lundberg, L.
/ APPLICANT: Stronqvist, M.
/ TITLE OF INVENTION: Expression Methods
/ FILE REFERENCE: 1754 SEQUENCE LISTING v2a.txt
/ CURRENT APPLICATION NUMBER: US/09/355.295B
/ CURRENT FILING DATE: 1999-07-18
/ PRIOR APPLICATION NUMBER: PCT/SE99/00648
/ PRIOR FILING DATE: 1999-04-21
/ NUMBER OF SEQ ID NOS: 5
/ SEQ ID NO 3
/ LENGTH: 745
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-355-295B-3

Query Match 1.5% Score 12; DB 4; Length 745;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 526 YWTFNPAKTGDPN 537
DB 490 YWTFNPAKTGDPN 501

RESULT 30
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US-09-347-878-32
/ Sequence 32, Application US/09347878C
/ Patent No. 6376210
/ GENERAL INFORMATION:
/ APPLICANT: Yuan, Chong
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
/ FILE REFERENCE: 25885-1651
/ CURRENT APPLICATION NUMBER: US/09/347.878C
/ CURRENT FILING DATE: 1999-07-06
/ NUMBER OF SEQ ID NOS: 75
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 32
/ LENGTH: 747
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-347-878-32

Query Match 1.5% Score 12; DB 4; Length 747;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 526 YWTFNPAKTGDPN 537
DB 490 YWTFNPAKTGDPN 501

RESULT 31
US-09-264-737-1
/ Sequence 1, Application US/09264737A
/ Patent No. 6107549
/ GENERAL INFORMATION:
/ APPLICANT: Feng, Paul C.C.
/ APPLICANT: Ruff, Thomas G.
/ TITLE OF INVENTION: Engineering Plant Resistance to Pyridines via
/ FILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance
/ CURRENT APPLICATION NUMBER: US/09/264.737A
/ CURRENT FILING DATE: 1999-03-09
/ EARLIER APPLICATION NUMBER: 60/077.377
/ EARLIER FILING DATE: 1998-03-10
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 539
/ TYPE: PRT
/ ORGANISM: Rabbit
/ US-09-264-737-1

Query Match 1.1% Score 9; DB 3; Length 539;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 125 EDGYLYNY 133
DB 36 EDGYLYNY 104

RESULT 32
US-09-264-737-2
/ Sequence 2, Application US/09264737A
/ Patent No. 6107549
/ GENERAL INFORMATION:
/ APPLICANT: Feng, Paul C.C.
/ APPLICANT: Ruff, Thomas G.
/ TITLE OF INVENTION: Engineering Plant Resistance to Pyridines via
/ FILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance
/ CURRENT APPLICATION NUMBER: US/09/264.737A
/ CURRENT FILING DATE: 1999-03-09
/ EARLIER APPLICATION NUMBER: 60/077.377
/ EARLIER FILING DATE: 1998-03-10
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn Ver. 2.0
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SEQ ID NO 2
LENGTH: 566
TYPE: PRT
ORGANISM: Rabbit
US-09-264-737-2

Query Match 1.1% Score 9; DB 3; Length 566;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYNLY 133
DB 115 EDCLYNLY 123

RESULT 33
US-08-845-295A-2
Sequence 2, Application US/08845295A
Patent No. 58,7490

GENERAL INFORMATION:
APPLICANT: Hubbs, John C.
TITLE OF INVENTION: Enzymatic Process for the Manufacture of
TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of
TITLE OF INVENTION: 2-Keto-L-Gulonic Acid
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eastman Chemical Company
STREET: P.O. Box 511
CITY: Kingsport
STATE: Tennessee
COUNTRY: USA
ZIP: 37662-5075
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,295A
FILING DATE: 25-April-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,879
FILING DATE: 17-May-1996
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70432
TELECOMMUNICATION INFORMATION:
TELEPHONE: 423-229-6189
TELEFAX: 423-229-1239
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: Protein
US-08-845-295A-2

Query Match 1.1% Score 9; DB 2; Length 584;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYNLY 133
DB 119 EDCLYNLY 127

RESULT 34
US-09-140-933-2
Sequence 2, Application US/09140933
Patent No. 6022719
GENERAL INFORMATION:

APPLICANT: Hubbs, John C.
TITLE OF INVENTION: Enzymatic Process for the Manufacture of
TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of
TITLE OF INVENTION: 2-Keto-L-Gulonic Acid
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eastman Chemical Company
STREET: P.O. Box 511
CITY: Kingsport
STATE: Tennessee
COUNTRY: USA
ZIP: 37662-5075
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/140,933
FILING DATE: 27-August-98
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,879; 08/845,295
FILING DATE: 17-May-96; 25-April-97
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70432
TELECOMMUNICATION INFORMATION:
TELEPHONE: 423-229-6189
TELEFAX: 423-229-1239
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: Protein
US-09-140-933-2

Query Match 1.1% Score 9; DB 3; Length 584;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYNLY 133
DB 119 EDCLYNLY 127

RESULT 35
US-09-146-661-2
Sequence 2, Application US/09146661
Patent No. 6136575
GENERAL INFORMATION:
APPLICANT: Hubbs, John C.
TITLE OF INVENTION: Enzymatic Process for the Manufacture of
TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of 2-Keto
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eastman Chemical Company
STREET: P.O. Box 511
CITY: Kingsport
STATE: Tennessee
COUNTRY: USA
ZIP: 37662-5075
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,661
FILING DATE: 03-September-98

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,879; 08/845,295
FILING DATE: 17-May-96; 25-April-97
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70432
TELECOMMUNICATION INFORMATION:
TELEPHONE: 423-229-6189
TELEFAX: 423-229-1239
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: protein
US-09-146-661-2

Query Match: 1.1%; Score 9; DB 3; Length 584;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNI 133
DB 119 EDCLYLNI 127

RESULT 36
US-09-150-515-2
Sequence 2, Application US/09150515
Patent No. 6271006
GENERAL INFORMATION:
APPLICANT: Hubbs, John C.
TITLE OF INVENTION: Enzymatic Process for the Manufacture of
TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of
TITLE OF INVENTION: 2-Keto-L-Gulonic Acid
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eastman Chemical Company
STREET: P.O. Box 511
CITY: Kingsport
STATE: Tennessee
COUNTRY: USA
ZIP: 37662-5075
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/150,515
FILING DATE: 09-SEP-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 63/017,879; 08/845,295
FILING DATE: 17-May-96; 25-April-97
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70432
TELECOMMUNICATION INFORMATION:
TELEPHONE: 423-229-6189
TELEFAX: 423-229-1239
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: protein
US-09-150-515-2

Query Match: 1.1%; Score 9; DB 3; Length 584;

Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNI 133
DB 119 EDCLYLNI 127

RESULT 37
US-08-462-884A-1
Sequence 2, Application US/08462884A
Patent No. 5624836
GENERAL INFORMATION:
APPLICANT: Lange III, Louis G
TITLE OF INVENTION: Splilburg, Curtis A
TITLE OF INVENTION: Mammalian Pancreatic Cholesterol
TITLE OF INVENTION: Esterase
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti
STREET: 10 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60636
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,884A
FILING DATE: Unknown
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: A. Blair Hughes
REGISTRATION NUMBER: 32,901
REFERENCE/DOCKET NUMBER: 99,852-J
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/715-1000
TELEFAX: 312/715-1234
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 597 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURES:
NAME/KEY: misc feature
LOCATION: 1..597
OTHER INFORMATION: /note= "Bovine pancreatic
OTHER INFORMATION: cholesterol esterase"
US-08-462-884A-1

Query Match: 1.1%; Score 9; DB 1; Length 597;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 EDCLYLNI 132
DB 95 EDCLYLNI 103

RESULT 38
US-08-461-881B-1
Sequence 1, Application US/08461881B
Patent No. 5792832
GENERAL INFORMATION:
APPLICANT: Lange III, Louis G
TITLE OF INVENTION: Splilburg, Curtis A
TITLE OF INVENTION: Mammalian Pancreatic
NUMBER OF SEQUENCES: 11
Cholesterol Esterase

1 CORRESPONDENCE ADDRESS:
2 ADDRESS: McDonnell Boenigsen Hulbert & Bergroff
3 STREET: 300 South Wacker Drive
4 CITY: Chicago
5 STATE: IL
6 COUNTRY: USA
7 ZIP: 60606
8
9 COMPUTER READABLE FORM:
10 MEDIUM TYPE: 3.5" hard disc
11 COMPUTER: IBM PC compatible
12 OPERATING SYSTEM: PC-DOS/MS-DOS
13 SOFTWARE: Patentin Release #1.0, Version #1.25
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/09/461,88-B
16 FILING DATE: June 5, 1995
17 CLASSIFICATION: 435
18 ATTORNEY/AGENT INFORMATION:
19 NAME: A. Blair Hughes
20 REGISTRATION NUMBER: 32,901
21 REFERENCE/DOCKET NUMBER: 89,852-J
22 TELECOMMUNICATION INFORMATION:
23 TELEPHONE: 312/913-0001
24 TELEFAX: 312/913-0002
25 TELEX: 910/221-5317
26 INFORMATION FOR SEQ ID NO: 1:
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 597 amino acids
29 TYPE: amino acid
30 TOPOLOGY: linear
31 MOLECULE TYPE: protein
32 FEATURE:
33 NAME/KEY: misc feature
34 LOCATION: 1..597
35 OTHER INFORMATION: /note="Bovine pancreatic
36 OTHER INFORMATION: cholesterol esterase"
37 US-08-461-88-B-1
38
39 Query Match 1.1%; Score 9; DB 1; Length 597;
40 Best Local Similarity 100.0%; Pred. No. 2.9;
41 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
42
43 QY 124 NEDCLYINI 132
44 DB 95 NEDCLYINI 103
45
46 RESULT 39
47 US-09-123-960-1
48 Sequence 1, Application US/09133960
49 Patent No. 5981293
50 GENERAL INFORMATION:
51 APPLICANT: Lange III, Louis G
52 APPLICANT: Spilburg, Curtis A
53 TITLE OF INVENTION: Mammalian Pancreatic
54 NUMBER OF SEQUENCES: 11
55 CORRESPONDENCE ADDRESS:
56 ADDRESSEE: McDonnell Boenigsen Hulbert & Bergroff
57 STREET: 300 South Wacker Drive
58 CITY: Chicago
59 STATE: IL
60 COUNTRY: USA
61 ZIP: 60606
62 COMPUTER READABLE FORM:
63 MEDIUM TYPE: 3.5" hard disc
64 COMPUTER: IBM PC compatible
65 OPERATING SYSTEM: PC-DOS/MS-DOS
66 SOFTWARE: Patentin Release #1.0, Version #1.25
67 CURRENT APPLICATION DATA:
68 APPLICATION NUMBER: US/09/123,960
69 FILING DATE:
70 CLASSIFICATION:
71 PRIOR APPLICATION DATA:
72 APPLICATION NUMBER: 08/461,881

1 FILING DATE: June 5, 1995
2 ATTORNEY/AGENT INFORMATION:
3 NAME: A. Blair Hughes
4 REGISTRATION NUMBER: 32,901
5 REFERENCE/DOCKET NUMBER: 89,852-K
6 TELECOMMUNICATION INFORMATION:
7 TELEPHONE: 312/913-0001
8 TELEFAX: 312/913-0002
9 TELEX: 910/221-5317
10 INFORMATION FOR SEQ ID NO: 1:
11 SEQUENCE CHARACTERISTICS:
12 LENGTH: 597 amino acids
13 TYPE: amino acid
14 MOLECULE TYPE: protein
15 FEATURE:
16 NAME/KEY: misc feature
17 LOCATION: 1..597
18 OTHER INFORMATION: /note="Bovine pancreatic
19 OTHER INFORMATION: cholesterol esterase"
20 US-09-123-960-1
21
22 Query Match 1.1%; Score 9; DB 2; Length 597;
23 Best Local Similarity 100.0%; Pred. No. 2.9;
24 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
25
26 QY 124 NEDCLYINI 132
27 DB 95 NEDCLYINI 103
28
29 RESULT 40
30 US-08-462-884A-3
31 Sequence 3, Application US/08462884A
32 Patent No. 5624836
33 GENERAL INFORMATION:
34 APPLICANT: Lange III, Louis G
35 APPLICANT: Spilburg, Curtis A
36 TITLE OF INVENTION: Mammalian Pancreatic Cholesterol
37 NUMBER OF SEQUENCES: 11
38 CORRESPONDENCE ADDRESS:
39 ADDRESSEE: Banner & Aliepreti
40 STREET: 10 South Wacker Drive
41 CITY: Chicago
42 STATE: IL
43 COUNTRY: USA
44 ZIP: 60606
45 COMPUTER READABLE FORM:
46 MEDIUM TYPE: Floppy disk
47 COMPUTER: IBM PC compatible
48 OPERATING SYSTEM: PC-DOS/MS-DOS
49 SOFTWARE: Patentin Release #1.0, Version #1.25
50 CURRENT APPLICATION DATA:
51 APPLICATION NUMBER: US/08/462,884A
52 FILING DATE: Unknown
53 CLASSIFICATION: 435
54 ATTORNEY/AGENT INFORMATION:
55 NAME: A. Blair Hughes
56 REGISTRATION NUMBER: 32,901
57 REFERENCE/DOCKET NUMBER: 89,852-C
58 TELECOMMUNICATION INFORMATION:
59 TELEPHONE: 312/715-1000
60 TELEFAX: 312/715-1234
61 TELEX: 910/221-5317
62 INFORMATION FOR SEQ ID NO: 3:
63 SEQUENCE CHARACTERISTICS:
64 LENGTH: 605 amino acids
65 TYPE: amino acid
66 TOPOLOGY: linear
67 MOLECULE TYPE: protein
68 US-08-462-884A-3

Query Match 1.1%; Score 9; DB 1; Length 605;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 124 NEDCLYINI 132
Db 103 NEDCLYINI 111

RESULT 41

US-08-461-881B-3
Sequence 3, Application US/08461881B
Patent No. 5792832
GENERAL INFORMATION:
APPLICANT: Lange III, Louis G
APPLICANT: Spilburg, Curtis A
TITLE OF INVENTION: Mammalian Pancreatic
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDowell, Boehnen Hubert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" hard disc
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,881B
FILING DATE: June 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: A. Blair Hughes
REGISTRATION NUMBER: 32,901
REFERENCE/DOCKET NUMBER: 89,852-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/913-0002
TELEFAX: 312/913-0002
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-881B-3

Query Match 1.1%; Score 9; DB 1; Length 605;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 124 NEDCLYINI 132
Db 103 NEDCLYINI 111

RESULT 42

US-09-123-960-3
Sequence 3, Application US/09123960
Patent No. 5981299
GENERAL INFORMATION:
APPLICANT: Lange III, Louis G
APPLICANT: Spilburg, Curtis A
TITLE OF INVENTION: Mammalian Pancreatic
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDowell, Boehnen Hubert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL

COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" hard disc
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,960
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,881
FILING DATE: June 5, 1995
ATTORNEY/AGENT INFORMATION:
NAME: A. Blair Hughes
REGISTRATION NUMBER: 32,901
REFERENCE/DOCKET NUMBER: 89,852-K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/913-0001
TELEFAX: 312/913-0002
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-123-960-3

Query Match 1.1%; Score 9; DB 2; Length 605;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 124 NEDCLYINI 132
Db 103 NEDCLYINI 111

RESULT 43

US-09-347-878-34
Sequence 34, Application US/09347878C
Patent No. 6176210
GENERAL INFORMATION:
APPLICANT: Yvan, Chong
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
FILE REFERENCE: 25885-165.
CURRENT APPLICATION NUMBER: US/09/347,878C
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 34
LENGTH: 606
TYPE: PRT
ORGANISM: Bos taurus
OTHER INFORMATION: Bovine pancreatic cholesterol esterase protein sequence
PUBLICATION INFORMATION:
PATENT DOCUMENT NUMBER: 08/462,884
PATENT FILING DATE: 1995-06-05
PUBLICATION DATE: 1997-04-29
US-09-347-878-34

Query Match 1.1%; Score 9; DB 4; Length 606;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 124 NEDCLYINI 132
Db 104 NEDCLYINI 112

RESULT 44

US-08-747-221B-11
Sequence 11, Application US/03747221B
Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: Silver, Gary M.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6063610e) Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610e) December 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: PC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-747-221B-11
Query March 1.0%; Score 8; DB 3; Length 137;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 125 EDCLYLNI 132
Db 112 EDCLYLNI 119
RESULT 45
US-09-005-051-11
Sequence 11, Application US/09005051
Patent No. 6291222
GENERAL INFORMATION:
APPLICANT: Silver, Gary M.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6291222e) Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/747,221
FILING DATE: No. 6291222e) December 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: PC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-051-11
Query March 1.0%; Score 8; DB 3; Length 137;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 125 EDCLYLNI 132
Db 112 EDCLYLNI 119
RESULT 46
US-09-827-171B-8
Sequence 8, Application US/09827171B
Patent No. 6254869
GENERAL INFORMATION:
APPLICANT: CAROLYN PETERSEN
APPLICANT: JIN-KING HUNG
TITLE OF INVENTION: CRYPTOPAIN VACCINES, ANTIBODIES, PROTEINS,
TITLE OF INVENTION: PEPTIDES, DNA AND RNAs FOR PROPHYLAXIS,
TITLE OF INVENTION: TREATMENT, DIAGNOSIS AND
TITLE OF INVENTION: DETECTION OF
TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIK A
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
STATE: California
COUNTRY: United States of America
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
COMPUTER: PC
OPERATING SYSTEM: WINDOWS
SOFTWARE: WordPerfect 6.0a WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,171B
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/014,233
FILING DATE: March 27, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hana Verry
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: (HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-1677
TELEFAX: (415) 324-1678
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids

TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Plasmodium vinckei
US-08-827-1718-8

Query Match 1.0%; Score 8; D3 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 677 VTIAGAS 684
DB 129 VTIAGAS 136

RESULT 47
US-08-747-2218-37
Sequence 37, Application US/087472218
Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
TITLE OF INVENTION: No. 6063610a1 Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,2218
FILING DATE: No. 6063610eember 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 528 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-747-2218-37
Query Match 1.0%; Score 8; D3 3; Length 528;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 527 WTNFAKTG 534
DB 472 WTNFAKTG 479

RESULT 48
US-03-005-051-37
Sequence 37, Application US/0305051
Patent No. 6231222
GENERAL INFORMATION:

APPLICANT: Silver, Gary W.
TITLE OF INVENTION: No. 6291222a1 Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/747,221
FILING DATE: No. 6291222eember 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 528 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-051-37
Query Match 1.0%; Score 8; D3 3; Length 528;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 527 WTNFAKTG 534
DB 472 WTNFAKTG 479

RESULT 49
US-08-362-525-12
Sequence 12, Application US/08362525
Patent No. 6027910
GENERAL INFORMATION:
APPLICANT: KIS, FRANCISCUS W.
APPLICANT: SCHREUDER, MAARTEN P.
APPLICANT: TOSCHKA, HOLGER Y.
TITLE OF INVENTION: PROCESS FOR IMMOBILIZING ENZYMES TO THE
TITLE OF INVENTION: CELL WALL OF A MICROBIAL CELL BY PRODUCING A FUSION
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-9918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,525
FILING DATE: 04-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92203080.5
FILING DATE: 08-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92203089.7
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/01763
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16, 773
REFERENCE/DOCKET NUMBER: 213289/T7020(V)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3003
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 12:
LENGTH: 563 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-525-12

Query Match 1.0%; Score 8; DB 3; Length 563;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 NEDCLYLN 131
DB 121 NEDCLYLN 128

RESULT 50
US-08-747-221B-54
Sequence 54, Application US/08747221B
Patent No. 60636-0
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
ATTORNEY/AGENT INFORMATION:
NAME: Wisniewski, Nancy
REGISTRATION NUMBER: No. 6063610e1 Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSER: Carol Talkington Verser, Ph.D.
ADDRESS: Heeka Corporation
STREET: 1925 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610e1 December 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: PC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-747-221B-54

Query Match 1.0%; Score 8; DB 3; Length 570;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCVLYN 132
DB 86 EDCVLYN 93

RESULT 51
US-08-747-221B-55
Sequence 55, Application US/08747221B
Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
ATTORNEY/AGENT INFORMATION:
NAME: Wisniewski, Nancy
REGISTRATION NUMBER: No. 6063610e1 Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSER: Carol Talkington Verser, Ph.D.
ADDRESS: Heeka Corporation
STREET: 1925 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610e1 December 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: PC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-747-221B-55

Query Match 1.0%; Score 8; DB 3; Length 570;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCVLYN 132
DB 86 EDCVLYN 93

RESULT 52
US-09-005-051-54
Sequence 54, Application US/09005051
Patent No. 629122
GENERAL INFORMATION:

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? APPLICANT: Silver, Gary M.
? APPLICANT: Wisniewski, Nancy
? TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nuclic Acid
? TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
? NUMBER OF SEQUENCES: 66
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Carol Talkington Verser, Ph.D.
? ADDRESSEE: Heska Corporation
? STREET: 1825 Sharp Point Drive
? CITY: Fort Collins
? STATE: Colorado
? COUNTRY: USA
? ZIP: 80525
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: Windows 95
? SOFTWARE: Wordperfect for Windows, Version 7.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/005,051
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/747,221
? FILING DATE: No. 6291222e1 December 12, 1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Verser, Carol Talkington
? REGISTRATION NUMBER: 37,459
? REFERENCE/DOCKET NUMBER: PC-1
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 970/493-7272
? TELEFAX: 970/484-9505
? INFORMATION FOR SEQ ID NO: 54:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 570 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
?
? US-09-005-051-54
?
? Query Match 1.0%; Score 8; DB 3; Length 570;
? Best Local Similarity 100.0%; Pred. No. 27;
? Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
?
? QY 125 EDCLYINI 132
? DB 96 EDCCLYINI 93
?
? RESULT 53
? US-09-005-051-55
? Sequence 55, Application US/09005051
? Patent No. 6291222
? GENERAL INFORMATION:
? APPLICANT: Silver, Gary M.
? APPLICANT: Wisniewski, Nancy
? TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nuclic Acid
? TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
? NUMBER OF SEQUENCES: 66
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Carol Talkington Verser, Ph.D.
? ADDRESSEE: Heska Corporation
? STREET: 1825 Sharp Point Drive
? CITY: Fort Collins
? STATE: Colorado
? COUNTRY: USA
? ZIP: 80525
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: Windows 95
? SOFTWARE: Wordperfect for Windows, Version 7.0
? CURRENT APPLICATION DATA:

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? APPLICATION NUMBER: US/09/005,051
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/747,221
? FILING DATE: No. 6291222e1 December 12, 1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Verser, Carol Talkington
? REGISTRATION NUMBER: 37,459
? REFERENCE/DOCKET NUMBER: PC-1
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 970/493-7272
? TELEFAX: 970/484-9505
? INFORMATION FOR SEQ ID NO: 55:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 570 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
?
? US-09-005-051-55
?
? Query Match 1.0%; Score 8; DB 3; Length 570;
? Best Local Similarity 100.0%; Pred. No. 27;
? Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
?
? QY 125 EDCLYINI 132
? DB 96 EDCCLYINI 93
?
? RESULT 54
? US-08-348-920-1
? Sequence 1, Application US/08348920
? Patent No. 5695750
? GENERAL INFORMATION:
? APPLICANT: Doctor, Bhupendra P.
? APPLICANT: Maxwell, Donald
? APPLICANT: Saxena, Ashima
? APPLICANT: Radic, Zoran
? APPLICANT: Taylor, Palmer
? TITLE OF INVENTION: Compositions for Use to Deactivate
? TITLE OF INVENTION: Organophosphates
? NUMBER OF SEQUENCES: 2
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: John F. Moran
? STREET: Off. of Command Judge Adv., HQ USAMRDC, Fort
? STREET: Detrick
? CITY: Frederick
? STATE: MD
? COUNTRY: US
? ZIP: 21702-5012
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentia Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/348,920
? FILING DATE: 25-NOV-1994
? CLASSIFICATION: 424
? ATTORNEY/AGENT INFORMATION:
? NAME: Hendricks, Gienaa
? REGISTRATION NUMBER: 32,535
? REFERENCE/DOCKET NUMBER: doc348,920
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (302) 619-7807
? TELEFAX: 301-619-7714
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 575 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: unknown

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MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-348-920-1

Query Match 1.0%; Score 8; DB 1; Length 575;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 EDCLYLNI 132
Db 92 EDCLYLNI 99

RESULT 55
US-08-348-920-2
Sequence 2, Application US/08348920
Patent No. 5695750
GENERAL INFORMATION:
APPLICANT: Doctor, Bhupendra P.
APPLICANT: Maxwell, Donald
APPLICANT: Saxena, Ashima
APPLICANT: Radic, Zoran
APPLICANT: Taylor, Palmer
TITLE OF INVENTION: Compositions for Use to Deactivate
TITLE OF INVENTION: C-ganophosphates
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. Moran
STREET: Off. of Command Judge Adv., HQ USAMRDC, Fort
STREET: Detrick
CITY: Frederick
STATE: MD
COUNTRY: US
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent-in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,920
FILING DATE: 25-Nov-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: ddc348,920
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-7807
TELEFAX: 301-619-7714
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-348-920-2

Query Match 1.0%; Score 8; DB 1; Length 575;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 EDCLYLNI 132
Db 92 EDCLYLNI 99

RESULT 56
US-08-747-221B-31
Sequence 31, Application US/08747221B
Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610ember 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/484-9505
TELEFAX: 970/493-7272
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 595 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-747-221B-31

Query Match 1.0%; Score 8; DB 3; Length 595;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 EDCLYLNI 132
Db 111 EDCLYLNI 118

RESULT 57
US-09-005-051-31
Sequence 31, Application US/09005051
Patent No. 6291222
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: No. 629122222222222222 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 595 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-051-31

Query Match 1.0%; Score 8; DB 3; Length 595;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNI 132
DB 111 EDCLYLNI 118

RESULT 58
US-08-747-221B-25
Sequence 25, Application US/08747221B
Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610e1 December 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 596 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-747-221B,25

Query Match 1.0%; Score 8; DB 3; Length 596;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNI 132
DB 112 EDCLYLNI 119

RESULT 59
US-09-005-051-25
Sequence 25, Application US/09005051
Patent No. 6291222
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: No. 629122222222222222 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 596 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-051-25

Query Match 1.0%; Score 8; DB 3; Length 596;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNI 132
DB 112 EDCLYLNI 119

RESULT 60
5200183-4
Patent No. 5200183
APPLICANT: TANG, JORDAN J.N.; WANG, CHI-SUN
TITLE OF INVENTION: RECOMBINANT BILE SALT ACTIVATED LIPASES
NUMBER OF SEQUENCES: 22
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,426
FILING DATE: 12-JUN-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 504,635
FILING DATE: 04-APR-1990
APPLICATION NUMBER: 122,410
FILING DATE: 19-NOV-1987
SEQ ID NO:4:
LENGTH: 723
5200183-4

Query Match 1.0%; Score 8; DB 6; Length 723;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCYLYNI 132
DB 79 EDCYLYNI 86

RESULT 61
US-09-252-991A-28373
Sequence 28373, Application US/03252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,789
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/034,193
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28373
LENGTH: 767
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28373

Query Match 1.0%; Score 8; DB 4; Length 767;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 453 PAVAADLH 463
DB 309 PAVAADLH 316

RESULT 62
US-09-735-934A-4
Sequence 4, Application US/09735934A
Patent No. 6372468
GENERAL INFORMATION:
APPLICANT: Li, Jiaxin et al
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: C1000851
CURRENT APPLICATION NUMBER: US/09/735,934A
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 894
TYPE: PRT
ORGANISM: Homo sapiens
US-09-735-934A-4

Query Match 1.0%; Score 8; DB 4; Length 894;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 EDEDIHQ 163
DB 767 EDEDIHQ 774

RESULT 63
US-10-060-332-4
Sequence 4, Application US/10060332
Patent No. 6528294
GENERAL INFORMATION:
APPLICANT: Li, Jiaxin et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: C1000851DIV
CURRENT APPLICATION NUMBER: US/10/060,332
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 894
TYPE: PRT
ORGANISM: Homo sapiens
US-10-060-332-4

Query Match 1.0%; Score 8; DB 4; Length 894;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 EDEDIHQ 163
DB 767 EDEDIHQ 774

RESULT 64
US-08-308-086-8
Sequence 8, Application US/08308086
Patent No. 5786454
GENERAL INFORMATION:
APPLICANT: Gabriel Wakman and Andrey Shaw
TITLE OF INVENTION: Modified SH2 Domains and Methods of Use
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patricia L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,086
FILING DATE: 09-16-97
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
US-08-308-086-8

Query Match: 0.9%; Score 7; DB 1; Length 95;
Best Local Similarity: 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 759 DYTLTLR 765
|||||
DB 35 DYTLTLR 41

RESULT 65

US-08-167-035-17
Sequence 17, Application US/08167035
Patent No. 5618691
GENERAL INFORMATION:
APPLICANT: Schlössinger, Joseph
APPLICANT: Skolnick, Edward Y.
APPLICANT: Margolis, Benjamin J.
TITLE OF INVENTION: NOVEL EXPRESSION CLONING METHOD FOR
IDENTIFYING TARGET PROTEINS FOR ENZYMOLOGIC TYPING
TITLE OF INVENTION: KINASES AND NOVEL TARGET PROTEINS
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: 10036-2711
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08167035
FILING DATE: 16-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 793-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-167-035-17

Query Match: 0.9%; Score 7; DB 1; Length 96;
Best Local Similarity: 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 759 DYTLTLR 765
|||||
DB 34 DYTLTLR 40

RESULT 66
US-08-208-887A-17
Sequence 17, Application US/08208887A
Patent No. 5677421
GENERAL INFORMATION:
APPLICANT: Schlössinger, Joseph
APPLICANT: Skolnick, Edward Y.
APPLICANT: Margolis, Benjamin J.
TITLE OF INVENTION: NOVEL EXPRESSION CLONING METHOD FOR
IDENTIFYING TARGET PROTEINS FOR ENZYMOLOGIC TYPING

TITLE OF INVENTION: KINASES AND NOVEL TARGET PROTEINS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: 10036-2711
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08208887A
FILING DATE: 11-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 793-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-208-887A-17

Query Match: 0.9%; Score 7; DB 1; Length 96;
Best Local Similarity: 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 759 DYTLTLR 765
|||||
DB 34 DYTLTLR 40

RESULT 67

US-08-479-078-20
Sequence 20, Application US/08479078
Patent No. 5814466
GENERAL INFORMATION:
APPLICANT: Rawson, Anthony
TITLE OF INVENTION: Method for Assaying for a Substance that
Affects an SH2-Phosphorylated Ligand Regulatory System
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bereskin & Parr
STREET: 40 King Street, West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08479078
FILING DATE: June 6, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Linda V. Kutydyk
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-154
TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-479-078-20

Query Match 0.9%; Score 7; DB 2; Length 96;
Best Local Similarity 100.0%; Preg. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 759 DYTTLR 765
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DB 35 DYTTLR 41

RESULT 68
US-08-539-005-17
Sequence 17, Application US/08539005
Patent No. 5858686
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Skolnick, Edward Y.
APPLICANT: Margolis, Benjamin L.
TITLE OF INVENTION: NOVEL EXPRESSION CLONING METHOD FOR
IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE
KINASES AND NOVEL TARGET PROTEINS
TITLE OF INVENTION: KINASES AND NOVEL TARGET PROTEINS
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: 10036-2711
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/539.005
FILING DATE: 4-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/167,035
FILING DATE: 16-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8664
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-539-005-17

Query Match 0.9%; Score 7; DB 2; Length 96;
Best Local Similarity 100.0%; Preg. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 759 DYTTLR 765

|||||
DB 34 DYTTLR 40

RESULT 69
US-09-280-598-19
Sequence 19, Application US/09280598
Patent No. 6391584
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Skolnick, Edward Y.
APPLICANT: Margolis, Benjamin L.
APPLICANT: App, Harold
TITLE OF INVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR
IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE
KINASES AND NOVEL TARGET PROTEINS
TITLE OF INVENTION: KINASES AND NOVEL TARGET PROTEINS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280.598
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/252,820
FILING DATE: 02-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-067
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8664
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-280-598-19

Query Match 0.9%; Score 7; DB 4; Length 96;
Best Local Similarity 100.0%; Preg. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 759 DYTTLR 765
|||||
DB 34 DYTTLR 40

RESULT 70
US-08-820-754-25
Sequence 25, Application US/08820754
Patent No. 5976835
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/820,754
FILING DATE: 19-MAR-1997
CLASSIFICATION: 53C
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 21-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
IMMEDIATE SOURCE:
CLONE: p85(alpha)N
US-08-820-754-25

Query Match 0.9%; Score 7; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 759 DYTLLR 765
|||
Db 39 DYTLLR 45

RESULT 71
US-08-956-652-25
Sequence 25, Application US/08956652
Patent No. 6033475
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN

TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,652
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 21-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
IMMEDIATE SOURCE:
CLONE: p85(alpha)N
US-08-956-652-25

Query Match 0.9%; Score 7; DB 3; Length 99;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 759 DYTLLR 765
|||
Db 39 DYTLLR 45

RESULT 72
US-08-956-869-25
Sequence 25, Application US/08956869
Patent No. 6030808
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong

TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,869
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/212,185
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
IMMEDIATE SOURCE:
CLONE: p85.alpha1N
US-08-956-869-25
Query Match 0.9% Score 7; DB 3; Length 99;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 759 DYTLLR 765
DB 39 DYTLLR 45
RESULT 73
US-08-948-547-25
Sequence 25, Application US/08948547
Patent No. 612418
GENERAL INFORMATION:
APPLICANT: Darrell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN

TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,547
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
IMMEDIATE SOURCE:
CLONE: p85.alpha1N
US-08-948-547-25
Query Match 0.9% Score 7; DB 3; Length 99;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 759 DYTLLR 765
DB 39 DYTLLR 45
RESULT 74
US-08-747-221B-8
Sequence 8, Application US/08747221B
Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: Silver, Gary M.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid
NUMBER OF SEQUENCES: 66

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CORRESPONDENCE ADDRESS:
ADDRESS: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 606361 December 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-747-221B-8

Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 103;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLN 131
DB 80 EDCLYLN 86

RESULT 75
US-09-005-051-8
Sequence 2, Application US/09005051
GENERAL INFORMATION:
PATENT NO. 6291222
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6291222 September 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
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REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-051-8

Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 103;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLN 131
DB 80 EDCLYLN 86
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Search completed: November 5, 2003, 15:26:50
Job time : 24 secs

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: November 5, 2003, 15:18:43, Search time 47 Seconds

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Title: US-09-978-423a-375

Perfect score: 816

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Searched: 1107863 seqs, 158726573 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

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Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARYS

Result No.	Score	Query Match	Length	ID	Description
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2	816	100.0	816	21	AAAB4296
3	816	100.0	816	21	AAAB3427
4	816	100.0	816	24	ABU61126
5	538	65.9	817	24	ABR82852
6	388	47.5	509	22	AAAB94127
7	388	47.5	509	24	ABR82853
8	326	40.0	816	23	AAAB49308
9	208	25.5	396	22	AAU87273

10	76	9.3	1.65	22	ABP17862	Human nervous syst
11	55	6.1	509	22	AAV93705	Human polypeptide
12	48	5.9	271	22	ABG10266	Novel human diagno
13	48	5.9	338	21	AAAB0734	Human CRFX ORF498
14	48	5.9	801	23	ABR07524	Human drug metabol
15	48	5.9	835	23	AAE25020	Human drug metabol
16	48	5.9	835	23	ABR97215	Novel human protei
17	48	5.9	835	23	ABR07675	Human carboxyleste
18	48	5.9	837	22	AAAB62400	Human MBSP2 polype
19	46	5.6	49	22	ABG51838	Human liver peptid
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22	32	3.9	229	21	AAAB4913	Human secreted pro
23	32	3.9	229	21	ABAB4914	Human secreted pro
24	32	3.8	726	22	ABG10264	Novel human diagno
25	31	3.8	144	22	AAO01845	Human polypeptide
26	28	3.4	81	22	AAU87570	Novel central nerv
27	28	3.4	81	22	AAU23324	Novel human enzyme
28	28	3.4	335	22	AAAB9345	Human polypeptide
29	28	3.4	419	22	ABG16824	Novel human diagno
30	26	3.2	165	22	ABG10269	Novel human diagno
31	26	2.6	134	22	AAO04336	Human polypeptide
32	22	2.2	228	23	ABG64991	Human albumin fusi
33	18	2.2	228	23	AAE21452	Human gene 1 encod
34	15	1.8	161	23	AAE21516	Human gene 1 encod
35	15	1.8	162	23	ABG64990	Human albumin fusi
36	15	1.8	162	23	AAE21473	Human gene 1 encod
37	12	1.5	359	21	AAAB54266	Human pancreatic c
38	12	1.5	535	15	AAAB58985	Bile salt-stimulat
39	12	1.5	538	16	AAAB75098	Recombinant bile s
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41	12	1.5	566	15	AAAB58981	Bile salt-stimulat
42	12	1.5	568	15	AAAB58982	Bile salt-stimulat
43	12	1.5	568	17	AAAB92558	Human bile salt-st
44	12	1.5	668	15	AAAB58983	Bile salt-stimulat
45	12	1.5	668	15	AAAB70445	Bile salt-stimulat
46	12	1.5	722	15	AAAB58984	Bile salt-stimulat
47	12	1.5	722	16	AAAB75107	Bile salt-activate
48	12	1.5	722	17	AAAB10050	Human bile salt-ac
49	12	1.5	722	17	AAAB98926	Human bile salt-ac
50	12	1.5	722	23	ABR04676	Human milk bile sa
51	12	1.5	722	23	AAU09894	Bile salt-stimulat
52	12	1.5	735	23	ABR41301	Human ovarian anti
53	12	1.5	742	12	AAAB14111	Human milk bile-sa
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55	12	1.5	744	15	AAAB45189	BSSL/CEL. Homo sa
56	12	1.5	745	13	AAAB20098	Bile salt-stimulat
57	12	1.5	745	15	AAAB58980	Bile salt-stimulat
58	12	1.5	745	17	AAAB99257	Human bile salt-st
59	12	1.5	745	20	AAAB32168	Human bile salt-st
60	12	1.5	745	21	AAAB08202	A human pancreatic
61	11	1.3	530	19	AAAB57667	C. felis esterase,
62	11	1.3	530	19	AAAB57667	Drosophila melano
63	11	1.3	517	22	ABR68593	Drosophila melano
64	10	1.2	537	22	ABR61304	Drosophila melano
65	9	1.1	92	23	AAO17545	Human carboxyleste
66	9	1.1	266	23	ABR69056	Human polypeptide
67	9	1.1	507	22	ABR61993	Human polypeptide
68	9	1.1	541	22	ABR57789	Drosophila melano
69	9	1.1	543	20	AAAB33146	Rabbit liver carbo
70	9	1.1	544	23	AAO18872	Recombinant porcin
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72	9	1.1	564	22	ABR60015	Drosophila melano
73	9	1.1	565	20	AAAB33145	Rabbit liver carbo
74	9	1.1	566	21	AAAB08202	Amino acid sequenc
75	9	1.1	566	22	AAAB73263	Human triacylglyce
76	9	1.1	567	23	AAO17544	Human liver carbox
77	9	1.1	568	24	ABR97363	Human acyl coenzym
78	9	1.1	574	23	ABR31485	D. melanogaster ju
79	9	1.1	575	23	ABR61004	Novel human protei
80	9	1.1	581	23	ABR79537	Human carboxyleste
81	9	1.1	581	23	ABR61005	Novel human protei
82	9	1.1	581	24	ABR54639	Human NOVX polypep

```
83      9      1.1      583      21      AAB43732      Human: Cancer assoc
84      9      1.1      584      19      AAM31601      P-9 liver esterase
85      9      1.1      597      12      AAR12384      Bovine pancreatic
86      3      1.1      642      23      AAE25025      Human drug metabol
87      9      1.1      764      22      ABG24276      Novel human diagra
88      9      1.1      803      22      ABB62003      Drosophila melanog
89      9      1.1      875      22      ABB60257      Novel human melanog
90      5      1.0      67      22      ABG13651      Acetylcholinestera
91      3      1.0      81      9      AAP92904      C. felis esterase,
92      5      1.0      137      19      AAM57853      Glutrocephalides fe
93      8      1.0      137      21      AAR12908      Human pancreatic c
94      8      1.0      144      21      AAB54392      Human G-protein cc
95      8      1.0      178      22      AAU04572      Human G-protein-cc
96      8      1.0      178      24      ABU60873      Novel human diagra
97      8      1.0      200      22      ABG13653      Novel human diagra
98      5      1.0      210      24      ABB81688      Human G-protein-cc
99      8      1.2      219      23      ABB90252      Human polypeptide
100     8      1.2      244      22      AAB85129      P. viticola cystein
```

ALIGNMENTS

RESULT 1

ID AAY41740 standard: Protein; 816 AA.

AC AAY41740;

DT 07-DEC-1999 (first entry)

DE Human PRO703 protein sequence.

KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;

KW probe: blood coagulation disorder; cancer; cellular adhesion disorder;

KW secreted protein; transmembrane protein.

XX Homo sapiens.

XX MOJ346281-A2.

PD 16-SEP-1995.

PF 08-MAR-1999; 99MO-US05C28.

XX 10-MAR-1998; 98US-0077450.

PR 11-MAR-1998; 98US-0077632.

PR 11-MAR-1998; 98US-0077641.

PR 11-MAR-1998; 98US-0077649.

PR 12-MAR-1998; 98US-0077791.

PR 13-MAR-1998; 98US-0078004.

PR 17-MAR-1998; 98US-0043220.

PR 20-MAR-1998; 98US-0078886.

PR 20-MAR-1998; 98US-0078910.

PR 20-MAR-1998; 98US-0078936.

PR 20-MAR-1998; 98US-0078939.

PR 25-MAR-1998; 98US-0079294.

PR 26-MAR-1998; 98US-0079656.

PR 27-MAR-1998; 98US-0079663.

PR 27-MAR-1998; 98US-0079664.

PR 27-MAR-1998; 98US-0079689.

PR 27-MAR-1998; 98US-0079728.

PR 27-MAR-1998; 98US-0079766.

PR 30-MAR-1998; 98US-0079920.

PR 30-MAR-1998; 98US-0079923.

PR 3-MAR-1998; 98US-0080105.

PR 3-MAR-1998; 98US-0080107.

PR 31-MAR-1998; 98US-0080165.

PR 31-MAR-1998; 98US-0080194.

PR 01-APR-1998; 98US-0080327.

PR 01-APR-1998; 98US-0080328.

PR 01-APR-1998; 98US-0080333.

PR 01-APR-1998; 98US-0080334.

PR 08-APR-1998; 98US-0091049.

PR 08-APR-1998; 98US-0091070.

PR 08-APR-1998; 98US-0091071.

PR 09-APR-1998; 98US-0091195.

PR 09-APR-1998; 98US-0091203.

PR 09-APR-1998; 98US-0091229.

PR 15-APR-1998; 98US-0091817.

PR 15-APR-1998; 98US-0091817.

PR 15-APR-1998; 98US-0091952.

PR 15-APR-1998; 98US-0091955.

PR 21-APR-1998; 98US-0092569.

PR 21-APR-1998; 98US-0092569.

PR 22-APR-1998; 98US-0092700.

PR 22-APR-1998; 98US-0092704.

PR 22-APR-1998; 98US-0092804.

PR 23-APR-1998; 98US-0092877.

PR 23-APR-1998; 98US-0092796.

PR 27-APR-1998; 98US-0093336.

PR 28-APR-1998; 98US-0093336.

PR 28-APR-1998; 98US-0093392.

PR 29-APR-1998; 98US-0093495.

PR 29-APR-1998; 98US-0093495.

PR 29-APR-1998; 98US-0093496.

PR 29-APR-1998; 98US-0093499.

PR 29-APR-1998; 98US-0093500.

PR 29-APR-1998; 98US-0093545.

PR 29-APR-1998; 98US-0093554.

PR 29-APR-1998; 98US-0093558.

PR 29-APR-1998; 98US-0093559.

PR 30-APR-1998; 98US-0093742.

PR 05-MAY-1998; 98US-0094366.

PR 06-MAY-1998; 98US-0094414.

PR 06-MAY-1998; 98US-0094441.

PR 07-MAY-1998; 98US-0094598.

PR 07-MAY-1998; 98US-0094600.

PR 07-MAY-1998; 98US-0094627.

PR 07-MAY-1998; 98US-0094639.

PR 07-MAY-1998; 98US-0094640.

PR 07-MAY-1998; 98US-0094643.

PR 13-MAY-1998; 98US-0095323.

PR 13-MAY-1998; 98US-0095338.

PR 13-MAY-1998; 98US-0095339.

PR 13-MAY-1998; 98US-0095573.

PR 15-MAY-1998; 98US-0095579.

PR 15-MAY-1998; 98US-0095580.

PR 15-MAY-1998; 98US-0095582.

PR 15-MAY-1998; 98US-0095689.

PR 15-MAY-1998; 98US-0095697.

PR 15-MAY-1998; 98US-0095700.

PR 15-MAY-1998; 98US-0095704.

PR 18-MAY-1998; 98US-0096023.

PR 22-MAY-1998; 98US-0096392.

PR 22-MAY-1998; 98US-0096414.

PR 22-MAY-1998; 98US-0096430.

PR 22-MAY-1998; 98US-0096486.

PR 28-MAY-1998; 98US-0096709.

PR 28-MAY-1998; 98US-0097106.

PR 28-MAY-1998; 98US-0097208.

PR 30-JUL-1998; 98US-0094651.

PR 11-SEP-1998; 98US-0090368.

XX (GETH) GENENTECH INC.

XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

XX WPI; 1999-551358/46.

XX N-PSDB; AA234209.

XX New secreted and transmembrane polypeptides and their polynucleotides,

XX useful for treating blood coagulation disorders, cancers and cellular

XX adhesion disorders -

XX Claim 12; Fig 151; 530pp; English.

XX

XX

XX The present invention describes secreted and transmembrane polypeptides
 CC and their polynucleotides. The nucleotide sequences are useful as
 CC sources of probes, primers, for chromosome mapping, and for generation
 CC of antisense sequences. They can also be used to create transgenic
 CC animals. The proteins can be used to treat a variety of diseases and
 CC disorders, depending on their function. Diseases that may be treated
 CC include blood coagulation disorders, cancers and cellular adhesion
 CC disorders. They may also be used to raise antibodies. AA33861 to
 CC AA33868, and AA33865 to AA33874 represent polynucleotide and
 CC polypeptide sequence given in the exemplification of the present
 CC invention.

XX Sequence 816 AA:

Query Match 100.0%; Score 816; DB 20; Length 816;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSNVLMWLTALAIKFTLDSQAVPVNLYGKIRGLTLPLEILGPVGYLGFVYA 60
 DB 1 MNSNVLMWLTALAIKFTLDSQAVPVNLYGKIRGLTLPLEILGPVGYLGFVYA 60
 QY 61 SEPTGRRFQPEPPSSWTGINTTQFAVCPQHLDESSLHDMPIFTNLDTLTYV 120
 DB 61 SEPTGRRFQPEPPSSWTGINTTQFAVCPQHLDESSLHDMPIFTNLDTLTYV 120
 QY 121 QCNEDCLYLNIVYPEDGANTKKNADQTSNDGDEDDHONSKKVWYVYHGSYME 180
 DB 121 QCNEDCLYLNIVYPEDGANTKKNADQTSNDGDEDDHONSKKVWYVYHGSYME 180
 QY 181 GCGNMIDGSIILASGVNIVITNYRLGILFSTSDQAAGKNGYLLDQIALWIEEWG 240
 DB 181 GCGNMIDGSIILASGVNIVITNYRLGILFSTSDQAAGKNGYLLDQIALWIEEWG 240
 QY 241 AFGGPKRYTIFSGSGAGSCVSLTSHSSEGLFQKALICSTALSSKAYVQYAKYTR 300
 DB 241 AFGGPKRYTIFSGSGAGSCVSLTSHSSEGLFQKALICSTALSSKAYVQYAKYTR 300
 QY 301 LADKVGCMMLDTDMVECLRNKVKELIQITTPATVHAFGSPVIGDVIDDQQLMEQ 360
 DB 301 LADKVGCMMLDTDMVECLRNKVKELIQITTPATVHAFGSPVIGDVIDDQQLMEQ 360
 QY 361 GEELNDIMLGNGGEGCLKFNGGIVDNEGVTPNPDPSYSFVNNLYGVEGKLTJET 420
 DB 361 GEELNDIMLGNGGEGCLKFNGGIVDNEGVTPNPDPSYSFVNNLYGVEGKLTJET 420
 QY 421 IKFMYTMAKDENPETRRKTLVALFTDQWVAPAVADLHAQVGSPTFFVAFYHGSSEM 480
 DB 421 IKFMYTMAKDENPETRRKTLVALFTDQWVAPAVADLHAQVGSPTFFVAFYHGSSEM 480
 QY 481 KSMNADSAHGEDEVYFGIPMIGFTELPSCNFSKCDVMSLAVMTYMTNFAKTQDPQV 540
 DB 481 KSMNADSAHGEDEVYFGIPMIGFTELPSCNFSKCDVMSLAVMTYMTNFAKTQDPQV 540
 QY 541 PCOTKFIHTKPRFEEVWASXVNFQDYLHGLKPRYEHYEAQVAFWELTSHLH 600
 DB 541 PCOTKFIHTKPRFEEVWASXVNFQDYLHGLKPRYEHYEAQVAFWELTSHLH 600
 QY 601 NEIFQVYSTTTRKVPDMTSPFYGTRRSFAKIMPTKPAIPANPNHSGSDPKTGED 660
 DB 601 NEIFQVYSTTTRKVPDMTSPFYGTRRSFAKIMPTKPAIPANPNHSGSDPKTGED 660
 QY 661 TTVLETRKQVSTELSVTAAGASLFLNLLAFALVYKCKRRETHRRSPQRNTND 720
 DB 661 TTVLETRKQVSTELSVTAAGASLFLNLLAFALVYKCKRRETHRRSPQRNTND 720
 QY 721 IAHQNEEISLQMKOLEHDEGCESLQADTLRLTCCPDYTTLERSDDILPLTPWTIT 780
 DB 721 IAHQNEEISLQMKOLEHDEGCESLQADTLRLTCCPDYTTLERSDDILPLTPWTIT 780
 QY 781 MIPNTLGGVPLHTNCTFGGQNSTNLPHGSHSTRV 816
 DB 781 MIPNTLGGVPLHTNCTFGGQNSTNLPHGSHSTRV 816

DB 781 MIPNTLGGVPLHTNCTFGGQNSTNLPHGSHSTRV 816

RESULT 2

AA344296

AA344296 standard; Protein; 816 AA.

AA344296;

08-FEB-2001 (first entry)

Human PRO701 (UNQ365) protein sequence SEQ ID NO:375.

Human: secreted protein; transmembrane protein; PRO; EST; cytosolic;

expressed sequence tag; detection; cancer.

Hom sapiens.

MO200053756-A2.

14-SEP-2000.

18-FEB-2000; 2000MO-US04341.

08-MAR-1999; 99MO-US05028.

12-MAR-1999; 99US-0123957.

29-MAR-1999; 99US-0126773.

21-APR-1999; 99US-0130232.

28-APR-1999; 99US-0131445.

14-MAY-1999; 99US-0134287.

23-JUN-1999; 99US-0141037.

26-JUL-1999; 99US-0145698.

29-OCT-1999; 99US-0162506.

30-NOV-1999; 99MO-US28313.

02-DEC-1999; 99MO-US28551.

16-DEC-1999; 99MO-US28565.

30-DEC-1999; 99MO-US30095.

30-DEC-1999; 99MO-US31243.

05-JAN-2000; 2000MO-US00219.

06-JAN-2000; 2000MO-US00277.

06-JAN-2000; 2000MO-US00376.

(SETH) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein D, Desnoyers J, Eaton DL,

Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME,

Coddard A, Godowski PJ, Grimaldi CC, Gurney AL, Hillan KJ,

Klajman LJ, Kuo SS, Napier MA, Pan J, Paori RF, Roy NA,

Shelton DL, Stewart TA, Tumas D, Williams PM, Wood W.

WFI: 2000-611443/58.

N-FSDB; AAC78552.

Novel PRO polypeptides and polynucleotides used in detection methods,
 to target bioactive molecules to specific cells, and to modulate
 cellular activities -
 Claim 12; Fig 151; 636p; English.

AAC78458 to AAC78599 represent polynucleotide and EST (expressed
 sequence tag) sequences which encode secreted or transmembrane PRO
 polypeptides. The PRO polynucleotides and polypeptides have cytostatic
 activity. The polynucleotides and polypeptides can be used for detecting
 the presence of PRO polypeptides in samples, for linking bioactive
 molecules to cells and for modulating biological activities of cells,
 using the polypeptides for specific targeting. The polypeptide targeting
 can be used to kill the target cells, e.g. for the treatment of cancers.
 The polypeptide pairs provide specific targeting of bioactive molecules
 to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
 the isolation of the PRO polynucleotide sequences.

Sequence 816 AA:

Query Match 100.0%; Score 816; DB 2.; Length 816;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MNSNVLLWLTALAIETTLDSQAQPVVNTVYKIRGLRPLPNEILGPEQYGVYPA 60
DB 1 MNSNVLLWLTALAIETTLDSQAQPVVNTVYKIRGLRPLPNEILGPEQYGVYPA 60
QY 61 SPTGRRRCFPPPPSSMTGINTTGFPAVCPQHLDERELTDCXNPIWETALDITMYV 120
DB 61 SPTGRRRCFPPPPSSMTGIRKTTTFFAACVCPQHLDERELTDCXNPIWETALDITMYV 120
QY 121 QQCNEQCLYLNIVPTEEDANTKQADDTSDRGEDEDIDQNSKKPPVYVINGSYVE 190
DB 121 QQCNEQCLYLNIVPTEEDANTKQADDTSDRGEDEDIDQNSKKPPVYVINGSYVE 180
QY 181 GTGNMIDGSLILASXGVYITITNYRGLIGFSTGQAAKKVGLDQCALRMKEENVG 240
DB 181 GTGNMIDGSLILASXGVYITITNYRGLIGFSTGQAAKKVGLDQCALRMKEENVG 240
QY 241 AFQGPFRVITIFSGAGASCVSILTSYHSEGFQXATQSGTALSXNANYQFAKXTRI 300
DB 241 AFQGPFRVITIFSGAGASCVSILTSYHSEGFQXATQSGTALSXNANYQFAKXTRI 300
QY 301 LADKVGCMMLDTTDMYECURNKVKELIQCTTPATYHIAFGFVIGDVIIPDQGIEMEQ 360
DB 301 LADKVGCMMLDTTDMYECURNKVKELIQCTTPATYHIAFGFVIGDVIIPDQGIEMEQ 360
QY 361 GEFINDIMLVNCGEGKLVNGLVINEGCVTPNPDPFSVSNLYNGYREGKTLRET 420
DB 361 GEFINDIMLVNCGEGKLVNGLVINEGCVTPNPDPFSVSNLYNGYREGKTLRET 420
QY 421 IKMYTDMADKEXPETRRKTLVALFTDQGVAPAVACADLHAGYSGFTFYAFYHQCSEY 480
DB 421 IKMYTDMADKEXPETRRKTLVALFTDQGVAPAVACADLHAGYSGFTFYAFYHQCSEY 480
QY 481 KPSMADSAHGDVYVYFGPMIGTELESCNFSKDCWLSAVMTYWTNPAFTGDPNPV 540
DB 481 KPSMADSAHGDVYVYFGPMIGTELESCNFSKDCWLSAVMTYWTNPAFTGDPNPV 540
QY 541 POEKFIFKPNFEEVAASKYKPKDLYLHGKRVSDHRAKVAFWELVPHLNL 600
DB 541 POEKFIFKPNFEEVAASKYKPKDLYLHGKRVSDHRAKVAFWELVPHLNL 600
QY 601 NEIFQVYSTTKVPPDMSFPYGTSPSPAKIMPTTKRPAITPANNPKSKDPKHTGED 660
DB 601 NEIFQVYSTTKVPPDMSFPYGTSPSPAKIMPTTKRPAITPANNPKSKDPKHTGED 660
QY 661 TTVLITKRDYSELSTVAVGASLFLNLLAFAALYYKCSRRIETHRPSPQNTTND 720
DB 661 TTVLITKRDYSELSTVAVGASLFLNLLAFAALYYKCSRRIETHRPSPQNTTND 720
QY 721 IAHIOEEIMSLQKLEIDHECESQADJTLRLTPEPYTLTLRRSPDICTLMPNTT 780
DB 721 IAHIOEEIMSLQKLEIDHECESQADJTLRLTPEPYTLTLRRSPDICTLMPNTT 780
QY 781 MIPNTLTGMQPLHTENTFSGGQNSINLPHGSHTRY 816
DB 781 MIPNTLTGMQPLHTENTFSGGQNSINLPHGSHTRY 816

```

RESULT 3
 AAB33427
 ID AAB33427 standard; Protein; 816 AA.

XX AAB33427;

XX 29-JAN-2001 (first entry)

DE Human PRO701 protein UNQ365 SEQ ID NO:67.

XX Human; immune related disease; diagnosis; arthritis; inflammatory; cardiac;

KM dermatological; antiarthritic; antirheumatic; immunosuppressive;
 KW haemostatic; antithyroid; antidiabetic; neurotic; neuoprotective;
 KW antinaemic; hepatotropic; vitruoid; antipsoriatic; antiallergic;
 KW antiaesthetic; systemic lupus erythematosus; rheumatoid arthritis;
 KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
 KW autoimmune thrombocytopaenia; immune-mediated renal disease;
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;
 KW inflammatory bowel disease; gluten-sensitive enteropathy;
 KW autoimmune disease; immune-mediated skin disease; allergic disease;
 KW immunological disease; transplantation associated disease;
 KW graft rejection; graft-versus-host-disease.
 KW Homo sapiens.
 KW W02000053758-A2.
 PD 14-SEP-2000.
 XX
 PF 02-MAR-2000; 2000MO-US05841.
 XX
 PR 08-MAR-1999; 99MO-US05028.
 PR 10-MAR-1999; 99US-0123618.
 PR 12-MAR-1999; 99US-0123957.
 PR 23-MAR-1999; 99US-0125775.
 PR 22-APR-1999; 99US-0128849.
 PR 20-APR-1999; 99MO-US08645.
 PR 28-APR-1999; 99US-0131445.
 PR 04-MAY-1999; 99US-0132371.
 PR 14-MAY-1999; 99US-0134287.
 PR 02-JUN-1999; 99MO-US12252.
 PR 23-JUN-1999; 99US-0144037.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.
 PR 01-SEP-1999; 99MO-US20211.
 PR 08-SEP-1999; 99MO-US20594.
 PR 13-SEP-1999; 99MO-US20944.
 PR 15-SEP-1999; 99MO-US21090.
 PR 15-SEP-1999; 99MO-US21547.
 PR 05-OCT-1999; 99MO-US23089.
 PR 29-OCT-1999; 99US-0162506.
 PR 29-NOV-1999; 99MO-US28214.
 PR 30-NOV-1999; 99MO-US28313.
 PR 30-NOV-1999; 99MO-US28409.
 PR 01-DEC-1999; 99MO-US28634.
 PR 01-DEC-1999; 99MO-US28634.
 PR 02-DEC-1999; 99MO-US28581.
 PR 02-DEC-1999; 99MO-US28584.
 PR 02-DEC-1999; 99MO-US28585.
 PR 16-DEC-1999; 99MO-US30095.
 PR 20-DEC-1999; 99MO-US30999.
 PR 30-DEC-1999; 99MO-US31274.
 PR 05-JAN-2000; 2000MO-US00219.
 PR 06-JAN-2000; 2000MO-US00277.
 PR 06-JAN-2000; 2000MO-US00376.
 PR 11-FEB-2000; 2000MO-US00365.
 PR 18-FEB-2000; 2000MO-US04341.
 PR 18-FEB-2000; 2000MO-US04342.
 PR 22-FEB-2000; 2000MO-US04414.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Ashkenazi A¹, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W,
 XX Kabakoff RC, Lu Y, Fan J, Pennica D, Shelton DL, Smith V,
 XX Stewart TA, Tumas D, Watanabe CX, Wood WI, Yan M;
 XX WPI: 2000-572271/53.
 DR N-PSDB: AAC58592.
 XX
 PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 immune related disorders, e.g. systemic lupus erythematosus, rheumatoid

PC arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
XX
PS Claim 33; Fig 28; 309pp; English.
XX
CC The present invention describes sixty four human PRO proteins which can
CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemo-lytic
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central
CC and peripheral nervous systems, hepatobiliary diseases, inflammatory
CC bowel disease, glucose-sensitive enteropathy and Whipple's disease.
CC autoimmune or immune-mediated skin diseases, allergic diseases,
CC immunological diseases of the lung, and transplantation associated
CC diseases including graft rejection and graft-versus-host-disease.
CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and
CC AAC33414 to AAC33477 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX

SQ Sequence 816 AA;

Query Match 100.0%; Score 816; DB 21; Length 816;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLNSNVLLMLTALAKFLILDSQAPVNTNYSKLGRTPLNELSGVEQLGAPYA 60
DB 1 MLNSNVLLMLTALA-KFLILDSQAPVNTNYSKLGRTPLNELSGVEQLGAPYA 60
QY 61 SPTGERRFQPPSPSSWTS:RNTQFAVCPHLPDPSLLHDM:PIWTFANQDTLTYV 120
DB 61 SPTGERRFQPPSPSSWTS:GRNCTQFAVCPHLPDPSLLHDM:PIWTFANQDTLTYV 120
QY 121 QDCNECCLYNIVPTEDGATTKNADITSDNDEDED:HDONSRRPVVYIHGSYWE 180
DB 121 QDCNECCLYNIVPTEDGATTKNADITSDNDEDED:HDONSRRPVVYIHGSYWE 180
QY 121 QDCNECCLYNIVPTEDGATTKNADITSDNDEDED:HDONSRRPVVYIHGSYWE 180
DB 121 QDCNECCLYNIVPTEDGATTKNADITSDNDEDED:HDONSRRPVVYIHGSYWE 180
QY 181 GTGNMIDGSLASGNVIVITNRLGTLGSLGDDAKNVCGLQIQNLKWEEDNNG 240
DB 181 GTGNMIDGSLASGNVIVITNRLGTLGSLGDDAKNVCGLQIQNLKWEEDNNG 240
QY 181 GTGNMIDGSLASGNVIVITNRLGTLGSLGDDAKNVCGLQIQNLKWEEDNNG 240
DB 181 GTGNMIDGSLASGNVIVITNRLGTLGSLGDDAKNVCGLQIQNLKWEEDNNG 240
QY 241 AFGGDPKRVITFGSGAGAGACVSLTTLHYSEGLFQKAI:CSGTLSSMAVNYOPAKTTR 300
DB 241 AFGGDPKRVITFGSGAGAGACVSLTTLHYSEGLFQKAI:CSGTLSSMAVNYOPAKTTR 300
QY 241 AFGGDPKRVITFGSGAGAGACVSLTTLHYSEGLFQKAI:CSGTLSSMAVNYOPAKTTR 300
DB 241 AFGGDPKRVITFGSGAGAGACVSLTTLHYSEGLFQKAI:CSGTLSSMAVNYOPAKTTR 300
QY 301 LADKVGCMPLDTTMEVCELEKKNKKEJ:QCTITATYHIAFGPVYIDCV:PDQFQIMEQ 360
DB 301 LADKVGCMPLDTTMEVCELEKKNKKEJ:QCTITATYHIAFGPVYIDCV:PDQFQIMEQ 360
QY 301 LADKVGCMPLDTTMEVCELEKKNKKEJ:QCTITATYHIAFGPVYIDCV:PDQFQIMEQ 360
DB 301 LADKVGCMPLDTTMEVCELEKKNKKEJ:QCTITATYHIAFGPVYIDCV:PDQFQIMEQ 360
QY 361 GEFNAYD:MGVNGEGKXYVDGIVDNEDGVTDPDPSSVNFQNLGYGPEGCTLRRT 420
DB 361 GEFNAYD:MGVNGEGKXYVDGIVDNEDGVTDPDPSSVNFQNLGYGPEGCTLRRT 420
QY 421 IKFMYTDADKENETRAKTLVALFTDQWAPAVAADLNAQVSPITYFAFYHHCQSEY 480
DB 421 IKFMYTDADKENETRAKTLVALFTDQWAPAVAADLNAQVSPITYFAFYHHCQSEY 480
QY 481 KPSWADSAHGDEVYVFGIPIWIGTELFSCNFSQNDVLSAVWVTYTNFAKTDPRQV 540
DB 481 KPSWADSAHGDEVYVFGIPIWIGTELFSCNFSQNDVLSAVWVTYTNFAKTDPRQV 540
QY 541 PODTKFHTKPRREEVAKSKYNPKDQYLH:GLKPRVRSYRATKXAFNLVYBPHJNL 600
DB 541 PODTKFHTKPRREEVAKSKYNPKDQYLH:GLKPRVRSYRATKXAFNLVYBPHJNL 600
QY 601 NEIFOVSTTTKVPFPMWTSFPGYRSPAKIAPTTRFAITPANNKSHKSDPKHTFED 660
DB 601 NEIFOVSTTTKVPFPMWTSFPGYRSPAKIAPTTRFAITPANNKSHKSDPKHTFED 660
QY 601 NEIFOVSTTTKVPFPMWTSFPGYRSPAKIAPTTRFAITPANNKSHKSDPKHTFED 660
DB 601 NEIFOVSTTTKVPFPMWTSFPGYRSPAKIAPTTRFAITPANNKSHKSDPKHTFED 660

QY 661 TVLIEITRDYSTEISVTIANVASTLFLNLTAPAAVYKKQKPRHETRRRPSQGNITND 720
DB 661 TVLIEITRDYSTEISVTIANVASTLFLNLTAPAAVYKKQKPRHETRRRPSQGNITND 720
QY 721 IAH:QNEEIMS:QKQQLSHDECESLQAHDTLRITCPEDYTLTRRSPDCLFMTPNIT 780
DB 721 IAH:QNEEIMS:QKQQLSHDECESLQAHDTLRITCPEDYTLTRRSPDCLFMTPNIT 780
QY 781 MIPNTLTKQPLHTPNTSSGQNS:NLFRGSHSTRV 816
DB 781 MIPNTLTKQPLHTPNTSSGQNS:NLFRGSHSTRV 816
RESULT 4
ABU61126
ID ABU61126 standard; Protein; 816 AA.
XX
AC ABU61126;
XX
XX 08-MAY-2003 (first entry)
XX
DE Human PRO701 polypeptide.
XX
KM Human; PRO polypeptide; secreted and transmembrane protein;
KM immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
KM cardiac insufficiency; nervous system disorder; kidney disorder;
KM bone disorder; cartilage disorder; arthritis; tumor; wound healing;
KM genetic disorder; cystostatic; antidiabetic; antiinflammatory;
KM antiarthritic; anti-tumor; vulnerary; antineoplastic; dermatological;
KM cardiant.
XX
XX Homo sapiens.
XX
XX US2002:69284-A1.
XX
PD 14-NOV-2002.
XX
XX 16-OCT-2001; 2001US-0978697.
XX
XX 07-OCT-1998; 98WO-US21141.
XX
XX 20-NOV-1998; 98WO-US24855.
XX
XX 05-JAN-1999; 99WO-US00106.
XX
XX 08-MAR-1999; 99WO-US05028.
XX
XX 10-FEB-1999; 99WO-US05190.
XX
XX 14-MAY-1999; 99WO-US10733.
XX
XX 02-JUN-1999; 99WO-US12252.
XX
XX 30-NOV-1999; 99WO-US28313.
XX
XX 02-DEC-1999; 99WO-US28551.
XX
XX 02-DEC-1999; 99WO-US28565.
XX
XX 16-DEC-1999; 99WO-US30095.
XX
XX 30-DEC-1999; 99WO-US31243.
XX
XX 30-DEC-1999; 99WO-US31274.
XX
XX 05-JAN-2000; 2000WO-US00219.
XX
XX 06-JAN-2000; 2000WO-US00277.
XX
XX 06-JAN-2000; 2000WO-US00376.
XX
XX 11-FEB-2000; 2000WO-US03565.
XX
XX 18-FEB-2000; 2000WO-US04341.
XX
XX 24-FEB-2000; 2000WO-US05004.
XX
XX 02-MAR-2000; 2000WO-US05841.
XX
XX 10-MAR-2000; 2000WO-US06319.
XX
XX 21-MAR-2000; 2000WO-US07532.
XX
XX 30-MAR-2000; 2000WO-US08439.
XX
XX 17-MAY-2000; 2000WO-US13705.
XX
XX 22-MAY-2000; 2000WO-US14042.
XX
XX 30-MAY-2000; 2000WO-US14941.
XX
XX 02-JUN-2000; 2000WO-US15264.
XX
XX 28-JUL-2000; 2000WO-US20710.
XX
XX 24-AUG-2000; 2000WO-US23328.
XX
XX 01-DEC-2000; 2000WO-US31678.
XX
XX 20-DEC-2000; 2000WO-US34956.
XX
XX 28-FEB-2001; 2001WO-US06520.
XX
XX 22-MAR-2001; 2001WO-US09552.

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PR 25-MAY-2001; 2001MO-US17932.
PR 01-JUN-2001; 2001MO-US17950.
PR 20-JUN-2001; 2001MO-US19692.
PR 29-JUN-2001; 2001MO-US21066.
PR 09-JUL-2001; 2001MO-US21735.
PR 17-OCT-1997; 97US-062250P.
PR 03-NOV-1997; 97US-064249P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066364P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077649P.
PR 12-MAR-1998; 98US-077791P.
PR 13-MAR-1998; 98US-078002P.
PR 20-MAR-1998; 98US-078886P.
PR 20-MAR-1998; 98US-078910P.
PR 20-MAR-1998; 98US-078536P.
PR 20-MAR-1998; 98US-078539P.
PR 25-MAR-1998; 98US-079294P.
PR 25-MAR-1998; 98US-079656P.
PR 27-MAR-1998; 98US-079663P.
PR 27-MAR-1998; 98US-079664P.
PR 27-MAR-1998; 98US-079689P.
PR 27-MAR-1998; 98US-079728P.
PR 27-MAR-1998; 98US-079786P.
PR 30-MAR-1998; 98US-079920P.
PR 30-MAR-1998; 98US-079922P.
PR 26-MAY-1981; 81US-0267223.
PR 17-MAR-1998; 98US-0040220.
PR 26-JUN-1995; 98US-0105413.
PR 07-OCT-1998; 98US-0168978.
PR 02-NOV-1998; 98US-0184216.
PR 06-NOV-1998; 98US-0187368.
PR 07-DEC-1998; 98US-0222054.
PR 22-DEC-1998; 98US-0228517.
PR 05-MAR-1999; 99US-0254465.
PR 10-MAR-1999; 99US-0265666.
PR 12-APR-1999; 99US-0284231.
PR 14-MAY-1999; 99US-0311832.
PR 14-MAY-1999; 99US-0380137.
PR 25-AUG-1999; 99US-0380138.
PR 25-AUG-1999; 99US-0380142.
PR 25-AUG-1999; 99US-0380129.
PR 08-NOV-2000; 2000US-C709238.
PR 27-NOV-2000; 2000US-C723749.
PR 20-DEC-2000; 2000US-C747253.
PR 22-MAR-2001; 2001US-0816744.
PR 22-MAR-2001; 2001US-081692C.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-085428C.
PR 01-JUN-2001; 2001US-0872635.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 30-JUL-2001; 2001US-0918585.

XX
XX (GETH ) GENENTECH INC.
XX
XX ASKhenazi A, Baker KP, Borstein D, Desnoyers L, Eaton D;
XX Ferrara N, Gilwardt E, Fong S, Gao W, Gelbar H, Gertsen ME;
XX Goddard A, Goldwast PJ, Grimaldi JC, Gurney AJ, Hillan KJ;
XX Klavavin IO, Kuo SS, Napier WA, Pan C, Paoni NF, Roy RA;
XX Shelton DJ, Stewart TA, Tumas D, Williams PM, Wood M;
XX
XX WPI; 2003-286163/28.
XX N-PSDB; ABX9258..
XX
XX Novel secreted and transmembrane polypeptides and polynucleotides
XX encoding them useful for treating cancer, kidney diseases, bone,
XX cartilage disorders and immune deficiencies.
XX
XX Claim 12; Fig 151; 459pp; English.
XX
XX

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Cc	The present invention relates to the isolation of novel human PRO
Cc	polypeptides, and the polynucleotide sequences encoding them. The
Cc	PRO polypeptides are secreted and transmembrane proteins. The PRO
Cc	polypeptides are useful for detecting other PRO polypeptides, for
Cc	linking bioactive molecules to cells expressing PRO polypeptides,
Cc	for mediating biological activities of cells expressing PRO
Cc	polypeptides, and for identifying agonists or antagonists. The
Cc	bioactive molecule maybe a toxin, radiolabel or antibody, and causes
Cc	apoptosis or death of the cell. The PRO polypeptides are useful for
Cc	treating immune disorders, diabetes or hyper- or hypo-insulinaemia,
Cc	cardiac insufficiency, nervous system disorders, kidney disorders,
Cc	bone and cartilage disorders or arthritis, tumours, and wound healing.
Cc	The polynucleotide sequences encoding PRO polypeptides are useful as
Cc	hybridisation probes, in chromosome and gene mapping, in the generation
Cc	of antisense RNA and DNA, in the preparation of PRO polypeptides, for
Cc	generating transgenic animals or knockout animals, for the genetic
Cc	analysis of individuals with genetic disorders, and in gene therapy.
Cc	AB61071-AB61164 represent the human PRO polypeptides of the
Cc	invention.
Cc	Note: The sequence data for this patent was obtained in electronic
Cc	format directly from the USPTO web site at
Cc	seqdata.uspto.gov/patidentry.htm.
Cc	xx
Sq	Sequence 316 AA;
Qy	Query Match 100.0%; Score 616; DB 24; Length 816;
Dz	Best Local Similarity 100.0%; P-adj. NO. 0;
Dz	Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 M L N S V L L M T A L A K E F T L D S Q A Y V W N T Y N K I R G L R T P L N E I L G P V E Q Y L G V Y A 60
Dz	1 M L N S V L L M T A L A K E F T L D S Q A Y V W N T Y N K I R G L R T P L N E I L G P V E Q Y L G V Y A 60
Qy	61 S P P G E R F O P E P P S S W T G R N T T G C A A V C P C L B E R S L H D M L P I F T A N L D T L M T Y V 120
Dz	61 S P P G E R F O P E P P S S W T G R N T T G C A A V C P C L B E R S L H D M L P I F T A N L D T L M T Y V 120
Qy	121 Q D Q M E D C L Y N I Y P T E D G A N T K K A G D I T S N D G E D C I H D O S K K R V M Y Y I H G S G Y M E 180
Dz	121 Q D Q M E D C L Y N I Y P T E D G A N T K K A G D I T S N D G E D C I H D O S K K R V M Y Y I H G S G Y M E 180
Qy	121 Q D Q M E D C L Y N I Y P T E D G A N T K K A G D I T S N D G E D C I H D O S K K R V M Y Y I H G S G Y M E 180
Dz	121 Q D Q M E D C L Y N I Y P T E D G A N T K K A G D I T S N D G E D C I H D O S K K R V M Y Y I H G S G Y M E 180
Qy	181 G T G M I D G S I L A S Y G N V I V I T I N Y R L G I G E L S T G D Q A K N Y G L D G I O A L R W L E E N V G 240
Dz	181 G T G M I D G S I L A S Y G N V I V I T I N Y R L G I G E L S T G D Q A K N Y G L D G I O A L R W L E E N V G 240
Qy	181 G T G M I D G S I L A S Y G N V I V I T I N Y R L G I G E L S T G D Q A K N Y G L D G I O A L R W L E E N V G 240
Dz	181 G T G M I D G S I L A S Y G N V I V I T I N Y R L G I G E L S T G D Q A K N Y G L D G I O A L R W L E E N V G 240
Qy	241 A F G G D P K R V I T F S G G A G A S C V S L T L S H Y S G L P O K A I O G S T L S S A N Y A Q P A K Y T R I 300
Dz	241 A F G G D P K R V I T F S G G A G A S C V S L T L S H Y S G L P O K A I O G S T L S S A N Y A Q P A K Y T R I 300
Qy	241 A F G G D P K R V I T F S G G A G A S C V S L T L S H Y S G L P O K A I O G S T L S S A N Y A Q P A K Y T R I 300
Dz	241 A F G G D P K R V I T F S G G A G A S C V S L T L S H Y S G L P O K A I O G S T L S S A N Y A Q P A K Y T R I 300
Qy	301 L A D R V G N M D T T I M V E C L R N K N K E L I O Q T I T P A T A H A E P V I D G D V I P D D P Q I L M E Q 360
Dz	301 L A D R V G N M D T T I M V E C L R N K N K E L I O Q T I T P A T A H A E P V I D G D V I P D D P Q I L M E Q 360
Qy	301 L A D R V G N M D T T I M V E C L R N K N K E L I O Q T I T P A T A H A E P V I D G D V I P D D P Q I L M E Q 360
Dz	301 L A D R V G N M D T T I M V E C L R N K N K E L I O Q T I T P A T A H A E P V I D G D V I P D D P Q I L M E Q 360
Qy	361 G E F L N Y D I M L C V N O G E G L K P F D G I V N D E D G T P N D P F S V S N F P D N L X G Y E G K D T L A E T 420
Dz	361 G E F L N Y D I M L C V N O G E G L K P F D G I V N D E D G T P N D P F S V S N F P D N L X G Y E G K D T L A E T 420
Qy	361 G E F L N Y D I M L C V N O G E G L K P F D G I V N D E D G T P N D P F S V S N F P D N L X G Y E G K D T L A E T 420
Dz	361 G E F L N Y D I M L C V N O G E G L K P F D G I V N D E D G T P N D P F S V S N F P D N L X G Y E G K D T L A E T 420
Qy	421 I K F W Y T M A D K E N E T R R K T V A L F T H Q W A P A V A D L H Q Y S A P T F Y A F Y H H C S E X 480
Dz	421 I K F W Y T M A D K E N E T R R K T V A L F T H Q W A P A V A D L H Q Y S A P T F Y A F Y H H C S E X 480
Qy	421 I K F W Y T M A D K E N E T R R K T V A L F T H Q W A P A V A D L H Q Y S A P T F Y A F Y H H C S E X 480
Dz	421 I K F W Y T M A D K E N E T R R K T V A L F T H Q W A P A V A D L H Q Y S A P T F Y A F Y H H C S E X 480
Qy	481 K P S A D S A H G D E V Y V G I P M I G T E L F S C N F S K D Y M L S A V M T Y W T N F A K T G D P N C V 540
Dz	481 K P S A D S A H G D E V Y V G I P M I G T E L F S C N F S K D Y M L S A V M T Y W T N F A K T G D P N C V 540
Qy	481 K P S A D S A H G D E V Y V G I P M I G T E L F S C N F S K D Y M L S A V M T Y W T N F A K T G D P N C V 540
Dz	481 K P S A D S A H G D E V Y V G I P M I G T E L F S C N F S K D Y M L S A V M T Y W T N F A K T G D P N C V 540
Qy	541 P O C K F I H T K N R E E E V A M S K Y N K D O L Y I G L K P R B D Y A R T K V A F M E L V P H L N L 600
Dz	541 P O C K F I H T K N R E E E V A M S K Y N K D O L Y I G L K P R B D Y A R T K V A F M E L V P H L N L 600
Qy	541 P O C K F I H T K N R E E E V A M S K Y N K D O L Y I G L K P R B D Y A R T K V A F M E L V P H L N L 600
Dz	541 P O C K F I H T K N R E E E V A M S K Y N K D O L Y I G L K P R B D Y A R T K V A F M E L V P H L N L 600
Qy	601 N E I F Q Y S T I T K V P P M T S F P Y S T R S S P A K I M E T T K G F A I T P A N N P G S K D P H K T G E D 660
Dz	601 N E I F Q Y S T I T K V P P M T S F P Y S T R S S P A K I M E T T K G F A I T P A N N P G S K D P H K T G E D 660
Qy	601 N E I F Q Y S T I T K V P P M T S F P Y S T R S S P A K I M E T T K G F A I T P A N N P G S K D P H K T G E D 660
Dz	601 N E I F Q Y S T I T K V P P M T S F P Y S T R S S P A K I M E T T K G F A I T P A N N P G S K D P H K T G E D 660

QY 661 TTVLIERKRDYSTELESTAVASALLFLNLAFALVYKKDKRHHETRRSPQNTTND 720
DB 662 TTVLIERKRDYSTELESTAVASALLFLNLAFALVYKKDKRHHETRRSPQNTTND 720
QY 721 IAHQNEIMSLQKQLEHDECESLQAHPTLRCTCPDQTLTLRRSPDCPLKNTTTC 780
DB 721 IAHQNEIMSLQKQLEHDECESLQAHPTLRCTCPDQTLTLRRSPDCPLKNTTTC 780
QY 781 MIPNTLTGKQPLHTFNTFFSGQNSTNLPHGSTRPV 816
DB 781 MIPNTLTGKQPLHTFNTFFSGQNSTNLPHGSTRPV 816

RESULT 5

AB882852
ID AB882852 standard; Protein: 817 AA.

XX AC AB882852;
XX D7 31-MAR-2003 (first entry)
XX DE C852 related polypeptide (Genbank identifier number GI# 6330941).
XX KM C852; p53; cytostatic; gene therapy; human; angiogenic; cancer;
XX OS carboxylesterase.
XX OS Homo sapiens.
XX PN M020029041-A2.
XX PD 12-DEC-2002.
XX PF 03-JUN-2002; 2002WO-US17314.
XX PR 05-JUN-2001; 2001US-296076P.
XX PR 10-OCT-2001; 2001US-328605P.
XX PR 15-FEB-2002; 2002US-357253P.
XX PA (EXEL-) EXELIXIS INC.
XX PI Friedman L, Plowman GD, Bevilin M, Francis-Lang H;
XX DR WPI; 2003-156848/15.
XX PT Identifying a candidate p53 pathway-modulating agent as therapeutic
XX PT targets for disorders associated with defective p53 function e.g.
XX PT cancer by contacting an assay system with a test agent where the system
XX PT provides reference activity.
XX ES Claim 13; Page 55-58; 60pp; English.

XX CC The invention relates to identifying a candidate p53 pathway modulating
XX CC agent. The method involves contacting an assay system comprising purified
XX CC C852 polypeptide or nucleic acid, or their functionally active fragment
XX CC or derivative, with a test agent under conditions where, but for the
XX CC presence of the test agent, the system provides a reference activity.
XX CC The methods are useful for identifying modulators of the p53 pathway as
XX CC therapeutic targets for disorders associated with defective p53 function,
XX CC such as angiogenic, apoptotic or cell proliferative disorders, e.g.
XX CC cancer. The modulators are useful as research reagents, diagnostics and
XX CC therapeutics. Sequences AB882851-53 represent C852 (carboxylesterase);
XX CC related polypeptide sequences.

XX SQ Sequence 817 AA;

Query Match 65.9%; Score 538; DB 24; Length 817;
Best Local Similarity 59.8%; Pred. No. 0;
Matches 658; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 159 DHHQNSKKPYVYTHHGGSTWEGTGMIDGSLASIGNVYVITINPLGLIGLSTGDA 218
DB 159 DHHQNSKKPYVYTHHGGSTWEGTGMIDGSLASIGNVYVITINPLGLIGLSTGDA 218

QY 219 AKGNVGLDDQCALPMTEENVGARGGDPKRTTIGSGAGACVSLTLSSHSEGLPQKAI 278
DB 219 AKGNVGLDDQCALPMTEENVGARGGDPKRTTIGSGAGACVSLTLSSHSEGLPQKAI 278
QY 279 TOSGTLSSKAVNVPAPAYRTILADKQCNMLCTTMCWECILRNKXVVELLQCTTTPAYH 338
DB 279 TOSGTLSSKAVNVPAPAYRTILADKQCNMLCTTMCWECILRNKXVVELLQCTTTPAYH 338
QY 339 IAFGEVIDGVIPDDPOLIMEQGEFLNVDIMLVNQGEGLEFVGVGVNEDGVTPNDEFE 398
DB 339 IAFGEVIDGVIPDDPOLIMEQGEFLNVDIMLVNQGEGLEFVGVGVNEDGVTPNDEFE 398
QY 399 SVSNFVNDLXGYPESKDTLRETIKPMYTDADKNEPETERKTLVALFTDQWVAPAVATA 458
DB 399 SVSNFVNDLXGYPESKDTLRETIKPMYTDADKNEPETERKTLVALFTDQWVAPAVATA 458
QY 458 DLHAQYGSPTFYAFYHHQSEMKPSMADSAHGDVYPVFGIPMIGFELSCNFSKQDV 517
DB 458 DLHAQYGSPTFYAFYHHQSEMKPSMADSAHGDVYPVFGIPMIGFELSCNFSKQDV 518
QY 518 MLSAVVMTYNTNFAKTGDPNPQVPDQTFIHTKPNRFEVAMSKYNPKDQLYJHIGLXPR 577
DB 518 MLSAVVMTYNTNFAKTGDPNPQVPDQTFIHTKPNRFEVAMSKYNPKDQLYJHIGLXPR 578
QY 578 VADHTRATKVAFWLELVYHLNLNLEIFQYVSTTTKVPPEMTSPFFYGRBSAKTWPTK 637
DB 578 VADHTRATKVAFWLELVYHLNLNLEIFQYVSTTTKVPPEMTSPFFYGRBSAKTWPTK 638
QY 638 RPAITPANPKSKDPKHTGPEDTVLLETREDYSTELESTAVASALLFLNLAFALY 697
DB 638 RPAITPANPKSKDPKHTGPEDTVLLETREDYSTELESTAVASALLFLNLAFALY 698
QY 698 YKXDKRREHTRRPSQPNITNDIAHIGNEIMSLQKQLEHDECESLQAHPTLRCTCP 757
DB 698 YKXDKRREHTRRPSQPNITNDIAHIGNEIMSLQKQLEHDECESLQAHPTLRCTCP 758
QY 758 PDYTLTLRRSPDDILMTPNTITMIPNTLTGKQPLHTFNTFFSGQNSTNLPHGSTRPV 816
DB 758 PDYTLTLRRSPDDILMTPNTITMIPNTLTGKQPLHTFNTFFSGQNSTNLPHGSTRPV 817

RESULT 6

AAE94127
ID AAE94127 standard; Protein: 509 AA.

XX AC AAE94127;
XX OS Homo sapiens.
XX PN EP1074617-A2.
XX PD 07-FEB-2001.
XX PF 28-JUL-2000; 2000EP-01:6126.
XX PR 29-JUL-1999; 99EP-0248036.
XX PR 27-AUG-1999; 99EP-0300253.
XX PR 11-JAN-2000; 2000JP-0118776.
XX PR 02-MAY-2000; 2000JP-0183767.
XX PR 09-JUN-2000; 2000JP-0241899.
XX PA (HELI-) HELIX RES INST.

XX PI Oca T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX DR WPI; 2001-318749/34.

XX primer sets for synthesizing polynucleotides, particularly the 5602
 27 full-length cDNAs defined in the specification, and for the detection
 28 and/or diagnosis of the abnormality of the proteins encoded by the
 29 full-length cDNAs -

XX Claim 8; SEQ ID 1481; 2537bp + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full length
 CC cDNAs easily without any specialised methods. AAB93156 to AAB13528 and
 CC AAB13633 to AAB18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAB13629 to AAB13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.

XX Sequence 509 AA;

Query Match 47.5%; Score 388; DB 22; Length 509;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 508; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 309 MLDTTDMVECLRNKKYKELIQCTTPATYHAFGVTGCVIPDPOQLMEGSEFLNYDI 368
 DB 1 MLDTTDMVECLRNKKYKELIQCTTPATYHAFGVTGCVIPDPOQLMEGSEFLNYDI 60
 QY MGVNCGEGKAFVDGIVNEDGVTNDFPSVSNFVNDLYGPEGKDLRETIKMYTDM 428
 DB 61 MGVNCGEGKAFVDGIVNEDGVTNDFPSVSNFVNDLYGPEGKDLRETIKMYTDM 120
 QY 429 ADKENPETERKTLVALFTDQWVAPAVA-ADLHAQYGSPTFYAFYHHQOSEMKPSWADS 487
 DB 121 ADKENPETERKTLVALFTDQWVAPAVATLHAQYGSPTFYAFYHHQOSEMKPSWADS 180
 QY 488 AHGDEVVYVFGIPMIGPTELFSCNSKQDVMLSAVMTYWTNFAKTGDPNPVQDTKFI 547
 DB 181 AHGDEVVYVFGIPMIGPTELFSCNSKQDVMLSAVMTYWTNFAKTGDPNPVQDTKFI 240
 QY 546 HTKPRFEEVAMSKNPKDQLYLH-GLKPRVDEVRATKVFMLEJVLHNLNEFOYV 607
 DB 241 HTKPRFEEVAMSKNPKDQLYLH-GLKPRVDEVRATKVFMLEJVLHNLNEFOYV 300
 QY 608 STTKVPPPDXTSPFYGRRSPPAKIMPTTKRPATIPANNPCHSDPHKTSGETTVLIET 667
 DB 301 STTKVPPPDXTSPFYGRRSPPAKIMPTTKRPATIPANNPCHSDPHKTSGETTVLIET 360
 QY 668 KRDYSTEILSVTLAVASCLFLNLAFAALYKPKBRBETHRRPSQNTNDAHONE 727
 DB 361 KRDYSTEILSVTLAVASCLFLNLAFAALYKPKBRBETHRRPSQNTNDAHONE 420
 QY 728 EINSQQKQLEHHECESICADTALITCPDPTVTLRRSPDIPFLMPTNTITPNTLT 787
 DB 421 EINSQQKQLEHHECESICADTALITCPDPTVTLRRSPDIPFLMPTNTITPNTLT 480
 QY 788 GNOPLATNTESGGGNSINLPHGSHTRV 816
 DB 481 GNOPLATNTESGGGNSINLPHGSHTRV 509

RESULT 7
 ID ABB82853
 AC ABB82853 standard; Protein; 509 AA.

XX ABB82853;

XX 31-MAR-2003 (first entry)

XX CES2 related polypeptide (GenBank identifier number GI# 18595051).

XX CES2, p53; cytosolic; gene therapy; human; angiogenic; cancer;

XX carboxylesterase.

XX Homo sapiens.

XX MO203295C41-A2.

XX 12-DEC-2002.

XX 03-JUN-2002; 2002WO-US17314.

XX 05-JUN-2001; 2001US-296576P.

XX 10-OCT-2001; 2001US-129605P.

XX 15-FEB-2002; 2002US-357253P.

XX (EXCL-) EXELIXIS INC.

XX Friedman L, Florman GD, Belvan M, Francis-Lang H;

XX WPI; 2003-156848/15.

XX identifying a candidate p53 pathway-modulating agent as therapeutic

XX targets for disorders associated with defective p53 function e.g.

XX cancer by contacting an assay system with a test agent where the system

XX provides reference activity -

XX Claim 13; Page 58-60; 60pp; English.

XX The invention relates to identifying a candidate p53 pathway modulating

XX agent. The method involves contacting an assay system comprising purified

XX CES2 polypeptide or nucleic acid, or their functionally active fragment

XX or derivative, with a test agent under conditions where, but for the

XX presence of the test agent, the system provides a reference activity.

XX The methods are useful for identifying modulators of the p53 pathway as

XX therapeutic targets for disorders associated with defective p53 function,

XX such as angiogenic, apoptotic or cell proliferative disorders, e.g.

XX cancer. The modulators are useful as research reagents, diagnostics and

XX therapeutics. Sequences ABB82851-53 represent CES2 (carboxylesterase)

XX related polypeptide sequences.

XX Sequence 509 AA;

QY 309 MLDTTDMVECLRNKKYKELIQCTTPATYHAFGVTGCVIPDPOQLMEGSEFLNYDI 368
 DB 1 MLDTTDMVECLRNKKYKELIQCTTPATYHAFGVTGCVIPDPOQLMEGSEFLNYDI 60
 QY MGVNCGEGKAFVDGIVNEDGVTNDFPSVSNFVNDLYGPEGKDLRETIKMYTDM 428
 DB 61 MGVNCGEGKAFVDGIVNEDGVTNDFPSVSNFVNDLYGPEGKDLRETIKMYTDM 120
 QY 429 ADKENPETERKTLVALFTDQWVAPAVA-ADLHAQYGSPTFYAFYHHQOSEMKPSWADS 487
 DB 121 ADKENPETERKTLVALFTDQWVAPAVATLHAQYGSPTFYAFYHHQOSEMKPSWADS 180
 QY 488 AHGDEVVYVFGIPMIGPTELFSCNSKQDVMLSAVMTYWTNFAKTGDPNPVQDTKFI 547
 DB 181 AHGDEVVYVFGIPMIGPTELFSCNSKQDVMLSAVMTYWTNFAKTGDPNPVQDTKFI 240

QY 548 HTKRNFEVAMSKYNPKQYLIHGCKERYCHRYATKVAFWELVPHLHNLEIFQV 607
 DB 241 HTKRNFEVAMSKYNPKQYLIHGCKERYCHRYATKVAFWELVPHLHNLEIFQV 300
 QY 608 STTKKVPDMTSPFYGRSPAKIWPTEKSPATTPANPNSKDPKXGPEDTYET 667
 DB 301 STTKKVPDMTSPFYGRSPAKIWPTEKSPATTPANPNSKDPKXGPEDTYET 360
 QY 668 KRDYSTEISVTIANGASLIJPLNIYAFALVYKCKRRHETRRRSPQNTNDAIIONE 727
 DB 361 KRDYSTEISVTIANGASLIJPLNIYAFALVYKCKRRHETRRRSPQNTNDAIIONE 420
 QY 728 EIMSLOMKOLEHDEHCESELCQAHDLRLTCPPDYTLTBRSPDIPPLATPTNTMINTLT 787
 DB 421 EIMSLOMKOLEHDEHCESELCQAHDLRLTCPPDYTLTBRSPDIPPLATPTNTMINTLT 480
 QY 788 GMOPHTENTFGSGONSTNLPKSHSTRV 816
 DB 481 GMOPHTENTFGSGONSTNLPKSHSTRV 509

RESULT 8
 AAM48908
 ID AAM48908 standard; Protein; 816 AA.
 AC AAM48908;
 XX
 XX
 CT 05-APR-2002 (first entry)
 DE Human neurocignin family member 46980 protein.
 KW Human neurocignin family; 46980; analgesic; neuroprotective; cytostatic;
 KW pain disorder; complex regional pain syndrome; causalgia; neuralgia;
 KW central pain; dysesthesia syndrome; carotidynia; neuronal disorder;
 KW cancer; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FN WO2000:94563-A2.
 PD 13-DEC-2001.
 XX
 XX 06-JUN-2001; 2001WO-US-8335.
 PR 06-JUN-2000; 2000US-209949P.
 XX
 XX 06-JUN-2000; 2000US-209949P.
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Curtis RAD;
 XX
 XX W21; 2002-147671/19.
 DR N-PSDB; ABA97533.
 XX
 PT New 46980 polypeptides and polynucleotides encoding them, useful for as
 PT diagnostic targets and therapeutic agents for controlling pain, pain
 PT disorders (e.g. complex regional pain syndrome, causalgia), neuronal
 PT disorders or cancer.
 XX
 XX Claim 9; Page 139; (23pp; English.
 CC The present invention provides the protein and coding sequences of a
 CC novel member of the human neurocignin family, designated 46980. The
 CC sequences can be used in the control of pain, to treat pain disorders
 CC such as complex regional pain syndrome, causalgia, neuralgia, central
 CC pain and dysesthesia syndrome and carotidynia, neuronal disorders, and
 CC cancer. The present sequence is the protein of the invention.
 XX
 SQ Sequence 816 AA;

Query Match 40.0%; Score 326; LB 23; Length 916;
 Best Local Similarity 99.6%; Pred. No. 0;

Matches 546; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 163 QNSKRPVWYITFGSSYMECTGMIDGSLASGVIVTNYRLGCTJGFLSTGDAAGN 222
 DB 162 QNSKRPVWYITFGSSYMECTGMIDGSLASGVIVTNYRLGCTJGFLSTGDAAGN 221
 QY 223 YGLLOICQALRWTEENNVCAFGGQPKRVITFGGAASCVSLTISHYSEGLFOKAIIOSG 282
 DB 222 YGLLOICQALRWTEENNVCAFGGQPKRVITFGGAASCVSLTISHYSEGLFOKAIIOSG 281
 QY 283 TALSSANVYQPAKXTRILADVQGNVLDITTYECLRNQVKELIQCTTPATYHIAFG 342
 DB 282 TALSSANVYQPAKXTRILADVQGNVLDITTYECLRNQVKELIQCTTPATYHIAFG 341
 QY 343 PVLDGQVPEDDPQIIMEQGEFLNYDIMGVNGBGLKRVNIGVNEGVTPNDFSVSN 402
 DB 342 PVLDGQVPEDDPQIIMEQGEFLNYDIMGVNGBGLKRVNIGVNEGVTPNDFSVSN 401
 QY 403 FVDNLYGYPEGKDTRETIKFMYTQADKNEPETERKTVALFTDQWAPVAVATDLHA 461
 DB 402 FVDNLYGYPEGKDTRETIKFMYTQADKNEPETERKTVALFTDQWAPVAVATDLHA 461
 QY 462 QYGSPTFYFAFYHGOSEKPKPSMADSAH3DEVYVFGI;PMISPTLE;FSCNFSKNDVMSA 521
 DB 462 QYGSPTFYFAFYHGOSEKPKPSMADSAH3DEVYVFGI;PMISPTLE;FSCNFSKNDVMSA 521
 QY 522 VVMTYTNPAKTGDRQVPQDTKTIHTKPNRFEVAMSKYNPKQYLIHGCKERYCH 581
 DB 522 VVMTYTNPAKTGDRQVPQDTKTIHTKPNRFEVAMSKYNPKQYLIHGCKERYCH 581
 QY 582 YRATKVAFWLELVPHLHNLEIFQVSTITKVPDMTSPFYGRSPAKIWPTEKSPA 641
 DB 582 YRATKVAFWLELVPHLHNLEIFQVSTITKVPDMTSPFYGRSPAKIWPTEKSPA 641
 QY 642 TPANPKSKDPRKXGPEDTYLIETKRDYSTEISVTIANGASLIJPLNIYAFALVYKCK 701
 DB 642 TPANPKSKDPRKXGPEDTYLIETKRDYSTEISVTIANGASLIJPLNIYAFALVYKCK 701
 QY 702 KRRHETRR 709
 DB 702 KRRHETRR 709

RESULT 9
 AAC87273
 ID AAC87273 standard; Protein; 396 AA.
 AC AAC87273;
 XX
 XX
 CT 05-JUN-2002 (first entry)
 DE Novel central nervous system protein #183.
 KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
 KW hyperproliferative disorder; neoplasia; cardiovascular disorder;
 KW cardiac arrest; cerebrovascular disorder; schizophrenia; angiodysplasia;
 KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
 KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
 KW adenocarcinoma; reproductive system disorder; testicular feminization;
 KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
 KW respiratory disorder; renal disorder; kidney failure; blood disorder;
 KW myocardial infarction; wound healing; cell proliferation; skin aging;
 KW food additive; food preservative; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FN WO200155318-A2.
 PD 02-AUG-2001.
 XX
 XX 17-JAN-2001; 2001WO-US01332.
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.

XX The invention describes an isolated nucleic acid molecule (i) encoding a
CC novel central nervous system protein. (ii) and polypeptides (iii) encoded
CC by (i), are used to treat a medical conditions and in diagnosis of a
CC pathological condition. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiotensin, nervous system disorders e.g. Alzheimer's disease and
CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
CC e.g. corneal infection, gastro-intestinal disorders e.g. dysphagia,
CC adenocarcinomas and irritable bowel syndrome, reproductive system
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
CC leukaemia, disorders involving neovascularisation e.g. malignancies,
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
CC acute kidney failure and blood related disorders e.g. myocardia,
CC infection. The polypeptides can also be used to aid wound healing and
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC maintain organs before transplantation, for supporting cell culture of
CC primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,

Query Match 25.5%; Score 208; DB 22; Length 396;
Best Local Similarity 100.0%; Pred. No. 6.1e-209;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 DHDQSKRPVWYTHGGSYMEGTGNTDGLSYAGNVVITNFRGLSTSGDDA 218
DB 128 DHDQSKRPVWYTHGGSYMEGTGNTDGLSYAGNVVITNFRGLSTSGDDA 187
QY 219 AKGVYGLDIOIALRWIENVAGFGSDPKRVTIFGSGAGSCVSLTSHSYGLPOKA 278
DB 188 AKGVYGLDIOIALRWIENVAGFGSDPKRVTIFGSGAGSCVSLTSHSYGLPOKA 247
QY 279 IQGCTALSWANVQPAKYTRILADKVGCMEDTTNMFELRNKYEELIQCTTPACTH 338
DB 248 IQGCTALSWANVQPAKYTRILADKVGCMEDTTNMFELRNKYEELIQCTTPACTH 307
QY 339 IAFGVIDGVIPDDPOLMEGGFENY 366
DB 308 IAFGVIDGVIPDDPOLMEGGFENY 335

RESULT 1C
ABBI7862
ID ABBI7862 standard; Protein: 165 AA.

AC ABBI7862:

CT 23-JAN-2002 (first entry)

XX Human nervous system related polypeptide SEQ ID NO 6519.

XX Human: nootropic; neuroprotective; cytosstatic; dermatological; vinuclide;
XX immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; vulnereary;
XX anti-parasitism; antischistosome; antileishmanial; antitubercular; cancer;
XX antitubercular; hepatoprotective; cerebroprotective; anti-inflammatory;
XX antileishmanial; antidiabetic; antitumor; antiparasitic; antifungal;
XX antiparasitic; cardiac; immune disorder; cardiovascular disorder;
XX neurological disease; infection; neurotropic; gene therapy; vaccine.

OS Homo sapiens.

XX WO200159663-A2.

XX 16-AUG-2001.

XX 17-JAN-2001; 2001WO-US01334.

XX 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0154664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0158123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0204467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218299.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226272.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 06-SEP-2000; 2000US-0231242.
PR 09-SEP-2000; 2000US-0231243.
PR 09-SEP-2000; 2000US-0231244.
PR 09-SEP-2000; 2000US-0231413.
PR 09-SEP-2000; 2000US-0231414.
PR 09-SEP-2000; 2000US-0232085.
PR 09-SEP-2000; 2000US-0232086.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0233397.
PR 14-SEP-2000; 2000US-0233398.
PR 14-SEP-2000; 2000US-0233399.
PR 14-SEP-2000; 2000US-0233399.
PR 14-SEP-2000; 2000US-0233400.
PR 14-SEP-2000; 2000US-0233401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.

PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240560.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 20-OCT-2000; 2000US-0242221.
 PR 01-NOV-2000; 2000US-0244674.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246539.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249266.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250391.
 PR 01-DEC-2000; 2000US-0251160.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251858.
 PR 08-DEC-2000; 2000US-0251859.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0251950.
 PR 11-DEC-2000; 2000US-0254037.
 PR 05-JAN-2001; 2001US-0255678.
 XX
 PA (HUMA-) HUMAN GENE SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 XX WPI: 2001-547565/60.
 DR N-PSDB: ABA14188.
 XX
 XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating nervous system
 PT cancers and metastases -

XX
 XX Claim 11; SEQ ID NO 65:9; 1701bp + Sequence listing; English.
 PS
 XX The invention relates to novel genes (ABA1004-AB21534) and proteins
 CC (ABA14678-AB21800) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
 CC
 SC Sequence 165 AA;
 Query Match 9.3%; Score 76; DB 22; Length 165;
 Best Local Similarity 100.0%; Pred. No. 8; Le-71;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 534 VPECHNLNEIFQVYVTTTKVPPDQTSFPGGRSPAKCMPTKRPATIPANPKRSKDP 653
 DB 54 VPHNLNLEIFQVYVTTTKVPPDQTSFPGGRSPAKCMPTKRPATIPANPKRSKDP 113
 QY 654 HKTGPEDTVLIEYKR 669
 DB 114 HKTGPEDTVLIEYKR 129
 RESULT 1:
 AAM93205
 ID AAM93205 standard; Protein; 509 AA.
 XX
 AC AAM93205;
 XX
 DT 06-NOV-2001 (first entry)
 DE Human polypeptide, SEQ ID NO: 2597.
 XX
 KM Human; full length cDNA; cDNA synthesis; oligo-capping.
 XX
 OS Homo sapiens.
 XX
 PN EPI130094-A2.
 XX
 PD 05-SEP-2001.
 XX
 PF 07-JUL-2000; 2000EP-0114C89.
 XX
 PR 08-JUL-1999; 99UP-0194486.
 PR 11-JAN-2000; 2000UP-0118774.
 PR 02-MAY-2000; 2000UP-0183765.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX
 DR WPI: 2001-524255/58.
 DR N-PSDB: AAK94113.
 XX
 XX 830 Primers useful for synthesizing full length cDNA clones and their
 PT use in genetic manipulation -
 XX
 PS Claim 6; SEQ ID NO 2597; 1380bp + sequence listing; English.

XX The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5' - and 3' - ends of the cDNA
CC molecules have been determined. Primers for synthesising the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is a polypeptide
CC encoded by a full length human cDNA of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ Sequence 509 AA;
Query Match 5.1%; Score 50; DB 22; Length 509;
Best Local Similarity 100.0%; Pred. No. 4,3e-43;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 510 CNFSKNDVMSAVVMTWTNTNPAKTGDPNQVPQDTKFIHTKPNFEFEVW 559
DB 212 CNFSKNDVMSAVVMTWTNTNPAKTGDPNQVPQDTKFIHTKPNFEFEVW 261
RESULT 12
ABG10266
ID ABG10266 standard; Protein; 271 AA.
XX
AC ABG10266;
XX
XT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #10257.
XX
KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
KM food supplement; medical imaging; diagnostic; genetic disorder;
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2301WO-US8631.
XX
PR 31-MAR-2000; 2003US-0540217.
PR 23-AUG-2000; 2003US-0649167.
XX
PA (HSE-) HSEF INC.
XX
PE Drmanac RT, Liu C, Tang YF;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS74453.
XX
PT New isolated polynucleotide and encoded polypeptides useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
NS Claim 20; SEQ ID No 40625; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical

CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG1010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 271 AA;
Query Match 5.9%; Score 48; DB 22; Length 271;
Best Local Similarity 100.0%; Pred. No. 3e-41;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 510 CNFSKNDVMSAVVMTWTNTNPAKTGDPNQVPQDTKFIHTKPNFEFEV 557
DB 184 CNFSKNDVMSAVVMTWTNTNPAKTGDPNQVPQDTKFIHTKPNFEFEV 231
RESULT 13
AAB40734
ID AAB40734 standard; Protein; 308 AA.
XX
AC AAB40734;
XX
XT 08-FEB-2001 (first entry)
XX
DE Human ORF498 polypeptide sequence SEQ ID NO:996.
XX
KM Human; open reading frame; ORF; detection; cytostatic; hepatotropic;
KM vulnerey; antiproliferative; antiparkinsonian; neurotropic; neuroprotective;
KM anticonvulsant; osteoparathic; antiarthritis; immunosuppressant; cardiac;
KM immunostimulant; thrombolytic; coagulant; vasotropic; antidabetic;
KM hypotensive; dermatologic; immunosuppressive; antiinflammatory;
KM antiviral; antibacterial; antifungal; antitumoric; antihydroly;
KM antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KM neurodegenerative disorder; osteoarthritis; graft vs host disease;
KM cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KM cholesterol ester storage; systemic lupus erythematosus; infection;
KM severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KM allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KM bone damage; cartilage damage; antiinflammatory disease; coagulation;
thrombosis; contraceptive.
XX
OS Homo sapiens.
XX
PN WO200056473-A2.
XX
PD 05-OCT-2000.
XX
PF 31-MAR-2000; 2000WO-US8621.
XX
PR 31-MAR-1999; 99US-0127607.
PR 02-APR-1999; 99US-0127636.
PR 05-APR-1999; 99US-0127728.
PR 30-MAR-2000; 2000US-0540763.
XX
PA (CJRA-) CUNAGEN CORP.
XX
PE Shinketsu RA, Teach M;
XX
DR WPI; 2000-602362/57.
DR N-PSDB; AAC74943.
XX
PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -
XX
PS Claim 11; Page 970-971; 5507pp; English.

XX AACT7446 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORF open reading frames 1 to 316. The ORF
 CC sequences have activities such as: cytostatic; hepatotropic; vulnerary;
 CC antiproliferative; antiparkinsonian; nootropic; neuroprotective;
 CC osteoprotic; anticonvulsant; antiallergic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotrophic;
 CC antidiabetic; hypotensive; dermatologic; immunosuppressive;
 CC antiinflammatory; antibacterial; antiviral; antifungal; antithyroid;
 CC antihypertensive; and antianemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORF-associated disorder. The
 CC nucleic acids can be used to express ORF proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, ap-astic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.

CC Sequence 309 AA;

Query Match 5.9%; Score 48; DB 21; Length 308;
 Best Local Similarity 100.0%; Pred. No. 3,4e-4;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 5-0 CNFSKNVWLSAVWMTWTFNFAKTGDPNPVPCDTKFTKPNREEV 557
 Db 287 CNFSKNVWLSAVWMTWTFNFAKTGDPNPVPCDTKFTKPNREEV 214

RESULT 14

AB07524

AC ABB07524;

Dt 23-APR-2002 (first entry)

DE Human drug metabolizing enzyme (DME) (ID: 7473875C21).

XX Drug metabolizing enzyme; DME; antiallergic; antineoplastic; antiasthmatic;
 KW osteopathic; antirheumatic; antiallergic; dermatologic; nephrotoxic;
 KW antiinflammatory; vulnerary; antibacterial; virtuous; antiparasitic;
 KW prozoocidal; fungicide; antihelminthic; cytostatic; ophthalmological;
 KW antiatherosclerotic; hepatotropic; antidiabetic; anorectic; human;
 KW thrombolytic; metabolic; anticonvulsant; antithyroid; gynecological;
 KW antianimal; anticancer; antididiabetic; laxative; enzyme.

XX Homo sapiens.

PN WO200204612-A2.

PD 17-JAN-2002.

PF 05-JUL-2001; 2001WO-US21324.

PR 07-JUL-2003; 2000US-216804P.

PR 14-JUL-2003; 2000US-218948P.

PR 21-JUL-2000; 2000US-220037P.

PR 28-JUL-2003; 2000US-221837P.

XX (INCY-1) INCYTE GENOMICS INC.

PI Baegun MR, Bruns CM, Das D, Ding L, Elliott VS, Ganahi AR;
 PI Haeffl A, Kearsley L, Khan FA, Lal P, Lee EA, Lu DM, Lu Y;
 PI Nguyen DB, Patterson C, Ramkumar C, Ring HZ, Santhakala MS;
 PI Yang Y, Thangavelu K, Thornton M, Tridibley CM, Walla NK, Xu Y;
 PI Yang J, Yao MG, Yue H;

DR WPI; 2002-164641/21.

DR N-PSDB; ABA94727.

PT Novel drug metabolizing enzymes and polynucleotides encoding the

PT enzymes, useful for treating, diagnosing or preventing

PT autoimmune/inflammatory, cell proliferative, developmental and

PT endocrine disorders

XX Claim 1; Page 148-149; 167pp; English.

CC The invention provides human drug metabolizing enzyme (DME) polypeptides
 CC and polynucleotides. DMEs can be expressed by standard recombinant
 CC methods. The DME polypeptides, polynucleotides, modulators and
 CC antibodies are useful from diagnosing, treating and preventing autoimmune
 CC /inflammatory (e.g. allergies, anemia, asthma, osteoporosis, rheumatoid
 CC arthritis, atopic dermatitis, glomerulonephritis and irritable bowel
 CC syndrome, trauma and bacterial, viral, parasitic, protozoal, fungal or
 CC hematologic infections), cell proliferative (e.g. cancer, atherosclerosis,
 CC and hepatitis), developmental (e.g. cerebral palsy and cataract),
 CC endocrine (e.g. thrombosis, goiter, hyperplasia, amenorrhea and
 CC gynecostasia), eye (e.g. iritis and glaucoma, metabolic (e.g. Addison's
 CC disease, diabetes and obesity), and gastrointestinal disorders (e.g.
 CC anorexia, nausea, abdominal angina, ulcerative colitis, diarrhea and
 CC constipation). The DME polypeptides are useful in drug screening
 CC techniques, and to analyse the proteome of a tissue or cell type. The DME
 CC polynucleotides are useful for creating knock-in humanized animals or
 CC transgenic animals to model human diseases, and in somatic or germline
 CC gene therapy. The present sequence represents a human DME polypeptide
 CC sequence.

CC Sequence 801 AA;

Query Match 5.9%; Score 48; DB 23; Length 801;
 Best Local Similarity 100.0%; Pred. No. 8.1e-41;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 5-0 CNFSKNVWLSAVWMTWTFNFAKTGDPNPVPCDTKFTKPNREEV 557
 Db 521 CNFSKNVWLSAVWMTWTFNFAKTGDPNPVPCDTKFTKPNREEV 568

RESULT 15

AAE25020

AC AAE25020;

CT 30-OCT-2002 (first entry)

DE Human drug metabolizing enzyme (DME-5).

XX Human; drug metabolizing enzyme; autoimmune; inflammatory disorder;
 KW acquired immunodeficiency syndrome; AIDS; atherosclerosis; psoriasis;
 KW proliferative disorder; arteriosclerosis; cirrhosis; hepatitis; cancer;
 KW asthma; neurological disorder; Alzheimer's disease; Huntington's disease;
 KW dementia; Parkinson's disease; developmental disorder; anemia; adenoma;
 KW drug screening; endocrine disorder; conjunctivitis; glaucoma; cataract;
 KW renal tubular acidosis; eye disorder; epilepsy; thrombosis; peptic ulcer;
 KW anorexia; metabolic disorder; cystic fibrosis; diabetes; liver disorder;
 KW goiter; gastrointestinal disorder; gene therapy; virtuous; anticonvulsant;
 KW anticonvulsant; nootropic; enzyme; DME-5.

XX Homo sapiens.

XX Key

XX Peptide

XX Protein

XX Peptide

XX Protein

Location/Qualifiers
 /label= Signal_peptide
 /note= Mature human DME-5"
 /label= Signal_peptide
 /note= Mature human DME-5"
 /note= "Mature human DME-5"

XX W02002166:6-A2.
 XX 28-FEB-2002.
 PD 21-AUG-2001; 2001WO-US26091.
 XX 21-AUG-2000; 2000US-226774P.
 XX 21-AUG-2000; 2000US-226774P.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Curtis RAJ;
 XX WPI; 2002-257916/30.
 DR N-PSDB; ABA955:99, ABA95230C.
 XX
 PT New carboxylesterase nucleic acid 33410, useful for the treatment and
 PT diagnosis of immune, cardiovascular, reproductive and cancerous
 PT disorders -
 XX
 XX Claim 1; Page 110; 123pp; English.
 XX
 CC The invention provides a novel carboxylesterase family member, designated
 CC 33410. Compounds that bind to or modulate the activity or expression of
 CC 33410, are useful for treating or preventing a disorder such as cellular
 CC proliferative or differentiative, neural, cardiovascular, prostatic, skin
 CC brain and skeletal muscular disorders, protein-protein interaction
 CC disorders, signal transduction disorders, immune (e.g. diabetes and
 CC rheumatoid arthritis), reproductive, cardiovascular (e.g. hypertension,
 CC atherosclerosis, coronary artery disease, arrhythmia, ischemic heart
 CC disease and angina pectoris), vascular disorders (e.g. varicose veins,
 CC Wegener's granulomatosis and wound healing) or cancerous disorders.
 CC Multiple sclerosis, Crohn's disease, ulcers, asthma, allergy, infection,
 CC kidney disease (glomerulonephritis), idiopathic thrombocytopenic purpura,
 CC hepatitis, tuberculosis, human immunodeficiency virus, Alzheimer's and
 CC Parkinson's. The 33410 polynucleotide and polypeptide are useful for
 CC diagnosis of a predisposition to a disorder, for evaluating the efficacy
 CC of a therapeutic or prophylactic disorder, for chromosome mapping, as
 CC immunogens, for drug screening, for the detection of mutations in the
 CC gene and for tissue typing. The present sequence represents the human
 CC carboxylesterase family member, 33410.
 XX
 XX Sequence 835 AA;
 SC
 Query Match 5.9%; Score 48; DB 23; Length 835;
 Best Local Similarity 100.0%; Pred. No. 8.4e-4;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 510 CNFSKNDVLSAVVMTYWTNFAKTDPNQPVQDTKFIHTKRNREEV 557
 DB 521 CNFSKNDVLSAVVMTYWTNFAKTDPNQPVQDTKFIHTKRNREEV 568
 RESULT 18
 AAB62400
 ID AAB62400 standard; Protein; 837 AA.
 XX
 AC AAB62400;
 XX
 DT 29-JUN-2001 (first entry)
 XX
 DE Human MBSP4 polypeptide (clone 21417374.0.9).
 XX
 KW MBSPX; cancer; preclampsia; immune system; neurologia; cyrostatic;
 KW gynecological; antiinflammation; neuroprotection; isotropic; relaxant;
 KW cardiant; dermatological; gene therapy; human; MBSP4.
 XX
 CS Homo sapiens.
 XX
 RN W0200127277-A2.
 XX
 PD 19-APR-2001.
 XX

PF 13-OCT-2000; 2000WO-US28480.
 XX
 XX 13-OCT-1999; 99US-0159231.
 PR 12-JAN-2000; 2000US-0175670.
 PR 12-OCT-2000; 2000US-0159231.
 XX
 XX (CURA-) CURAGEN CORP.
 XX
 PA Shimkete RA, Liechtenstein H, Boldog FL;
 PI WPI; 2001-282030/29.
 DR N-PSDB; AAF82996.
 XX
 XX Novel human polynucleotide sequences and the membrane bound or secreted
 PT polypeptides encoded by these sequences, designated MBSPX -
 XX
 XX Claim 1; Page 26-29; 157pp; English.
 XX
 CC The invention relates to novel polypeptides, termed MBSPX and
 CC polynucleotides encoding the MBSPX polypeptides. The MBSPX polypeptide,
 CC nucleic acid and an MBSPX antibody are useful for treating or preventing
 CC a pathology associated with the protein especially in humans. The MBSPX
 CC nucleic acid can be used to express MBSPX protein (e.g. via a recombinant
 CC expression vector in a host cell in gene therapy applications), or to
 CC detect MBSPX mRNA in a biological sample or a genetic lesion in a MBSPX
 CC gene. Disorders associated with insufficient or excessive production of
 CC MBSPX protein include cancer, preclampsia, immune system disorders and
 CC inflammation, neurological disorders, cardiovascular disorders, and skin
 CC and muscle abnormalities. The anti-MBSPX antibodies can be used to detect
 CC and isolate MBSPX proteins and modulate MBSPX activity. The present
 CC sequence represents the amino acid sequence of MBSP4, a human neurolygin
 CC homologue.
 XX
 XX Sequence 837 AA;
 SC
 Query Match 5.9%; Score 48; DB 22; Length 837;
 Best Local Similarity 100.0%; Pred. No. 8.4e-4;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 510 CNFSKNDVLSAVVMTYWTNFAKTDPNQPVQDTKFIHTKRNREEV 557
 DB 521 CNFSKNDVLSAVVMTYWTNFAKTDPNQPVQDTKFIHTKRNREEV 568
 RESULT 19
 AAB51838
 ID AAB51838 standard; Peptide; 49 AA.
 XX
 AC AAB51838;
 XX
 DT 25-FEB-2003 (first entry)
 XX
 DE Human liver peptide, SEQ ID No 30486.
 XX
 KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
 KW hypercholesterolaemia; coronary heart disease.
 XX
 CS Homo sapiens.
 XX
 PN W0200157273-A2.
 XX
 PD 09-AUG-2001.
 XX
 DE 30-JAN-2001; 2001WO-US00664.
 XX
 XX 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX

PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488896/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human adult liver.
XX
PS Claim 27; SEQ ID No 30486; 658bp; English.
XX
CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridizes at high
CC stringency to a nucleic acid molecule expressed in the human adult
CC liver. (I) may be used for predicting, measuring and displaying gene
CC expression in samples derived from human adult liver. The genes
CC identified may be involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinemia, hyperlipidaemia and hypercholesterolaemia which
CC is associated with coronary heart disease. ABG47348-ABG59930 represent
CC human liver single exon encoded peptides of the invention.
CC Note: The sequence information for this patent does not appear in the
CC printed specification but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 49 AA;
XX
Query Match 5.6%; Score 46; DB 22; Length 49;
Best Local Similarity 100.0%; Pred. No. 7, 9e-40;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 163 QNSKKPVMVYIHGGSYMEGTGNTDGSILASYSYGVIVITIKYRLGI 208
DB 4 QNSKKPVMVYIHGGSYMEGTGNTDGSILASYSYGVIVITIKYRLGI 49
XX
RESULT 20
ABG10270
ID ABG10270 standard; Protein; 1434 AA.
XX
AC ABG10270;
XX
EC 13-FEB-2002 (first entry);
XX
DE Novel human diagnostic protein #0261.
XX
KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
KM food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PI 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US58631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS74457.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

PS Claim 20; SEQ ID No 40623; 133bp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridization probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on RNA and
CC amino acid sequences. ABG00010-ABG03077 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1434 AA;
XX
Query Match 5.3%; Score 43; DB 22; Length 1434;
Best Local Similarity 100.0%; Pred. No. 2, 4e-35;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 515 NDVMSAVVMTYMTNFAKTGDPNQPVECTFPIHKPKRFEV 557
DB 267 NDVMSAVVMTYMTNFAKTGDPNQPVECTFPIHKPKRFEV 309
XX
RESULT 21
ABP43803
ID ABP43803 standard; Protein; 828 AA.
XX
AC ABP43803;
XX
DT 26-FEB-2003 (first entry)
XX
DE 3 isoform protein.
XX
KM Neuroprotective; immunomodulator; cancer; chromosome Xq13.1;
KM cytoskeletal; anti-inflammatory; gene therapy; nutritional supplement;
KM wound; burn; ulcer; Alzheimer's disease; Huntington's disease;
KM amyotrophic lateral sclerosis; autoimmune disorder; inflammation;
KM vulvectomy.
XX
OS Homo sapiens.
XX
PN WO200223111-A2.
XX
PI 18-APR-2002.
XX
PF 11-OCT-2001; 2001WO-US27760.
XX
PR 12-OCT-2000; 2000US-0687527.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
XX
DR Xue AC, Yang Y, Wehrman T, Drmanac RT;
XX
DR WPI; 2002-426278/45.
DR N-PSDB; ABG61047.
XX
PT New polypeptides and their encoded proteins, useful as nutritional
PT sources or supplements, or in gene therapy, particularly for treating
PT wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or
PT inflammation.

XX Claim 20; SEQ ID # 705; 357pp - sequence listing; English.

PS

XX The invention relates to 446 newly isolated polynucleotide sequences.

CC

CC The activity of polynucleotides of the invention may be described as,

CC anti-inflammatory, neuroprotective, immunomodulatory, cytostatic and

CC anti-inflammatory. Compositions comprising nucleic acids of the invention

CC are useful for treating a mammalian subject, or as nutritional sources or

CC supplements. These are useful in gene therapy, particularly for treating

CC wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,

CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or

CC inflammation. The nucleic acids and polypeptides are also useful in

CC diagnostic and research methods. The sequences given in records

CC AB643544-AB643989 represent polypeptides encoded by polynucleotides of

CC the invention.

CC NOTE: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WPO

CC at http://wipo.int/pdb/published_pdb_sequences.

CC

CC

XX Sequence 828 AA:

SO

Query March 4, 2003; Score 35; DB 23; Length 828;

Base Local Similarity 100.0%; Pred.No. 3,66-27;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0

CY 167 KPVWVYHGGSYVEGTGNNIDGSLASVGVYVIT 201

2b 180 KPVWVYHGGSYVEGTGNNIDGSLASVGVYVIT 214

RESULT 22

AA644913

ID AAB44913 standard; Protein; 229 AA.

XX

AC AAB44913:

XX

XX 09-FEB-2001 (first entry)

XX

XX Human secreted protein encoded by gene 42 homologue.

DE

XX

XX Human secreted protein; cytosolic; antiarthritic; antiasthmatic;

KW immunosuppressive; antiarteriosclerotic; antiinflammatory; neuropro-

KW tect; neuroprotective; antidiabetic; tranquiliser; antibacterial;

KW antipneumatic; antiarthritic; antineumatic; cardiac; anti-HIV;

KW autoimmune disorder; allergic condition; cardiovascular disorder;

KW cancer; neurological disease; tissue repair.

XX

XX Homo sapiens.

CS

XX

XX WO200005176-A2.

XX

XX 21-SEP-2000.

XX

XX 09-MAR-2000; 2000MO-US06057.

XX

XX 12-MAR-1999; 99US-0124142.

PR 11-JUN-1999; 99US-0138597.

PR 03-DEC-1999; 99US-0168666.

XX

XX (HUMA-1) HUMAN GENOME SCI INC.

PA

XX

XX Rosen CA, Ruben SM, Kotsakoulis G;

PI

XX

XX WPI; 2000-638176/61.

XX

XX Novel 49 human secreted proteins useful for diagnosis, prevention and

XX treatment of disorders including neurological, cell proliferative,

XX cardiovascular, and autoimmune/inflammatory disorders and microbial

XX infections.

XX

XX Disclosure; Page 359-400; 435pp; English.

XX

XX This invention describes a novel isolated polypeptide (i) comprising an

```
CC amino acid sequence at least 95 % identical to a polypeptide sequence
CC selected from 49 polypeptides encoded by polynucleotide sequences
CC included in American Type Culture Collection (ATCC) deposit number
CC C03917, defined in the specification. The products of the invention have
CC cytosolic, antiaerobic, antiaerobic, immunosuppressive, neurotrophic;
CC antiarteriosclerotic, antifibrotic, antiproliferative, antibacterial,
CC angiogenic, vasorelaxant, antithrombotic, antiproliferative, antiaerobic,
CC antineoplastic, cardiac and anti-HIV activity. (2) or a nucleic acid (II)
CC encoding (I) is useful for preventing, treating or ameliorating a medical
CC condition and for diagnosing a pathological condition or susceptibility
CC to the condition. (I) is useful for identifying a binding partner which
CC affects the activity of the polypeptide and for identifying an activity
CC in a biological sample. (I), (II) or an antibody (IV) specific to (I) is
CC also useful for treating or preventing a disease, disorder or condition
CC associated with aberrant expression of (I). Diseases treated or diagnosed
CC include immune disorders such as autoimmune diseases, blood protein
CC disorders, anemia, allergic reactions and conditions such as asthma,
CC organ rejection or graft-versus-host disease, inflammation, hyper-
CC proliferative disorders, cardiovascular disorders such as arteriolestenal
CC fistula, arrhythmias, arteriosclerosis, coronary thrombosis, organ
CC regeneration, cancer, neovascular glaucoma, diabetic retinopathy,
CC rheumatoid arthritis, psoriasis, diseases associated with increased
CC apoptosis that include acquired immunodeficiency syndrome (AIDS),
CC neurological diseases such as Parkinson's disease, viral, bacterial,
CC fungal or parasitic diseases. They are also used to repair, replace or
CC protect tissue damage by congenital defects, to treat trauma, in surgery,
CC including cosmetic plastic surgery, to treat fibrosis, reperfusion injury
CC or systemic cytokine damage, to stimulate chondrocyte growth, to prevent
CC skin aging due to sunburn, to change a mammal's mental state or physical
CC state by influencing biorhythms, cardiac rhythms, depression, memory,
CC stress and for accelerating wound healing. (I), (II) and/or their agonist
CC or antagonist are useful as food additives or preservatives to increase
CC or decrease storage capabilities, fat content, lipid, protein,
CC carbohydrate, vitamin, mineral or other nutritional components. (I) is
CC useful for screening therapeutic compounds. (II) is useful in forensic
CC biology for detecting DNA sequences and as diagnostic probes for
CC detecting the presence of specific mRNA in a particular cell type.
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XX 12-MAR-1999; 99JUS-0124142;
PR 11-JUN-1999; 99JUS-0138597;
XX 03-DEC-1999; 99JUS-0168666;
PA (HUMA-) HUMAN GEMOKE SCI INC.
PI Rosen CA, Ruben SW, Koratsoulis G;
XX WPI; 2000-638176/61.
XX
XX Novel 49 human secreted proteins useful for diagnosis, prevention and
PT treatment of disorders including neurological, cell proliferative,
PT cardiovascular, and autoimmune/inflammatory disorders and microbial
PT infections -
XX
XX Disclosure; Page 402; 405pp; English.
XX
XX This invention describes a novel isolated polypeptide (I) comprising an
XX amino acid sequence at least 95 % identical to a polypeptide sequence
XX selected from 49 polypeptides encoded by polynucleotide sequences
XX included in American Type Culture Collection (ATCC) deposit number
XX 203917, defined in the specification. The products of the invention have
XX cytosstatic, antiarthritic, antiasthmatic, immunosuppressive, neurotropic,
XX antiarteriosclerotic, antiinflammatory, neuroprotective, antidiabetic,
XX tranquiliser, vulnerary, antibacterial, antiparasitic, antiarrhythmic,
XX antineoplastic, cardiant and anti-HIV activity. (I) or a nucleic acid (II)
XX encoding (I) is useful for preventing, treating or ameliorating a medical
XX condition and for diagnosing a pathological condition or susceptibility
XX to the condition. (I) is useful for identifying a binding partner which
XX affects the activity of the polypeptide and for identifying an activity
XX in a biological sample. (I), (II) or an antibody (IV) specific to (I) is
XX also useful for treating or preventing a disease, disorder or condition
XX associated with aberrant expression of (I). Diseases treated or diagnosed
XX include immune disorders such as autoimmune diseases, blood protein
XX disorders, anemia, allergic reactions and conditions such as asthma,
XX organ rejection or graft-versus-host disease, inflammation, hyper
XX proliferative disorders, cardiovascular disorders such as arterioarterial
XX fistula, arrhythmias, arteriosclerosis, coronary thrombosis, organ
XX regeneration, cancer, neovascular glaucoma, diabetic retinopathy,
XX rheumatoid arthritis, psoriasis, diseases associated with increased
XX apoptosis that include acquired immunodeficiency syndrome (AIDS),
XX neurological diseases such as Parkinson's disease, viral, bacterial,
XX fungal or parasitic diseases. They are also used to repair, replace or
XX protect tissue damage by congenital defects, to treat trauma, in surgery,
XX including cosmetic plastic surgery, to treat fibrosis, reperfusion injury
XX or systemic cytokine damage, to stimulate chondrocyte growth, to prevent
XX skin aging due to sunburn, to change a mammal's mental state or physical
XX state by influencing biorythms, cardiac rhythms, depression, memory,
XX stress and for accelerating wound healing. (I), (II) and/or their agonist
XX or antagonist are useful as food additives or preservatives to increase
XX or decrease storage capabilities, fat content, lipid, protein,
XX carbohydrate, vitamin, mineral or other nutritional components. (I) is
XX useful for screening therapeutic compounds. (I) is useful in forensic
XX biology for detecting DNA sequences and as diagnostic probes for
XX detecting the presence of specific mRNA in a particular cell type.
XX
XX Sequence 229 AA;
XX
XX Query Match 3.9%; Score 32; DB 21; Length 229;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-24;
XX Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 399 SVSNFVNLYGYPGSKCTLAETIKFWMTDMAD 430
XX |||||
XX 108 SVSNFVNLYGYPGSKOTLRITKFWMTDMAD 139

```

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XX 13-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #10255.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensics;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001-WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HUSE-) HUSEQ INC.
XX
XX Dmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
XX N-PSDB; AAS74451.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity -
XX
XX C'tain 20; SEQ ID NO 40623; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC (II). (II) is useful for generating antibodies against it, detecting or
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (II) and its binding partners are useful in medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. AAG0010-AAG03377 represent novel human
XX CC diagnostic amino acid sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 726 AA;
XX
XX Query Match 3.9%; Score 32; DB 22; Length 726;
XX Best Local Similarity 100.0%; Pred. No. 4.3e-24;
XX Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 510 CNFSKRDWLSAVMTYTCNFAKTCPPQPPV 541
XX |||||
XX 272 CNFSKRDWLSAVMTYTCNFAKTCPPQPPV 303

```

RESULT 24
 ABG10264
 ID ABG10264 standard; Protein: 726 AA.
 AC
 XX ABG10264;
 AC

RESULT 25
 AAC01845
 ID AAC01845 standard; Protein: 144 AA.
 AC
 XX AAC01845;
 AC
 XX 06-NOV-2001 (first entry)

XX Human polypeptide SEQ ID NO 15737.
D2
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; hematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
FN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-C515126.
XX
PR 18-MAY-2000; 2000US-C577409.
XX
PA (H5SE-) H5SEQ .NC.
XX
PI Targ YC, Liu C, Dermanac RT;
XX
DR MPI, 2001-5:4835/56.
XX
DR N-PSDB; AA181776.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
XX disorders and treating e.g. leukemia, inflammation and immune
XX disorders.
PS Claim 20; SEQ ID NO 15737; 1339pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AA173941-AA173941) and
CC the encoded proteins (AA000010-AA013910) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, hematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 144 AA;
Query Match 3.8%; Score 31; DB 22; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 355 CILMEGGEFLNYDMLGVNCGEGKXFDGIV 365
Db 80 CILMEGGEFLNYDMLGVNCGEGKXFDGIV 110
RSDUT 26
AAU81573
ID AAU81570 standard; Protein; 8: AA.
XX
AC AAU81570;
XX
DT 05-JUN-2002 (first entry);
XX
DE Novel central nervous system protein #480.
XX
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischemia; angiosclerosis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;

KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy.
XX
OS Homo sapiens.
XX
FN WO200155318-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JUN-2001; 2001WO-US01332.
XX
PR 31-JAN-2000; 2000US-0179065.
XX
PR 04-FEB-2000; 2000US-0180628.
XX
PR 24-FEB-2000; 2000US-0184664.
XX
PR 02-MAR-2000; 2000US-0186350.
XX
PR 16-MAR-2000; 2000US-0189874.
XX
PR 17-MAR-2000; 2000US-0190076.
XX
PR 18-APR-2000; 2000US-0198123.
XX
PR 19-MAY-2000; 2000US-0205515.
XX
PR 07-JUN-2000; 2000US-0214886.
XX
PR 28-JUN-2000; 2000US-0214886.
XX
PR 30-JUN-2000; 2000US-0215135.
XX
PR 07-JUL-2000; 2000US-0216647.
XX
PR 07-JUL-2000; 2000US-0216880.
XX
PR 11-JUL-2000; 2000US-0217487.
XX
PR 11-JUL-2000; 2000US-0217496.
XX
PR 14-JUL-2000; 2000US-0218290.
XX
PR 26-JUL-2000; 2000US-0220963.
XX
PR 26-JUL-2000; 2000US-0220964.
XX
PR 14-AUG-2000; 2000US-0224518.
XX
PR 14-AUG-2000; 2000US-0224519.
XX
PR 14-AUG-2000; 2000US-0225213.
XX
PR 14-AUG-2000; 2000US-0225214.
XX
PR 14-AUG-2000; 2000US-0225266.
XX
PR 14-AUG-2000; 2000US-0225267.
XX
PR 14-AUG-2000; 2000US-0225268.
XX
PR 14-AUG-2000; 2000US-0225270.
XX
PR 14-AUG-2000; 2000US-0225447.
XX
PR 14-AUG-2000; 2000US-0225757.
XX
PR 14-AUG-2000; 2000US-0225758.
XX
PR 14-AUG-2000; 2000US-0225759.
XX
PR 18-AUG-2000; 2000US-0226279.
XX
PR 22-AUG-2000; 2000US-0226681.
XX
PR 22-AUG-2000; 2000US-0226686.
XX
PR 23-AUG-2000; 2000US-0227009.
XX
PR 30-AUG-2000; 2000US-0228924.
XX
PR 01-SEP-2000; 2000US-0229387.
XX
PR 01-SEP-2000; 2000US-0229343.
XX
PR 01-SEP-2000; 2000US-0229344.
XX
PR 01-SEP-2000; 2000US-0229345.
XX
PR 05-SEP-2000; 2000US-0229349.
XX
PR 05-SEP-2000; 2000US-0229513.
XX
PR 06-SEP-2000; 2000US-0230437.
XX
PR 06-SEP-2000; 2000US-0230438.
XX
PR 08-SEP-2000; 2000US-0231243.
XX
PR 08-SEP-2000; 2000US-0231242.
XX
PR 08-SEP-2000; 2000US-0231243.
XX
PR 08-SEP-2000; 2000US-0231244.
XX
PR 08-SEP-2000; 2000US-0231413.
XX
PR 08-SEP-2000; 2000US-0231414.
XX
PR 08-SEP-2000; 2000US-0232080.
XX
PR 08-SEP-2000; 2000US-0232081.
XX
PR 12-SEP-2000; 2000US-0231968.
XX
PR 14-SEP-2000; 2000US-0232397.
XX
PR 14-SEP-2000; 2000US-0232398.
XX
PR 14-SEP-2000; 2000US-0232399.
XX
PR 14-SEP-2000; 2000US-0232400.
XX
PR 14-SEP-2000; 2000US-0232401.
XX
PR 14-SEP-2000; 2000US-0233063.
XX
PR 14-SEP-2000; 2000US-0233064.

[illegible]

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PR 08-DEC-2000; 2000US-0251965.
PR 08-DEC-2000; 2000US-0251950.
PR 11-DEC-2000; 2000US-0254057.
PR 05-JAN-2001; 2001US-0259678.
XX
XX
XX (HCCA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-58.633/65.
XX N-PSDB; ABK43900.
XX
XX New isolated nucleic acid encoding a protein for diagnosing
PT preventing, treating or ameliorating medical conditions and used as
PT food additives or preservatives.
XX
XX Claim 3; SEQ ID NO 1088; 837pp; English.
XX
XX The invention describes an isolated nucleic acid molecule (1) encoding a
XX novel central nervous system protein. (1) and polypeptides (11) encoded
XX by (1), are used to treat a medical condition and in diagnosis of a
XX pathological condition. Disorders which are diagnosed or treated include
XX autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
XX disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
XX e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
XX angiogenesis, nervous system disorders e.g. Alzheimer's disease and
XX arylotrophic lateral sclerosis, infections caused by bacteria, viruses
XX e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
XX e.g. Corneal infection, gastrointestinal disorders e.g. dysphagia,
XX adenocarcinomas and irritable bowel syndrome, reproductive system
XX disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
XX and pituitary dwarfism, cancers and disorders at the cellular level e.g.
XX leukaemia, disorders involving neovascularisation e.g. malignancies,
XX respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
XX acute kidney failure and blood related disorders e.g. myocardial
XX infarction. The polypeptides can also be used to aid wound healing and
XX epithelial cell proliferation, to prevent skin aging due to sunburn, to
XX maintain organs before transplantation, for supporting cell culture of
XX primary tissues, to regenerate tissues and in chemotaxis. The
XX polypeptides can also be used as a food additive or preservative to
XX increase or decrease storage capabilities, fat content, lipid, protein,
XX
XX
XX Query Match: 3.4%; Score 28; DB 22; Length 81;
XX Best Local Similarity 100.0%; Pred. No. 9, 5e-21;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 46 EILGPECYLCVPASPTGRRROPE 73
XX ||||| ||||| ||||| |||||
XX 35 EILGPECYLCVPASPTGRRROPE 62
XX
XX RESCUE 27
XX AAU23224
XX AAU23224 standard; Protein; 81 AA.
XX
XX AAU23224;
XX
XX 17-DEC-2001 (first entry)
XX
XX DE Novel human enzyme polypeptide #310.
XX
XX Human: cytochrome oxidase; transferase; hydrolase; lyase; secretase;
XX lyase; hyperproliferative disorder; immunodeficiency disorder;
XX autoimmune disorder; neurological disorder; metabolic disorder;
XX inflammatory disorder; cardiovascular disorder; reproductive disorder;
XX blood-related disorder; infectious disorder; cytostatic; anti arthritic;
XX nephrotoxic; anticoagulant.
XX
XX CS Homo sapiens.
XX
XX W0200155301-A2.
XX
XX 02-AUG-2001.

```

[illegible]

XX Novel polypeptides and polynucleotides useful for diagnosing,
 PT preventing, treating neural, immune system, muscular, reproductive,
 PT pulmonary, cardiovascular, renal, proliferative disorders and cancerous
 PT diseases -

XX
 PS Claim 11; SEQ ID No 1220; 1180bp; English.

XX
 CC The present invention relates to the isolation of novel human enzyme
 CC polypeptides, and the cDNA AAS40795-AAS41684 and genomic sequences
 CC encoding them. The enzyme polypeptides of the invention may comprise the
 CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
 CC isomerases or ligases. The sequences of the invention are useful in the
 CC diagnosis, treatment, prevention and/or prognosis of a wide range of
 CC disorders including hyperproliferative disorders (e.g. cancer),
 CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders
 CC (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),
 CC metabolic disorders (e.g. phenylketonuria), inflammatory disorders
 CC (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis),
 CC blood-related disorders (e.g. haemophilia), reproductive disorders
 CC (e.g. infertility) and infectious disorders (e.g. influenza). The
 CC polynucleotides of the invention can also be used in gene therapy.

CC AAT22915-AAT23814 represent the novel human enzyme polypeptides of the
 CC invention.

CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WFO
 CC at ftp.wipo.int/pub/published_pat_sequences.

XX
 SQ Sequence 81 AA;

XX
 Query Match 3.4%; Score 28; DB 22; Length 81;
 Best Local Similarity 100.0%; Pred. No. 5,5e-21;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 46 EILGVECYLVGFYASPTGRRRPPPE 73
 DB 35 EILGVECYLVGFYASPTGRRRPPPE 62

RESULT 28
 AAM93345
 ID AAM93345 standard; Protein: 335 AA.

XX
 AC AAM93345;

XX
 DT 06-NOV-2001 (first entry);

XX
 DE Human polypeptide, SEQ ID NO: 2889.

XX
 KM Human: full length cDNA; cDNA synthesis; oligo-capping.

XX
 OS Homo sapiens.

XX
 PN EP130094-A2.

XX
 PD 05-SEP-2001.

XX
 PF 07-JUL-2000; 2000EP-0114083.

XX
 PR 09-JUL-1999; 99JP-0194496.

XX
 PR 11-JAN-2000; 2000JP-0119774.

XX
 PR 02-MAY-2000; 2000JP-0189765.

XX
 PA (HELI-) HELIX RES INST.

XX
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX WPI; 2001-524255/58.
 DR N-PSDB; AAK94265.

XX
 PT 830 Primers useful for synthesizing full length cDNA clones and their
 PT use in genetic manipulation -

XX
 PS Claim 8; SEQ ID NO 2889; 1180bp + sequence listing; English.

XX
 CC The invention relates to primers for synthesizing full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been
 CC isolated and nucleotide sequences of 5' and 3' ends of the cDNA
 CC molecules have been determined. Primers for synthesizing the full length
 CC cDNA are useful for clarifying the function of the protein encoded by
 CC the cDNA. The full length clones were obtained by construction of full
 CC length enriched cDNA libraries that were synthesised by the oligo-capping
 CC method. The primers enable the production of the full length cDNA easily
 CC without any special methods. The present sequence is a polypeptide
 CC encoded by a full length human cDNA of the invention.

CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in CD-ROM format directly from EPO.

XX
 SQ Sequence 335 AA;

XX
 Query Match 3.4%; Score 28; DB 22; Length 335;
 Best Local Similarity 100.0%; Pred. No. 3,5e-20;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 510 CFFSKNDYMSAVMTWYTPAKTGDPN 537
 DB 31 CFFSKNDYMSAVMTWYTPAKTGDPN 58

RESULT 29
 ABG16624
 ID ABG16624 standard; Protein: 419 AA.

XX
 AC ABG16624;

XX
 DT 18-FEB-2002 (first entry)

XX
 DE Novel human diagnostic protein #16615.

XX
 KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder.

XX
 OS Homo sapiens.

XX
 PN WO200175067-A2.

XX
 PD 11-OCT-2001.

XX
 PF 30-MAR-2001; 2001WC-US08631.

XX
 PR 31-MAR-2000; 2000US-0540217.

XX
 PR 23-APR-2000; 2000US-0649167.

XX
 PA (HYSE-) HYSEQ INC.

XX
 PN Dmanac RT, Liu C, Tang YT;
 F- N-PSDB; AAS60811.

XX
 DR WPI; 2001-639362/73.

XX
 PT New isolated polynucleotide and encoded polypeptides useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -

XX
 PS Claim 20; SEQ ID No 46983; 103bp; English.

XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (II) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or

CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (I). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG3377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at [ftp://wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
 XX
 XX
 SQ Sequence 419 AA;
 Query Match: 3.4%; Score 28; DB 22; Length 419;
 Best Local Similarity 100.0%; Pred. No. 4.3e-28;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 46 ELGPFVECYLGVFVNASPTGRRFPQPE 73
 |||||
 Db 66 ELGPFVECYLGVFVNASPTGRRFPQPE 73
 RESULT 33
 ASG10269
 ID ABG10269 standard; Protein; 165 AA.
 XX
 AC ABG10269;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #10269.
 XX
 KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US308631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PDB; AAS74456.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID NO 40628; 103bp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridization probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (II) is useful in gene therapy techniques
 CC to restore normal activity of (I) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical

CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG3377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at [ftp://wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
 XX
 XX
 SQ Sequence 165 AA;
 Query Match: 3.2%; Score 26; DB 22; Length 65;
 Best Local Similarity 100.0%; Pred. No. 2.3e-18;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 209 LGFLSTGDMAGNYGJLDQIQALRW 234
 |||||
 Db 91 LGFLSTGDMAGNYGJLDQIQALRW 116
 RESULT 31
 AAC04336
 ID AAC04336 standard; Protein; 134 AA.
 XX
 AC AAC04336;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 18228.
 XX
 KM Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KM tissue growth factor; immunomodulatory; cancer; leukaemia;
 KM nervous system disorders; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200164835-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-US04927.
 XX
 PR 28-FEB-2000; 2000US-0515126.
 PR 19-MAY-2000; 2000US-0577409.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-514838/56.
 DR N-PDB; AA184267.
 XX
 PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -
 XX
 PS Claim 20; SEQ ID NO 18228; 1399pp + Sequence Listing; English.
 XX
 CC The invention relates to human polynucleotides (AA179941-AA179941) and
 CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibit activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.

CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp://ipo.int/pub/published_pat_sequences.

XX Sequence 134 AA:

Query Match 2.6%; Score 21; DB 22; Length 134;
 Best Local Similarity 100.0%; Pred. No. 3.3e-43;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 669 RGYSTELSVTIAVGSLLFLFN 689
 DB 50 RGYSTELSVTIAVGSLLFLFN 70

RESULT 32
 ABG64991

ID ABG64991 standard; Protein; 228 AA.

AC ABG64991;

DT 27-AUG-2002 (first entry)

DE Human albumin fusion protein; #1666.

XX Albumin fusion protein; therapeutic protein X; human albumin; HA;
 XX human serum albumin; HSA; cancer; reproductive disorder;
 XX digestive disorder; immune disorder; endocrine disorder;
 XX haematopoietic disorder; neural disorder; connective disorder;
 XX cytostatic; antifertility; antiinflammatory; antitumor;
 XX immunomodulator; anti-HIV; antidiabetic; haemostatic; neurotropic;
 XX neuropsychiatric; antiparkinsonian; antimicrobial; neuroleptic;
 KW osteopathic; antithrombotic.

OS Homo sapiens.
 OS Synthetic.

FN WO200177137-A1.

PD 18-OCT-2001.

PE 12-APR-2001; 2001WO-US11988.

PR 12-APR-2000; 2000US-229358P.

PR 23-APR-2000; 2000US-199384P.

PR 21-DEC-2000; 2000US-256931P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Haseltine WA;

DR WPI; 2002-010886/C1.

PT New fusion protein for treating disease e.g. diabetes comprises an
 PT albumin fused to a therapeutic protein -

PS Claim 1; Page 1662-1663; 2102pp; English.

XX The present invention relates to albumin fusion proteins comprising a
 CC therapeutic protein X and human albumin (HA), also known as human serum
 CC albumin, HSA). The proteins are useful for treating a disease or
 CC disorder that may be modulated by therapeutic protein X. The albumin
 CC extends the shelf-life of protein X, and may increase its biological
 CC in vivo activity. The protein is useful for treating and
 CC diagnosing disorders such as cancer, reproductive disorders, digestive
 CC disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders
 CC (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders
 CC (e.g. diabetes), haematopoietic disorders, neural disorders
 CC (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jakob disease,
 CC encephalomyelitis, meningitis, schizophrenia), and connective disorders
 CC (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin
 CC fusion proteins of the invention.

SQ Sequence 228 AA:

Query Match 2.2%; Score 18; DB 23; Length 228;
 Best Local Similarity 100.0%; Pred. No. 7.6e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 KPMVYIHGGSYMEGTGN 184
 DB 173 KPMVYIHGGSYMEGTGN 190

RESULT 33
 AAE21452

ID AAE21452 standard; Protein; 228 AA.

AC AAE21452;

DT 01-JUL-2002 (first entry)

DE Human gene 1 encoded secreted protein HAMH20, SEQ ID NO:68.

XX Human; secreted protein; gene therapy; autoimmune disease; vitamin;
 KW rheumatoid arthritis; hyperproliferative disorder; neoplasia; breast;
 KW liver; cardiovascular; cardiac arrest; cerebrovascular; infection;
 KW cerebral ischaemia; angiogenesis; nervous system; Alzheimer's disease;
 KW ocular; corneal infection; wound healing; neuroprotective; skin aging;
 KW transplantation; chemotaxis; food additive; preservative; vitreous;
 KW storage capability; mineral; cofactor; immunosuppressive; cytostatic;
 KW antiproliferative; cardiac; vasotropic; cerebroprotective; neurotropic;
 KW fungicide; ophthalmological; sunburn; virucide; antibacterial.

OS Homo sapiens.

FN Key Location/Qualifiers
 FT Peptide 1..45
 FT /label= Signal_peptide
 FT Protein 46..228
 FT /label= Mature_secreted_protein

PD WO200224719-A1.

PE 26-MAR-2002.

PR 17-JAN-2001; 2001WO-US01565.

PR 20-SEP-2000; 2000US-234210P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Komatsu G, Baker KP, Birse CE, Soppet DR, Olsen HS;

DR Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fischella M;

DR Ni J;

DR WPI; 2002-258042/30.

DR N-PSDB; AAD33812.

PT New nucleic acid molecules encoding 21 human secreted proteins for
 PT diagnosing or treating e.g. autoimmune diseases, hyperproliferative
 PT disorders, and cardiovascular disorders, and used as food additives or
 PT preservatives -

PS Claim 11; Page 467; 519pp; English.

XX AAD33812-AAD33868 represent cDNAs corresponding to 21 human secreted
 CC protein genes, and AAE21452-AAE21508 represent the proteins they encode.
 CC AAE21509-AAE21517 represent human secreted protein fragments. The genes
 CC and their corresponding secreted proteins are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Pathological conditions can be diagnosed by determining the
 CC amount of the new protein in a sample or by determining the presence of
 CC mutations in the new genes. Specific uses are described for each of the
 CC 21 genes, based on the tissues in which they are most highly expressed,
 CC and include developing products for the diagnosis or treatment of

CC disorders such as autoimmune diseases e.g. rheumatoid arthritis,
 CC hyperproliferative disorders e.g. neoplasms of the breast or liver.
 CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
 CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
 CC Alzheimer's disease, infections caused by bacteria, viruses and fungi
 CC and ocular disorders e.g. corneal infection. The polypeptides of the
 CC invention can also be used to aid wound healing and epithelial cell
 CC proliferation, to prevent skin aging due to sunburn, to maintain organs
 CC before transplantation, for supporting cell culture of primary tissues,
 CC to regenerate tissues and in chemotaxis. They can also be used as a food
 CC additive or preservative to increase or decrease storage capabilities,
 CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
 CC and other nutritional components. The present sequence represents a
 CC human secreted protein of the invention.

CC Sequence 228 AA;

Query Match 2.2%; Score 18; EB 23; Length 228;

Best Local Similarity 100.0%; Pred. No. 7.6e-10;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 173 KPMWYIHGSGYVECTGN 190

RESULT 34

ID AAE21516 standard; Protein; 161 AA.

XX AAE21516;

DT 01-JUL-2002 (first entry)

XX Human gene 1 encoded secreted protein fragment #1.

XX Human: secreted protein; gene therapy; autoimmune disease; vitamin;
 KM rheumatoid arthritis; hyperproliferative disorder; neoplasm; breast;
 KM liver; cardiovascular; cardiac arrest; cerebrovascular; infection;
 KM cerebral ischaemia; angiogenesis; nervous system; Alzheimer's disease;
 KM ocular; corneal infection; wound healing; neuroprotective; skin aging;
 KM transplantation; chemotaxis; food additive; preservative; vitamin;
 KM storage capability; mineral; cofactor; immunosuppressive; cytostatic;
 KM antiproliferative; cardiac; vasotropic; cerebroprotective; nocotropic;
 KM fungicide; optalmalogical; sunburn; virucide; antibacterial.

XX Homo sapiens.

XX Key Location/Qualifiers

FT MISC-difference 133 /label= Unknown

FT MISC-difference 14. /label= Unknown

FT MISC-difference 153 /label= Unknown

FT MISC-difference 160 /label= Unknown

XX MO230224719-A1.

XX 28-MAR-2002.

XX 17-JAN-2001; 2001WO-US01565.

XX 20-SEP-2000; 2000US-234210P.

XX (HUMAN) HUMAN GENOME SCI INC.

XX Rosen CA, Komatsculis GA, Baker KP, Birse CE, Soppet DR, Oster HS,

PI Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fiacella N,

XX WIPI, 2002-258042/30.

XX New nucleic acid molecules encoding 21 human secreted proteins for
 PT diagnosing or treating e.g. autoimmune diseases, hyperproliferative
 PT disorders, and cardiovascular disorders, and used as food additives or
 PT preservatives -

XX PS Disclosure; Page 8; 51pp; English.

CC ADD3812-ADD3868 represent cDNAs corresponding to 21 human secreted
 CC protein genes, and AAE21452-AAE21508 represent the proteins they encode.
 CC AAE21509-AAE21517 represent human secreted protein fragments. The genes
 CC and their corresponding secreted proteins are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Pathological conditions can be diagnosed by determining the
 CC amount of the new protein in a sample or by determining the presence of
 CC mutations in the new genes. Specific uses are described for each of the
 CC 21 genes, based on the tissues in which they are most highly expressed,
 CC and include developing products for the diagnosis or treatment of
 CC disorders such as autoimmune diseases e.g. rheumatoid arthritis,
 CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
 CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
 CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
 CC Alzheimer's disease, infections caused by bacteria, viruses and fungi;
 CC and ocular disorders e.g. corneal infection. The polypeptides of the
 CC invention can also be used to aid wound healing and epithelial cell
 CC proliferation, to prevent skin aging due to sunburn, to maintain organs
 CC before transplantation, for supporting cell culture of primary tissues,
 CC to regenerate tissues and in chemotaxis. They can also be used as a food
 CC additive or preservative to increase or decrease storage capabilities,
 CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
 CC and other nutritional components. The present sequence represents human
 CC secreted protein fragment referred to in the disclosure of the invention.

XX Sequence 161 AA;

Query Match 1.8%; Score 15; EB 23; Length 161;

Best Local Similarity 100.0%; Pred. No. 7.6e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 87 PPTGRRRFPPEPPS 101

RESULT 35

ID ABG64990 standard; Protein; 162 AA.

XX ABG64990;

DT 27-AUG-2002 (first entry)

XX Human albumin fusion protein #1665.

XX Albumin fusion protein; therapeutic protein X; human albumin; HA;
 KM human serum albumin; HSA; cancer; reproductive disorder;
 KM digestive disorder; immune disorder; endocrine disorder;
 KM hematopoietic disorder; neural disorder; connective disorder;
 KM cytostatic; antifertility; antiinflammatory; anticancer;
 KM immunomodulator; anti-HIV; antidiabetic; haemostatic; nocotropic;
 KM neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
 KM osteopathic; antiarthritic.

XX Homo sapiens.

XX Synthetic.

XX WO200177137-A1.

XX 18-OCT-2001.

XX 12-APR-2001; 2001WO-US11988.

XX 12-APR-2000; 2000US-229358P.

```

PR 25-APR-2000; 2000US-199384P.
PR 21-DEC-2000; 2000US-255931P.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
XX Rosen CA, Haseltine WA.
XX WPI; 2002-010886/01.
XX
XX New fusion protein for treating disease e.g. diabetes comprises an
XX albumin fused to a therapeutic protein.
XX
XX Claim 1; Page 1662; 2102pp; English.
XX
XX The present invention relates to albumin fusion proteins comprising a
XX therapeutic protein X and human albumin (HA), also known as human serum
XX albumin, HSA). The proteins are useful for treating a disease or
XX disorder that may be modulated by therapeutic protein X. The albumin
XX extends the shelf-life of protein X, and may increase its biological
XX in vitro/in vivo activity. The protein is useful for treating and
XX diagnosing disorders such as cancer, reproductive disorders, digestive
XX disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders
XX (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders
XX (e.g. diabetes), haematopoietic disorders, neural disorders
XX (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, and connective
XX tissue disorders, meningitis, schizophrenia), and connective
XX tissue disorders (e.g. osteoporosis, arthritis). ABG51326-ABG5518 represent albumin
XX fusion proteins of the invention.
XX
XX Sequence 162 AA:
XX
XX Query Match 1.8%; Score 15; DB 23; Length 162;
XX Best Local Similarity 100.0%; Pred. No. 7.8e-07;
XX Matches 15; Conservative 0; Mismatches 0; Gaps 0;
XX
XX QY 62 PPTGRRRFPPEPPS 76
XX |||||||||
XX DB 88 PPTGRRRFPPEPPS 102
XX
XX RESULT 16
XX AAE21473
XX AAE21473 standard; Protein; 162 AA.
XX
XX AC AAE21473;
XX
XX DT 01-JULY-2002 (first entry)
XX
XX DE Human gene 1 encoded secreted protein HMMH20, SEQ ID NO:89.
XX
XX Human; secreted protein; gene therapy; autoimmune disease; vitamin;
XX rheumatoid arthritis; hyperproliferative disorder; neoplasm; breast;
XX liver; cardiovascular; cardiac arrest; cerebrovascular; infection;
XX cerebral ischaemia; angioneurotic; nervous system; Alzheimer's disease;
XX ocular; corneal infection; wound healing; neuroprotective; skin aging;
XX transplantation; cholestasis; food additives; preservative; vitamin;
XX storage capability; mineral; cofactor; immunosuppressive; cytotoxic;
XX antiproliferative; cardiac; vasodilator; cerebroprotective; neurotrophic;
XX fungicide; ophthalmological; sunburn; vitruole; antibacterial.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..45
XX FT /label= Signal_peptide
XX FT Protein 46..162
XX FT /label= Mature_secreted_protein
XX FT Misc-difference 134
XX FT /label= Unknown
XX FT /note= "Encoded by NCG"
XX FT 142
XX FT Misc-difference 142
XX FT /label= Unknown
XX FT /note= "Encoded by GNT"

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FT Misc-difference 154
FT /label= Unknown
FT /note= "Encoded by NCG"
FT Misc-difference 161
FT /label= Unknown
FT /note= "Encoded by NCG"
XX
XX WO200224719-A1.
XX
XX 28-MAR-2002.
XX
XX 17-JAN-2001; 2001WO-US01565.
XX
XX 20-SEP-2000; 2000US-234210P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Komatsu GA, Baker KP, Birse CE, Soppet DR, Olsen HS;
XX Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fischeita M;
XX N. G.
XX
XX WPI; 2002-258042/30.
XX
XX N-PDB: AAD33833.
XX
XX New nucleic acid molecules encoding 21 human secreted proteins for
XX diagnosing or treating e.g. autoimmune diseases, hyperproliferative
XX disorders, and cardiovascular disorders, and used as food additives or
XX preservatives.
XX
XX Claim 11; Page 483-484; 519pp; English.
XX
XX AAD33812-AAD33868 represent cDNAs corresponding to 21 human secreted
XX protein genes, and AAE21452-AAE21508 represent the proteins they encode.
XX CC AAE21509-AAE21517 represent human secreted protein fragments. The genes
XX and their corresponding secreted proteins are useful for preventing,
XX treating or ameliorating medical conditions, e.g., by protein or gene
XX therapy. Pathological conditions can be diagnosed by determining the
XX amount of the new protein in a sample or by determining the presence of
XX mutations in the new genes. Specific uses are described for each of the
XX 21 genes, based on the tissues in which they are most highly expressed,
XX and include developing products for the diagnosis or treatment of
XX disorders such as autoimmune diseases e.g. rheumatoid arthritis,
XX hyperproliferative disorders e.g. neoplasms of the breast or liver,
XX cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
XX e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
XX Alzheimer's disease, infections caused by bacteria, viruses and fungi
XX and ocular disorders e.g. corneal infection. The polypeptides of the
XX invention can also be used to aid wound healing and epithelial cell
XX proliferation, to prevent skin aging due to sunburn, to maintain organs
XX before transplantation, for supporting cell culture of primary tissues,
XX to regenerate tissues and in chemotaxis. They can also be used as a food
XX additive or preservative to increase or decrease storage capabilities,
XX fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
XX and other nutritional components. The present sequence represents a
XX human secreted protein of the invention.
XX
XX Sequence 162 AA:
XX
XX Query Match 1.8%; Score 15; DB 23; Length 162;
XX Best Local Similarity 100.0%; Pred. No. 7.8e-07;
XX Matches 15; Conservative 0; Mismatches 0; Gaps 0;
XX
XX QY 62 PPTGRRRFPPEPPS 76
XX |||||||||
XX DB 88 PPTGRRRFPPEPPS 102
XX
XX RESULT 37
XX AAB54266
XX ID AAB54266 standard; Protein; 359 AA.
XX
XX AC AAB54266;
XX

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D1 09-MAR-2001 (first entry)
XX
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:719.
XX
KM Human: pancreas; pancreatic cancer; pancreatic cancer antigen;
KM detection; diagnosis; identification; cytostatic; neuroprotective;
KM neurotropic; immunomodulatory; relaxant; contraceptive; gynaecological;
KM antinflammatory; cardiact; gene therapy; chromosome mapping;
KM linkage analysis; tissue identification; tissue typing; forensic;
KM neural; immune system; muscular; reproductive; gastrointestinal;
KM pulmonary; cardiovascular; renal; proliferative.
XX
OS Homo sapiens.
XX
PN WO200055320-A1.
XX
PD 21-SEP-2003.
XX
PF 08-MAR-2003; 203CWO-US05989.
XX
FR 12-MAR-1999; 99US-0124270.
XX
PA (HUKA-) HUKAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SY;
XX
DR WPI: 2000-579444/54.
DR N-PSDB: AAC99231.
XX
XX
PT New nucleic acid that is a pancreatic cancer antigen for preventing,
PT treating, or ameliorating a medical condition, particularly pancreatic
PT cancer, or for use in assays for diagnosing a pathological condition -
PS Claim 1; Page 1159-1160; 1379pp; English.
XX
XX
CC AAC98773 to AAC99231 encode the human pancreatic cancer associated
CC proteins, called pancreatic cancer antigens, given in AAB5406 to
CC AAB54466. The human pancreatic cancer antigens have cytostatic,
CC neuroprotective, neurotropic, immunomodulatory, relaxant, contraceptive,
CC gynaecological, cardiact and antinflammatory activities, and can be used
CC in gene therapy. The polynucleotide and proteins can be used for
CC preventing, treating, or ameliorating a medical condition or in assays
CC for diagnosing a pathological condition or a susceptibility to one in a
CC subject. Binding partners to the proteins and the activity of the
CC proteins can be identified. The pancreatic cancer antigens can be used to
CC detect, treat or prevent pancreatic disorders, especially cancer.
CC Agonists and antagonists to the antigens can be screened for. The
CC pancreatic cancer antigen polynucleotides can be screened for. The
CC acid hybridisation probes that can be used in chromosome mapping, linkage
CC analysis, tissue identification and/or typing and a variety of forensic
CC and diagnostic methods. The proteins can be used to generate antibodies
CC which are used to purify, detect and target the polypeptides, including
CC both in vivo and in vitro diagnostic and therapeutic methods. The
CC proteins can be used to treat or prevent neural, immune system, muscular,
CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
CC sequences used in the exemplification of the present invention.
XX
XX
SQ Sequence 359 AA;
XX
XX
Query Match 1.5%; Score 12; DB 21; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AC AAR58985;
XX
XX
DT 25-MAR-2003 (updated)
DT 03-MAY-1995 (first entry)
XX
DE Bile salt-stimulated lipase (variant A).
XX
KM Bile salt stimulated lipase; BSSL; glycoprotein; esterase;
KM acetyl cholinesterase; cystic fibrosis; chronic pancreatitis;
KM fat malabsorption; vitamins; dietary lipids; food supplement.
XX
XX
OS Homo sapiens.
XX
PN WO9420610-A1.
XX
PD 15-SEP-1994.
XX
PF 25-FEB-1994; 94WO-SB00160.
XX
FR 01-MAR-1993; 93SE-0000686.
FR 04-MAR-1993; 93SE-0000722.
XX
XX
PA (ASTR) ASTRA AB.
XX
PI Blaeckberg L, Edlund M, Hansson L, Hernell O, Lundberg L;
PI Strömqvist K, Toernell J;
XX
DR WPI: 1994-303018/37.
XX
XX
PT Bile salt-stimulated lipase variants and coding sequences - used
PT to produce prods. for treatment of a pathological condition
PT related to exocrine pancreatic insufficiency
XX
XX
PS Example 1.1.2; Page 57-58; 102pp; English.
XX
XX
CC Bile salt-stimulated lipase (BSSL) is a single chain glycoprotein
CC which is highly glycosylated. The N-terminal half of the protein
CC shows a homology to acetyl cholinesterase and some other esterases.
CC BSSL variant polypeptides can be used for the treatment of a
CC pathological condition related to exocrine pancreatic insufficiency
CC such as cystic fibrosis, chronic pancreatitis, fat malabsorption or
CC malabsorption of fat soluble vitamins for improvement of utilisation
CC of dietary lipids, particularly in preterm born infants. They can
CC also be used as supplements for infant food formulations. The BSSL
CC variants have maintained catalytic activity but contain less
CC glycosylation sites than native BSSL. This variant is a deletion
CC mutant lacking the C-terminal 187 amino acids of the wild-type
CC protein (See AAR58980).
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 535 AA;
XX
XX
Query Match 1.5%; Score 12; DB 15; Length 535;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

CY 526 YWTFNFAKTGDPN 537
DB 192 YWTFNFAKTGDPN 203

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RESULT 39
AAR58985
ID AAR58985 standard; protein; 535 AA.
XX
DE Recombinant bile salt-activated lipase.
XX
KM Bile salt activated lipase; BAL; C-terminal repeat.
XX

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XX Mammalia.
CS
XX
XX JP07111891-A.
XX
XX 02-MAY-1995.
XX
XX 30-SEP-1993; 93JP-0245079.
XX
XX 30-SEP-1993; 93JP-0245079.
XX
XX (MEIP ) MEIJI MILK PROD CO LTD.
XX
XX WPI; 1995-1963:8/26.
XX
XX N-PSDB; AAQ90569.
XX
XX New recombinant bile salt-activated lipase(s); cDNA encoding them
XX and vectors - useful for high level expression of the lipase(s) by
XX fermenter-culturing.
XX
XX Claim 1; Page 3-10; 31pp; Japanese.
XX
XX New lipases are ones in which 1-15 repeats of any of the sequences
XX AA875099-R75105 (encoded by AAQ90570-Q90576) are attached to the C-
XX terminus of the bile salt-activated lipase (BAL) of sequence AA875098
XX (encoded by AAQ90568) and/or in which the amino acid sequence SMTGS
XX (encoded by AAQ90578) is attached to the N-terminus of the BAL. The
XX recombinant lipases can be produced by fermentation in Pichia
XX pastoris GS 115 transformed host cells.
XX
XX Sequence 538 AA:
SQ
Query Match 1.5%; Score 12; DB 16; Length 538;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 526 YWTFNPAKTGDPN 537
DB 467 YWTFNPAKTGDPN 478
RESULT 40
AAW10058
ID AAW10058 standard; Protein; 538 AA.
XX
XX AAW10058;
XX
XX 28-FEB-1997 (first entry);
XX
XX Human wild-type bile salt-activated lipase.
XX
XX BAL; bile salt-activated lipase; C-terminal repeat; recombinant;
XX high yield; Pichia pastoris GS115; plasmid; transformation; pH12301;
XX fermentation.
XX
XX Homo sapiens.
XX
XX JF09228779-A.
XX
XX 10-SEP-1996.
XX
XX 28-FEB-1995; 95GF-0030889.
XX
XX 28-FEB-1995; 95GP-0039859.
XX
XX (MEIP ) MEIJI MILK PROD CO LTD.
XX
XX WPI; 1996-453:45/45.
XX
XX N-PSDB; AAT47862.
XX
XX High yield expression of recombinant bile salt activated lipase -
XX in plasmid pH12301 transformed Pichia pastoris GS115

```

```

PS Disclosure; Page 6-8; 12pp; Japanese.
XX
XX AAW10058 represents human wild-type mature bile salt-activated lipase
XX (BAL). The invention is directed to the recombinant production of
XX this enzyme at a high yield. This was achieved by the addition of
XX cDNA encoding a repeat region consisting of 16 repeats of an 11
XX amino acid sequence at the 3'-end of cDNA encoding the wild-type
XX protein. Seven possible sequences are given in the specification
XX for the 11 amino acid repeats (see AAW10050-W10057) expressed by
XX the recombinant BAL cDNA (see AAT47861). Recombinant BAL, having
XX the C-terminal repeats (see AAW10058) was expressed in Pichia pastoris
XX that had been transformed by plasmid pH12301 and cultured at 15-30
XX deg.C. at not more than 20% dissolved oxygen. This process resulted
XX in a markedly high yield of BAL enzyme.
XX
XX Sequence 538 AA:
SQ
Query Match 1.5%; Score 12; DB 17; Length 538;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 526 YWTFNPAKTGDPN 537
DB 467 YWTFNPAKTGDPN 478
RESULT 41
AAR58981
ID AAR58981 standard; protein; 546 AA.
XX
XX AAR58981;
XX
XX 25-MAR-2003 (updated)
XX
XX 03-MAY-1995 (first entry)
XX
XX Bile salt-stimulated lipase (variant B).
XX
XX Bile salt-stimulated lipase; BSL; glycoprotein; esterase;
XX acetyl cholinesterase; cystic fibrosis; chronic pancreatitis;
XX fat malabsorption; vitamins; dietary lipids; food supplement.
XX
XX Homo sapiens.
XX
XX WO9420610-A1.
XX
XX 15-SEP-1994.
XX
XX 25-FEB-1994; 94MO-SE06160.
XX
XX 01-MAR-1993; 93SE-0006686.
XX
XX 04-MAR-1993; 93SE-0006722.
XX
XX (ASTR ) ASTRA AB.
XX
XX Blackberg L, Edlund M, Hansson L, Hernell O, Lundberg L,
XX Stromqvist M, Toernell C;
XX
XX WPI; 1994-303:18/37.
XX
XX Bile salt-stimulated lipase variants and coding sequences - used
XX to produce prods. for treatment of a pathological condition
XX related to exocrine pancreatic insufficiency
XX
XX Claim 6; Page 58-60; 102pp; English.
XX
XX Bile salt-stimulated lipase (BSL) is a single chain glycoprotein
XX which is highly glycosylated. The N-terminal half of the protein
XX shows a homology to acetyl cholinesterase and some other esterases.
XX BSL variant polypeptides can be used for the treatment of a
XX pathological condition related to exocrine pancreatic insufficiency
XX such as cystic fibrosis, chronic pancreatitis, fat malabsorption or
XX malabsorption of fat soluble vitamins for improvement of utilisation
XX of dietary lipids, particularly in preterm born infants. They can

```

CC also be used as supplements for infant food formulations. The BSSL
 CC variants have maintained catalytic activity but contain less
 CC glycosylation sites than native BSSL.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 546 AA:

Query Match 1.5%; Score 12; DB 15; Length 546;
 Best Local Similarity 100.0%; Pred. No. 0.0035;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 WWTNFAKTGDPN 537
 |||||
 DB 467 WWTNFAKTGDPN 478

RESULT 42
 AAR58982
 ID AAR58982 standard; protein; 568 AA.

AC AAR58982;
 XX
 DT 25-MAR-2003 (updated)
 DT 03-MAY-1995 (first entry)

DE Bile salt-stimulated lipase (variant C).

XX Bile salt-stimulated lipase; BSSL; glycoprotein; esterase;
 KM acetyl cholinesterase; cystic fibrosis; chronic pancreatitis;
 KW fat malabsorption; vitamins; dietary lipids; food supplement.

XX Homo sapiens.

XX WC9420610-A1.

XX PD 15-SEP-1994.

XX PF 25-FEB-1994; 94WC-SE0016C.

XX PR 01-MAR-1993; 93SE-000066.

XX PR 04-MAR-1993; 93SE-0000722.

XX PA (ASTR) ASTRA AB.

XX Bjaeckberg L, Edlund M, Hansson L, Herrell C, Lundberg J;
 PI Stromqvist M, Tjernell J;

XX WPI; 1994-103018/37.

XX Bile salt-stimulated lipase variants and coding sequences - used
 PT to produce prods. for treatment of a pathological condition
 PT related to exocrine pancreatic insufficiency

XX Claim 6; Page 60-62; 102pp; English.

XX Bile salt-stimulated lipase (BSSL) is a single chain glycoprotein
 CC which is highly glycosylated. The N-terminal half of the protein
 CC shows a homology to acetyl cholinesterase and some other esterases.
 CC BSSL variant polypeptides can be used for the treatment of a
 CC pathological condition related to exocrine pancreatic insufficiency
 CC such as cystic fibrosis, chronic pancreatitis, fat malabsorption or
 CC malabsorption of fat soluble vitamins for improvement of utilization
 CC of dietary lipids, particularly in preterm born infants. They can
 CC also be used as supplements for infant food formulations. The BSSL
 CC variants have maintained catalytic activity but contain less
 CC glycosylation sites than native BSSL.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX

SQ Sequence 568 AA:

Query Match 1.5%; Score 12; DB 15; Length 568;

Best Local Similarity 100.0%; Pred. No. 0.0035;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 WWTNFAKTGDPN 537
 |||||
 DB 467 WWTNFAKTGDPN 478

RESULT 43
 AAR9258
 ID AAR9258 standard; protein; 568 AA.

AC AAR9258;

XX
 DT 05-DEC-1996 (first entry)

DE Human bile salt-stimulated lipase variant BSSL-C.

XX Bile salt-stimulated lipase; BSSL; lipid digestion; fat absorption;
 KW infant feed; Pichia pastoris.

XX Synthetic.

XX GN229065-A.

XX PD 25-SEP-1996.

XX PF 22-MAR-1996; 96GB-C006023.

XX PR 24-MAY-1995; 95SE-C001939.

XX PR 23-MAR-1995; 95IN-C000351.

XX PA (ASTR) ASTRA AB.

XX Das G;

XX WPI; 1996-415084/42.

XX New recombinant DNA coding for bile salt stimulated lipase and
 PT secretory signal sequence - controlled by Pichia pastoris promoter
 PT allows prodn. of correctly processed lipase in P. pastoris, useful
 PT as additive for infant feeds to improve fat absorption

XX Claim 4; Page 32-33; 36pp; English.

XX BSSL-C (AAR9258) is a variant of human bile salt-stimulated lipase
 CC (BSSL). It has deletions at residues 536-568 and 591-711, i.e.
 CC it lacks the 11-amino acid repeats found in the C-terminal region
 CC of the native protein. Expression studies, using C127 host cells and
 CC a bovine papilloma virus expression vector, showed that BSSL-C
 CC can be expressed in an active form. A mutated BSSL gene was used
 CC to produce recombinant, active BSSL-C in transformed Pichia
 CC pastoris cells. BSSL-C can be used in infant feed formulations.

XX Sequence 568 AA:

Query Match 1.5%; Score 12; DB 17; Length 568;
 Best Local Similarity 100.0%; Pred. No. 0.0035;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 WWTNFAKTGDPN 537
 |||||
 DB 467 WWTNFAKTGDPN 478

RESULT 44

XX AAR58983
 ID AAR58983 standard; protein; 568 AA.

AC AAR58983;

XX
 DT 25-MAR-2003 (updated)
 DT 03-MAY-1995 (first entry)

```

XX DE Bile salt-stimulated lipase variant.
XX
XX KW Bile salt-stimulated lipase; BSSL; glycoprotein; esterase;
XX KM acetyl cholinesterase; cystic fibrosis; chronic pancreatitis;
XX KM fat malabsorption; vitamins; dietary lipids; food supplement.
XX
XX OS Homo sapiens.
XX
XX PN WC9420610-A1.
XX
XX PD 15-SEP-1994.
XX
XX PF 25-FEB-1994; 94WO-SE00160.
XX
XX PR 01-MAR-1993; 93SE-0000686.
XX PR 04-MAR-1993; 93SE-0000722.
XX
XX PA (ASTR ) ASTR A B.
XX
XX PI Bjaeckberg L, Edlund M, Hansson L, Hernell O, Lundberg L;
XX PI Stroemqvist M, Toernell J;
XX
XX PS WPI: 1994-303018/37.
XX
XX PT Bile salt-stimulated lipase variants and coding sequences - used
XX PT to produce prods. for treatment of a pathological condition
XX PT related to exocrine pancreatic insufficiency
XX
XX PS Claim 6: Page 68-70; 102pp; English.
XX
XX CC Bile salt-stimulated lipase (BSSL) is a single chain glycoprotein
XX CC which is highly glycosylated. The N-terminal half of the protein
XX CC shows a homology to acetyl cholinesterase and some other esterases.
XX CC BSSL variant polypeptides can be used for the treatment of a
XX CC pathological condition related to exocrine pancreatic insufficiency
XX CC such as cystic fibrosis, chronic pancreatitis, fat malabsorption or
XX CC malabsorption of fat soluble vitamins for improvement of utilisation
XX CC of dietary lipids, particularly in preterm born infants. They can
XX CC also be used as supplements for infant food formulations. The BSSL
XX CC variants have maintained catalytic activity but contain less
XX CC glycosylation sites than native BSSL. This variant lacks amino
XX CC acids 632-708 (inclusive) of the amino acid sequence given in AAR58980.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX CC (Updated on 25-MAR-2003 to correct PI field.)
XX
XX SQ Sequence 668 AA;
XX
XX Query Match 1.5%; Score 12; DB 15; Length 668;
XX Best Local Similarity 100.0%; Pred. No. 0.004;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 526 YWTFNAKTGDPN 537
XX |||||
XX DB 490 YWTFNAKTGDPN 501
XX
XX RESULT 45
XX AAR70145
XX ID AAR70145 standard; Protein; 668 AA.
XX
XX AC AAR70145;
XX
XX XX
XX DT 25-MAR-2003 (updated);
XX DT 03-MAY-1995 (first entry);
XX
XX DE Bile salt-stimulated lipase (variant T).
XX
XX KM Bile salt-stimulated lipase; BSSL; glycoprotein; esterase;
XX KM acetyl cholinesterase; cystic fibrosis; chronic pancreatitis;
XX KM fat malabsorption; vitamins; dietary lipids; food supplement.
XX
XX OS Homo sapiens.

```

```

XX XX WC9420610-A1.
XX
XX PD 15-SEP-1994.
XX
XX PF 25-FEB-1994; 94WO-SE00160.
XX
XX PR 01-MAR-1993; 93SE-0000686.
XX PR 04-MAR-1993; 93SE-0000722.
XX
XX PA (ASTR ) ASTR A B.
XX
XX PI Bjaeckberg L, Edlund M, Hansson L, Hernell O, Lundberg L;
XX PI Stroemqvist M, Toernell J;
XX
XX PS WPI: 1994-303018/37.
XX PS N-PSDB; AAQ71874.
XX
XX PT Bile salt-stimulated lipase variants and coding sequences - used
XX PT to produce prods. for treatment of a pathological condition
XX PT related to exocrine pancreatic insufficiency
XX
XX PS Example 3.1: Page 68-70; 102pp; English.
XX
XX CC Bile salt-stimulated lipase (BSSL) is a single chain glycoprotein
XX CC which is highly glycosylated. The N-terminal half of the protein
XX CC shows a homology to acetyl cholinesterase and some other esterases.
XX CC BSSL variant polypeptides can be used for the treatment of a
XX CC pathological condition related to exocrine pancreatic insufficiency
XX CC such as cystic fibrosis, chronic pancreatitis, fat malabsorption or
XX CC malabsorption of fat soluble vitamins for improvement of utilisation
XX CC of dietary lipids, particularly in preterm born infants. They can
XX CC also be used as supplements for infant food formulations. The BSSL
XX CC variants have maintained catalytic activity but contain less
XX CC glycosylation sites than native BSSL. Variant T has exactly 77
XX CC amino acids or seven repeats less than the full length BSSL
XX CC described in AAR58980.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX CC (Updated on 25-MAR-2003 to correct PI field.)
XX
XX SQ Sequence 668 AA;
XX
XX Query Match 1.5%; Score 12; DB 15; Length 668;
XX Best Local Similarity 100.0%; Pred. No. 0.004;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 526 YWTFNAKTGDPN 537
XX |||||
XX DB 490 YWTFNAKTGDPN 501
XX
XX RESULT 46
XX AAR58984
XX ID AAR58984 standard; protein; 722 AA.
XX
XX AC AAR58984;
XX
XX XX
XX DT 25-MAR-2003 (updated)
XX DT 03-MAY-1995 (first entry);
XX
XX DE Bile salt-stimulated lipase (variant N).
XX
XX KM Bile salt-stimulated lipase; BSSL; glycoprotein; esterase;
XX KM acetyl cholinesterase; cystic fibrosis; chronic pancreatitis;
XX KM fat malabsorption; vitamins; dietary lipids; food supplement.
XX
XX OS Homo sapiens.
XX
XX PN WC9420610-A1.
XX
XX PD 15-SEP-1994.
XX
XX PF 25-FEB-1994; 94WO-SE00160.

```

```

XX 01-MAR-1993; 93SE-0000686.
PR 04-MAR-1993; 93SE-0000722.
XX
XX (ASTR ) ASTRA AB.
XX
XX Blaeckberg L, Edlund M, Hansson L, Harnell O, Lundberg U,
PI Stoenqvist M, Toernell U;
DR WPI; 1994-03018/37.
XX
XX Bile salt-stimulated lipase variants and coding sequences - used
PT to produce prods. for treatment of a pathological condition
XX related to exocrine pancreatic insufficiency
XX
XX Claim 8; Page 62-64; 102pp; English.
XX
XX Bile salt-stimulated lipase (BSSL) is a single chain glycoprotein
CC which is highly glycosylated. The N-terminal half of the protein
CC shows a homology to acetyl cholinesterase and some other esterases.
CC BSSL variant polypeptides can be used for the treatment of a
CC pathological condition related to exocrine pancreatic insufficiency
CC such as cystic fibrosis, chronic pancreatitis, fat malabsorption or
CC malabsorption of fat soluble vitamins for improvement of utilization
CC of dietary lipids, particularly in preterm born infants. They can
CC also be used as supplements for infant food formulations. The BSSL
CC variants have maintained catalytic activity but contain less
CC glycosylation sites than native BSSL.
CC (Updated on 25-MAR-2003 to correct FN field.)
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 722 AA;

Query Match 1.5%; Score 12; DB 15; Length 722;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTFNFAKTGDPN 537
DQ 467 YWTFNFAKTGDPN 478

RESULT 47
AA075107
ID AA075107 standard; Protein; 722 AA.
XX
XX AA075107;
AC
XX
XX 01-FEB-1996 (first entry);
DT
XX
XX Bile salt-activated lipase with 16 C-terminal 11-mer repeats.
DE
XX
XX Bile salt activated lipase; BAL; C-terminal repeat.
KW
XX
XX Mammalia.
OS
XX
XX Key Location/Qualifiers
FH 539..722
FT Region /note="contains 16 copies of imperfect 11mer
FT repeats; the region is made up from a
FT combination of 7 different sequences"
XX
XX JPO7111991-A.
XX
XX 02-MAY-1995.
PD
XX
XX 30-SEP-1993; 93JP-0245079.
PF
XX
XX 30-SEP-1993; 93JP-0245079.
PR
XX
XX (MEIP ) MEIJI MILK PROD CO LTD.
PA
XX
XX WPI; 1995-196318/26.

```

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DR N-PSDB; AA090579.
XX
XX New recombinant bile salt-activated lipase(s), DNA encoding them
PT and vectors - useful for high level expression of the lipase(s) by
FT fermenter-culturing.
XX
XX Disclosure; Page 10-13; 31pp; Japanese.
XX
XX New lipases are ones in which 1-15 repeats of any of the sequences
CC AA075099-R75105 (encoded by AA090570-090576) are attached to the C-
CC terminus of the bile salt-activated lipase (BAL) of sequence AA075098
CC (encoded by AA090569) and/or in which the amino acid sequence SHYGS
CC (encoded by AA090578) is attached to the N-terminus of the BAL. The
CC recombinant lipases can be produced by fermentation in Pichia
CC pastoris GS 115 transformed host cells. The present sequence
CC is a protein with 16 copies of the undecapeptide imperfect
CC repeats at the BAL C-terminus.
XX
SQ Sequence 722 AA;

Query Match 1.5%; Score 12; DB 16; Length 722;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTFNFAKTGDPN 537
DQ 467 YWTFNFAKTGDPN 478

RESULT 48
AA010050
ID AA010050 standard; Protein; 722 AA.
XX
XX AA010050;
AC
XX
XX 28-FEB-1997 (first entry);
DT
XX
XX Human bile salt-activated lipase with C-terminal repeat region.
DE
XX
XX BAL; bile salt-activated lipase; C-terminal repeat; recombinant;
KW high yield; Pichia pastoris GS115; plasmid; transformation; PH1301;
XX fermentation.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 539..714
FT Region /label=repeat region
FT /note="region of 16 repeated 11 amino acid
FT motifs, see also AA010051-57"
XX
XX JPC0228779-A.
XX
XX 10-SEP-1996.
PD
XX
XX 28-FEB-1995; 95JP-0039889.
PF
XX
XX 28-FEB-1995; 95JP-0039889.
PR
XX
XX (MEIP ) MEIJI MILK PROD CO LTD.
PA
XX
XX WPI; 1996-459145/46.
XX
XX N-PSDB; AA047861.
XX
XX High yield expression of recombinant bile salt activated lipase -
PT in plasmid PH1301 transformed Pichia pastoris GS115
XX
XX Disclosure; Page 9-11; 12pp; Japanese.
XX
XX AA010050 is human mature bile salt-activated lipase (BAL), which has a
CC repeat region consisting of 16 repeats of an 11 amino acid sequence
CC attached to its C-terminus. Seven possible sequences are given in the
CC specification for the 11 amino acid repeat sequence. The invention is

```

CC directed to the recombinant production of BAL at a high yield.
 CC Recombinant BAL, having the C-terminal repeats (see AAW10051-M10057) was
 CC expressed in *Pichia pastoris* that had been transformed by plasmid
 CC PH1301 and cultured at 15-30 deg C at not more than 20% dissolved
 CC oxygen. This process resulted in a markedly high yield of BAL enzyme.

XX Sequence 722 AA:

Query Match 1:5% Score 12; DB 17; Length 722;
 Best Local Similarity 100.0%; Pred. No. 0.0043;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTFPAKTGDPN 537
 |||||
 DB 467 YWTFPAKTGDPN 478

RESULT 49
 AAR98926
 ID AAR98926 standard; Protein: 722 AA.

XX AAR98926;

XX 31-OCT-1996 (first entry);

XX Human bile salt-activated lipase.

XX Bile salt-activated lipase; BAL; Cholesterol; transgenic animal;

KW milk; hyperlipoproteinaemia; hypercholesterolaemia; atherosclerosis;

KM pancreatitis; therapy; drug delivery.

XX Homo sapiens.

XX Location/Qualifiers

FT Key 539..722

FT /label=C-tail

FT 539..549

FT /label=Proline-rich_region

FT 550..560

FT /label=Proline-rich_region

FT 561..571

FT /label=Proline-rich_region

FT 572..582

FT /label=Proline-rich_region

FT 583..593

FT /label=Proline-rich_region

FT 594..604

FT /label=Proline-rich_region

FT 605..615

FT /label=Proline-rich_region

FT 616..626

FT /label=Proline-rich_region

FT 627..637

FT /label=Proline-rich_region

FT 638..648

FT /label=Proline-rich_region

FT 649..659

FT /label=Proline-rich_region

FT 660..670

FT /label=Proline-rich_region

FT 671..681

FT /label=Proline-rich_region

FT 682..692

FT /label=Proline-rich_region

FT 693..703

FT /label=Proline-rich_region

FT 704..714

FT /label=Proline-rich_region

XX WO9617054-A1.

XX 06-JUN-1996.

PF 01-DEC-1995; 95MO-US15647.

XX 07-JUN-1995; 95US-0482262.

XX 01-DEC-1994; 94US-0347718.

PR 07-JUN-1995; 95US-0479160.

XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.

XX Tang JUN, Wang C;

PI WPI, 1996-277774/28.

XX Reducing intestinal absorption of cholesterol - by administering a

PT C-tail protein comprising the carboxy region of human bile salt

PR lipase or deriv.

XX Claim 1: Page 79-81; 99pp; English.

XX The human bile salt-activated lipase (BAL) mature protein (AAR98926)

XX includes a carboxy-terminal tail contg. 16 copies of a proline-

XX rich consensus repeat sequence (AAR98928). The C-tail can compete

XX with BAL for binding to receptors on the intestinal surface

XX to inhibit uptake of cholesterol. It can be used to treat

XX hyperlipoproteinaemia and hypercholesterolaemia and associated

XX disease states and as a drug delivery agent. The C-tail can be

XX obtd. by protease digestion of natural BAL, expressed in eukaryotic

XX host cells (see also AAT34787), or secreted in the milk of

XX transgenic animals.

XX Sequence 722 AA;

Query Match 1.5% Score 12; DB 17; Length 722;
 Best Local Similarity 100.0%; Pred. No. 0.0043;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTFPAKTGDPN 537
 |||||
 DB 467 YWTFPAKTGDPN 478

RESULT 50

AB804676

ID AB804676 standard; Protein: 722 AA.

XX AB804676;

XX 06-MAR-2002 (first entry)

XX Human milk bile salt-stimulated lipase (BSL) protein SEQ ID NO:2.

XX Human; milk; bile salt-stimulated lipase; BSL; hypotensive; cardiant;

XX antidiabetic; nephrotropic; acetylcholinesterase inhibitor; food;

XX pharmaceutical; nutritional; hypertension; myocardial infarction;

XX left ventricular systolic dysfunction; diabetes mellitus;

KW progressive renal impairment; renal failure.

XX Homo sapiens.

XX WO200101368-A2.

XX 01-NOV-2001.

XX 19-APR-2001; 2001WO-US12776.

XX 21-APR-2000; 2000US-19968CP.

XX (MONS) MONSANTO TECHNOLOGY LLC.

XX Kobzeff CM;

XX WPI: 2002-066434/09.

XX N-PSDB; AB804403.

PT Producing the hypotensive tripeptide Val Pro Pro for use in
PT pharmaceutical, nutritional and food compositions, comprises first
PT producing recombinant Bile Salt Stimulated Lipase
XX
PS Disclosure, Page 26-29; 29pp; English.
XX
CC The present invention describes a method of producing polypeptides
CC containing VPP (Val Pro Pro). The method comprises: (a) obtaining a
CC recombinant expression vector containing a nucleic acid encoding
CC recombinant bile salt-stimulated lipase (BSSL) polypeptide;
CC (b) inserting the recombinant expression vector into a host cell;
CC (c) growing the host cell to express a protein encoded by the
CC recombinant vector; and (d) purifying the recombinant protein from the
CC host cell. BSSL has hypotensive, cardiant, antidiabetic and
CC nephrotropic activities, and is an acetylcholinesterase inhibitor. The
CC method is used to produce VPP which can be used in pharmaceutical, food
CC and nutritional compositions. The VPP produced by the method can be used
CC in the diagnosis, treatment and prophylaxis of hypertension and related
CC conditions such as left ventricular systolic dysfunction, myocardial
CC infarction, diabetes mellitus and progressive renal impairment/failure.
CC The present sequence represents human milk BSSL. The carboxy-terminal
CC region of human milk BSSL contains 16 proline-rich repeating units of
CC :1 amino acid, and each repeating unit contains the tripeptide VPP
CC Taking the protein particularly advantageous for use in the present
CC invention.
XX
SQ Sequence 722 AA:

Query Match 1.5%; Score 12; DB 23; Length 722;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTFNFAKTGDPN 537
|||
DB 467 YWTFNFAKTGDPN 478

RESULT 51
AA009894
ID AA009894 standard; Protein: 722 AA.
AC
XX AAU09894;
XX
CT 26-FEB-2002 (first entry)
XX
DE Bile Salt Stimulated Lipase (BSSL).
XX
KW Human; BSSL; hypotensive; cardiant; antidiabetic; nephrotropic;
KW bile salt stimulated lipase; antihypertensive tripeptide VPP; food;
KW transgenic animal; milk; pharmaceutical; nutritional; hypertension;
KW myocardial infarction; left ventricular systolic dysfunction;
KW diabetes mellitus; renal failure.
XX
OS Homo sapiens.
XX
PN MO20C181366-A2.
XX
PD 01-NOV-2001.
XX
PF 19-APR-2001; 2001WO-US12672.
XX
PR 21-APR-2000; 2000US-199675P.
XX
PA (MONS) MONSANTO TECHNOLOGY LLC.
XX
PI Kobzaeff JM;
XX
XX MPI: 2002-041393/05.
DR N-PSDB; AAS18538.
XX
PT Producing anti-hypertensive tripeptide, VPP, useful in pharmaceutical,
PT nutritional and food compositions, comprises purifying the polypeptide
PT from bile salt stimulated lipase expressed in the milk of a transgenic

PT nonhuman mammal -
XX
XX Disclosure, Page 22-25; 25pp; English.
PS
CC The invention relates to a method of producing a polypeptide containing
CC antihypertensive tripeptide VPP (Val-Pro-Pro). The method comprises:
CC (a) collecting milk from a transgenic non-human mammal where the animal
CC has been engineered to express and secrete a recombinant Bile Salt
CC Stimulated Lipase (BSSL) polypeptide into their milk; and (b) purifying
CC the polypeptide from the milk. The method is used for production of a
CC polypeptide containing VPP which can be used in pharmaceutical, food and
CC nutritional compositions. The VPP produced can be used in the diagnosis,
CC treatment and prophylaxis of hypertension and related conditions such as
CC left ventricular systolic dysfunction, myocardial infarction, diabetes
CC mellitus and progressive renal impairment/failure. The method allows
CC industrial scale production of polypeptides containing VPP compared to
CC the low amounts present in the prior art fermentation of cow's milk.
CC Bile Salt Stimulated Lipase has a carboxy-terminal region which contains
CC 16 repeats of VPP and accumulates to 1% of the total milk protein. The
CC present sequence represents the amino acid sequence of bile salt
CC stimulated lipase.
XX
SQ Sequence 722 AA:

Query Match 1.5%; Score 12; DB 23; Length 722;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTFNFAKTGDPN 537
|||
DB 467 YWTFNFAKTGDPN 478

RESULT 52
ABP41901
ID ABP41901 standard; Protein: 735 AA.
AC
XX ABP41901;
XX
CT 22-AUG-2002 (first entry)
XX
DE Human ovarian antigen HTPFW87, SEQ ID NO:3033.
XX
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumor;
KW ovarian cancer; breast cancer; tumor; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive.
XX
OS Homo sapiens.
XX
PN MO20C200677-A1.
XX
PD 03-JAN-2002.
XX
PF 07-JUN-2001; 2001WO-US18569.
XX
PR 07-JUN-2000; 2000US-209467P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
XX MPI: 2002-147878/19.
DR N-PSDB; AB054978.
XX
PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT useful in the prevention, treatment and diagnosis of cancer (e.g.

```

FT ovarian cancer), immune disorders, cardiovascular disorders and
FT neurological diseases -
PS Claim 11; SEQ ID NO 3033; 2022bp; English.
XX
CC The invention relates to 2:75 novel human ovarian antigens (ABP4-034-
CC ABP4328) and to CDKs encoding them (ABQ5431-ABQ5435), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovarian and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumors of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dyspareunia), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxo
CC shock syndrome), inflammatory conditions (e.g., mastitis, gonorrhea and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, and the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 735 AA;

```

Query Match 1.5%; Score 12; DB 23; Length 735;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 526 YWTFNPAKTGDPN 537
DB 493 YWTFNPAKTGDPN 502

RESULT 53
AAR14311
ID AAR14311 standard; Protein; 742 AA.
XX
AC AAR14311;
XX
DT 13-JAN-1992 (first entry)
XX
DE Human milk bile-salt activated lipase.
XX
KM premature baby; fat absorption; baby food.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 559..734
FT /label=repeat_region
FT /note="16 repeats of similar 11 amino acid motif"
FT Peptide 1..20
FT /label=signal_peptide
FT Modified-site 207
FT /label=N-linked_glycosylation_site
FT /note="potential"
FT Active-site 214
FT /label=active_site_serine
FN W09115234-A.

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XX
PD 17-OCT-1991.
XX
EF 04-APR-1991; 91WO-US02328.
XX
XX 12-JUN-1990; 90US-0537426.
PR 04-APR-1990; 90US-0504635.
XX
PA (OKLA-) OKLAHOMA MED RES FO.
XX
FI Tang JLN, Wang CS;
XX
DR WPI; 1991-324964/44.
DR N-PSDB; AAQ14186.
XX
PT New recombinant Bile salt activated lipase(s) - used in improving
PT infant nutrition, to treat diseases concerned with lipid
PT digestion and as probes for studying BSL or related lipase(s);
XX
XX Claim 15; Fig 2; 36pp; English.
XX
XX This sequence is deduced from a combination of two cDNA clones
XX (G10-2 and G10-3) isolated from a lactating human breast tissue
XX cDNA library. Screening was with probes based on the 61-residue
XX amino acid sequence of the N-terminal cleavage fragment of BSL.
XX The C-terminal region consists of 16 similar 11 amino acid repeats;
XX about a third of the residues in this region are proline. Human BSL
XX is a glycoprotein and a potential N-glycosylation site has been
XX identified.
XX
SQ Sequence 742 AA;

```

Query Match 1.5%; Score 12; DB 12; Length 742;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 526 YWTFNPAKTGDPN 537
DB 487 YWTFNPAKTGDPN 498

RESULT 54
AAR98927
ID AAR98927 standard; Protein; 742 AA.
XX
AC AAR98927;
XX
DT 31-OCT-1996 (first entry)
XX
DE Human bile salt-activated lipase precursor.
XX
KM Bile salt-activated lipase; BSL; cholesterol; transgenic animal;
KM milk; hyperlipoproteinaemia; hypercholesterolaemia; atherosclerosis;
KM pancreatitis; therapy; drug delivery.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..26
FT /label=Sig_peptide
FT Modified-site 187
FT /label=N-glycosylation_site
FT Modified-site 194
FT /label=N-glycosylation_site
FT Region 559..742
FT /label=C-tail
FT Region 559..569
FT /label=proline-rich_region
FT Region 570..580
FT /label=proline-rich_region
FT Region 581..591
FT /label=proline-rich_region
FT Region 592..602

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FT /label= Proline-rich_region
 FT 603..623
 FT /label= Proline-rich_region
 FT 614..624
 FT /label= Proline-rich_region
 FT 625..635
 FT /label= Proline-rich_region
 FT 636..646
 FT /label= Proline-rich_region
 FT 647..657
 FT /label= Proline-rich_region
 FT 658..668
 FT /label= Proline-rich_region
 FT 669..679
 FT /label= Proline-rich_region
 FT 680..690
 FT /label= Proline-rich_region
 FT 691..701
 FT /label= Proline-rich_region
 FT 702..712
 FT /label= Proline-rich_region
 FT 713..723
 FT /label= Proline-rich_region
 FT 724..734
 FT /label= Proline-rich_region

PN W09617054-A1.
 PD 06-JUN-1996.
 PF 01-DEC-1995; 95MO-US15647.
 PR 07-JUN-1995; 95US-0482262.
 PR 01-DEC-1994; 94US-034718.
 PR 07-JUN-1995; 95US-0479152.
 PA (OXIA-) CHIAHOYA MEDICAL RES FOUND.
 XX
 XX Tang JCN, Wang C;
 XX WPI; 1996-277774/28.
 DR N-PCDB; AAT34787.
 XX

PT Reducing intestinal absorption of cholesterol - by administering a
 PT C-tail protein comprising the carboxy region of human bile salt
 PT lipase or deriv.

PS Disclosure; Page 82-84; 99pp; English.

XX The human bile salt-activated lipase (BAL) precursor (AAR98927)
 CC includes a carboxy-terminal tail consisting of a proline-
 CC rich consensus repeat sequence (AAR98928). The C-tail can complete
 CC with BAL for binding to receptors on the intestinal surface
 CC to inhibit uptake of cholesterol. It can be used to treat
 CC hyperlipoproteinemia and hypercholesterolaemia and associated
 CC disease states and as a drug delivery agent. BAL or its C-tail
 CC can be obtained by protease digestion of natural BAL expressed in
 CC eukaryotic host cells (see also AAT34787), or secreted in the milk
 CC of transgenic animals.

CC Sequence 742 AA;

Query Match 1.5%; Score 12; DB 17; Length 742;
 Best Local Similarity 100.0%; Pred. No. 0.0044;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTFNAKTGDPN 537
 DB 487 YWTFNAKTGDPN 488

RESULT 55
 AAR45189.

ID AAR45189 standard; Protein; 744 AA.
 XX
 AC AAR45189;
 XX
 DT 25-MAR-2003 (updated)
 DT 27-JUN-1994 (first entry)
 DE BSSL/CEL.
 XX
 KM BSSL: biologically functional bile salt stimulated lipase; CE;
 KM carboxyl ester lipase; hybridisation; milk protein; transgenic;
 KM infant milk substitute; oral; specific; lipolysis; vitamin; bile;
 KM lipid malabsorption; cystic fibrosis; chronic pancreatitis;
 KM digestion.
 XX
 CS Homo sapiens.
 XX
 PN W09325669-A1.
 XX
 PD 23-DEC-1993.
 XX
 PF 03-JUN-1993; 93MO-SE00515.
 XX
 PR 11-JUN-1992; 92SE-0001809.
 PR 12-JUN-1992; 92SE-0001826.
 PR 03-JUL-1992; 92SE-0002088.
 PR 19-MAR-1993; 93SE-0000902.
 XX
 PA (ASTR) ASTRA AB.
 XX
 PE Bjurell KG, Carlsson PN, Enerback CSM, Hansson SU,
 PE Laddberg JFF, Nilsson CA, Tornell UBF, Toerne-L UBF;
 PE Enerback CSM;
 XX
 DR WPI; 1994-007327/31.
 DR N-PCDB; AAO54222.
 XX
 XX
 PT DNA encoding bile salt-stimulated lipase/carboxyl ester lipase -
 PT expressed by transgenic non-human mammals and used as human milk
 PT substitute, contains intron sequences
 XX
 PS Claim 1; Page 43-51; 76pp; English.

XX The primers (AAQ54223-28) are used to amplify fragments of the
 CC BSSL / CEU gene, (AAQ54222). Which encodes a bile salt-stimulated
 CC lipase / carboxyl ester lipase which when expressed by transgenic
 CC animals can be used as a human milk substitute. The BSSL is designed
 CC to pass through the stomach and is activated in the small intestine.
 CC As it has a broad substrate specificity it can mediate the complete
 CC digestion of most dietary lipids.
 CC (updated on 25-MAR-2003 to correct PN field.)
 CC

CC Sequence 744 AA;

Query Match 1.5%; Score 12; DB 15; Length 744;
 Best Local Similarity 100.0%; Pred. No. 0.0044;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTFNAKTGDPN 537
 DB 489 YWTFNAKTGDPN 500

RESULT 56
 AAR20098
 ID AAR20098 standard; Protein; 745 AA.
 XX
 AC AAR20098;
 XX
 DT 24-MAR-1992 (first entry)
 XX
 DE Bile-salt stimulated lipase.

XX

```

KW BSSL; fat malabsorption.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /note= "signal peptide"
FT 24..745
FT Peptide /note= "mature peptide"
XX
PK WC9113923-A.
XX
PD -2-DEC-1991.
XX
PF 30-MAY-1991; 9:WO-SE0381.
XX
PR 01-JUN-1990; 90SE-0301955.
XX
PA (ASTR) ASTRA AB.
XX
PI Bjurset G, Blackberg L, Carlsson P, Enerback S, Hernell O,
PI Nilsson U, Olivecrona T;
XX
DR WPI, 1992-07429/01.
DR N-PSDB; AAQ20252.
XX
PT New human bile-salt stimulated lipase derivs. - useful to treat
PT pathological conditions related to chronic pancreatitis, cystic
PT fibrosis, etc.
XX
PS Claim 1; Fig 2; 54pp; English.
XX
CC The amino acid sequence is that of bile-salt stimulated lipase
CC (BSSL) which may be produced in large amounts through the use of
CC recombinant techniques. BSSL is used in pharmaceutical compns.
CC useful for the treatment of a condition related to exocrine
CC pancreatic insufficiency, cystic fibrosis, chronic pancreatitis,
CC fat malabsorption of any etiology, malabsorption of fat soluble
CC vitamins, fat malabsorption due to physiological reasons, e.g. in
CC new-born infants, etc. BSSL is suitable for oral admin.
XX
SQ Sequence 745 AA;
XX
Query Match 1.5%; Score 12; DB 13; Length 745;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 526 YWTFNPAKTGDPN 537
DB 490 YWTFNPAKTGDPN 501
XX
RESULT 57
AAR58980
ID AAR58980 standard; protein; 745 AA.
XX
AC AAR58980;
XX
DT 25-MAR-2003 (updated;
DT 03-MAY-1995 (first entry)
XX
DE Bile salt-stimulated lipase.
XX
KW Bile salt-stimulated lipase; BSSL; glycoprotein; esterase;
KW acetylcholinesterase; cystic fibrosis; chronic pancreatitis;
KW fat malabsorption; vitamins; dietary lipids; food supplement.
XX
OS Homo sapiens.
XX
PN WO9420610-A1.
XX
PD 15-SEP-1994.
XX

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PF 25-FEB-1994; 94WO-SE00160.
XX
PR 01-MAR-1993; 93SE-CC00686.
PR 04-MAR-1993; 93SE-0000722.
XX
PA (ASTR) ASTRA AB.
XX
PI Blackberg L, Edlund M, Hansson L, Hernell O, Lundberg L;
PI Stromqvist M, Toernell J;
XX
DR WPI, 1994-003018/37.
DR N-PSDB; AAQ83221.
XX
PT Bile salt-stimulated lipase variants and coding sequences - used
PT to produce prods. for treatment of a pathological condition
PT related to exocrine pancreatic insufficiency
XX
PS Disclosure; Page 52-54; 102pp; English.
XX
CC Bile salt-stimulated lipase (BSSL) is a single chain glycoprotein
CC which is highly glycosylated. The N-terminal half of the protein
CC shows a homology to acetyl cholinesterase and some other esterases.
CC BSSL variant polypeptides can be used for the treatment of a
CC pathological condition related to exocrine pancreatic insufficiency
CC such as cystic fibrosis, chronic pancreatitis, fat malabsorption or
CC malabsorption of fat soluble vitamins for improvement of utilisation
CC of dietary lipids, particularly in preterm born infants. They can
CC also be used as supplements for infant food formulations.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 745 AA;
XX
Query Match 1.5%; Score 12; DB 15; Length 745;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 526 YWTFNPAKTGDPN 537
DB 490 YWTFNPAKTGDPN 501
XX
RESULT 58
AAR99257
ID AAR99257 standard; Protein; 745 AA.
XX
AC AAR99257;
XX
DT 05-DEC-1996 (first entry)
XX
DE Human bile salt-stimulated lipase.
XX
KW Bile salt-stimulated lipase; BSSL; lipid digestion; fat absorption;
KW infant feed; Pichia pastoris.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= Sig_peptide
FT 24..745
FT Protein /label= Mat protein
FT /note= "Claim 5"
XX
FT Region 536..546
FT /label= Repeat_unit
FT Region 547..557
FT /label= Repeat_unit
FT Region 558..568
FT /label= Repeat_unit
FT Region 569..579
FT /label= Repeat_unit
FT Region 580..590
FT /label= Repeat_unit
XX

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FT      Region      591..601      /label= Repeat_unit
FT      Region      602..612      /label= Repeat_unit
FT      Region      613..623      /label= Repeat_unit
FT      Region      624..634      /label= Repeat_unit
FT      Region      635..645      /label= Repeat_unit
FT      Region      646..656      /label= Repeat_unit
FT      Region      657..667      /label= Repeat_unit
FT      Region      668..678      /label= Repeat_unit
FT      Region      679..689      /label= Repeat_unit
FT      Region      690..700      /label= Repeat_unit
FT      Region      701..711      /label= Repeat_unit
FT      Region      /label= Repeat_unit

XX      GB2293085-A.
XX
XX      25-SEP-1996.
XX
XX      22-MAR-1996; 96GB-0006023.
XX
XX      24-MAY-1995; 95SE-0001933.
XX      21-MAR-1995; 95IN-0003351.
XX
XX      (ASTR 1 ASTRA AB.
XX
XX      Das G.
XX
XX      WPI: 1996-415384/42.
XX      N-PSDB; AA135253.
XX
XX      New recombinant DNA coding for bile salt stimulated lipase and
XX      secretory signal sequence - controlled by pLacIa pastoris promoter
XX      allows produ. of correctly processed lipase in P. pastoris, useful
XX      as additive for infant foods to improve fat absorption
XX
XX      Claim 2; Page 27-29; 38pg; English.
XX
XX      Human bile salt-stimulated lipase (BSSL; EC-3.1.1.1) plays a
XX      critical role in the digestion of milk lipids in breast-fed infants
XX      and is believed to be the major rate-limiting factor in fat
XX      absorption, partic. in premature infants. Recombinant BSSL
XX      can be produced cost-effectively, in properly processed form,
XX      in Pichia pastoris host cells utilising vectors that incorporate
XX      a BSSL nucleic acid (see also AA135250), an appropriate signal
XX      sequence and pref. the P. pastoris methano. oxidase promoter.
XX      The BSSL is useful in infant feed formulations.
XX
XX      Sequence      745 AA:
XX
XX      Query Match      1.5%; Score 12; DB 17; Length 745;
XX      Best Local Similarity 100.0%; Pred. No. 0.0044;
XX      Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      526 YWTFNAKTGDPN 537
XX      |||:|||||
XX      490 YWTFNAKTGDPN 501
XX
XX      RESULT 59
XX      ID      AA032168
XX      AC      AAY32168 standard; Protein: 745 AA.
XX      AC      AAY32168;

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DT      01-FEB-2000 (first entry)
DE
XX      Human bile salt-stimulated lipase.
XX
XX      Bile salt-stimulated lipase; BSSL; human; transgenic sheep;
KW      transgenic mammal; milk; pancreatic insufficiency; lipid;
XX      preterm infant; nutrition; cystic fibrosis.
XX
XX      Homo sapiens.
OS
XX
XX      Key
XX      Location/Qualifiers
XX      Peptide
XX      1..23
XX      /note="signal peptide"
XX      FT
XX      24..745
XX      Protein
XX      /note="mature protein, specifically claimed in
XX      Claim 10"
XX      FT
XX      Claim 10"
XX      MO9954443-A1.
XX      PN
XX      28-OCT-1999.
XX      FD
XX      21-APR-1993; 99MO-SE00648.
XX      PF
XX      22-APR-1998; 98SE-0001424.
XX      PR
XX      (ASTR ) ASTRAB.
XX      PA
XX      (PLLT-) PPLTHERAPEUTICS.
XX
XX      Dairyville W. Lundberg L, Stromqvist M;
XX      WPI; 1999-634002/54.
XX      DR
XX      N-PSDB; AA220299, AA220300.
XX
XX      New recombinant human bile salt-stimulated lipase produced by
XX      transgenic mammals, used for treating diseases related to exocrine
XX      pancreatic insufficiency and improving utilization of dietary lipids in
XX      preterm born infants.
XX      FT
XX      preterm born infants.
XX      PS
XX      Claim 9; Page 56-58; 67pg; English.
XX
XX      The present sequence represents human bile salt-stimulated lipase
XX      (BSSL). The invention relates to human recombinant BSSL obtainable
XX      from transgenic sheep. The invention also relates to transgenic
XX      sheep whose germ cells and somatic cells contain a recombinant
XX      nucleotide molecule encoding BSSL. The nucleotide sequence can be
XX      introduced as a BSSL genomic sequence including introns (see
XX      AA220299, or as cDNA (see AA220300)). Methods are provided for
XX      producing the transgenic animals, and methods for producing human
XX      BSSL derived from the transgenic animals. The recombinant BSSL,
XX      produced in the sheep's milk, is glycosylated and fully active.
XX      The BSSL is used in the treatment of diseases relating to exocrine
XX      pancreatic insufficiency, e.g. as a consequence of cystic fibrosis
XX      (claimed), and for improvement of the utilization of dietary lipids
XX      in preterm born infants (claimed).
XX
XX      Sequence 745 AA:
XX
XX      Query Match 1.5%; Score 12; DB 20; Length 745;
XX      Best Local Similarity 100.0%; Pired. No. 0.0044;
XX      Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      526. YWTFPAKTGDPN 537
XX      |||||||
XX      490 YWTFPAKTGDPN 501
XX
RESULT 60
ID AAB08201 standard; Protein; 745 AA.
AC AAB08201.
XX
XX 04-DEC-2000 (first entry)

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```

XX      A human pancreatic cholesterol esterase polypeptide.
XX      Human; pancreatic cholesterol esterase gene; cholesterol metabolism;
XX      restriction fragment length polymorphism; RFLP.
XX      Homo sapiens.
XX      US6107025-A.
XX      FN
XX      22-AUG-2000.
XX      PD
XX      09-JAN-1995.    JACS-0370223.
XX      PF
XX      15-JUL-1991.    9JUS-0730204.
XX      PR      26-APR-1993.    9JUS-C0533C8.
XX      XX
XX      (KUMA/) KUMAR B V.
XX      PA      (LANG/) LANG T G.
XX      PI      Kumar BV, Lange LG:
XX      DR      WPI: 2000-566209/55.
XX      DR      N-PSTB; AA63883.
XX      XX
XX      PT      Use of restriction fragment length polymorphism in gene encoding
XX      PT      pancreatic cholesterol esterases in human for detecting patterns of
XX      PT      particular polymorphism to identify particular genetic variants for
XX      PS      treatment -
XX      XX
XX      Disclosure; Fig 2A-G; 34pp; English.
XX      XX
XX      The present sequence represents a human pancreatic cholesterol esterase
XX      CC      protein. The specification describes methods for detecting restriction
XX      CC      fragment length polymorphisms (RFLPs) in the human pancreatic
XX      CC      cholesterol esterase gene. The method comprises isolating DNA,
XX      CC      digesting the DNA with a restriction enzyme, separating the digested
XX      CC      fragments, transferring onto a membrane, hybridizing fragments with a
XX      CC      detectably-labeled nucleic acid probe complementary to a portion of
XX      CC      the gene and detecting pattern of hybridized fragments. The method is
XX      CC      used for RFLP analysis to identify individuals with a particular genetic
XX      CC      variant of the human pancreatic cholesterol esterase gene. This
XX      CC      provides for the prevention or alleviation of disease states related
XX      CC      to cholesterol metabolism.
XX      SC
XX      Sequence       745 AA:
XX
XX      Query Match          1.5%; Score 32; DB 21; Length 745;
XX      Best Local Similarity 100.0%, Pred.No. 0.0044;
XX      Matches 12; Conservative 0; Mismatches 0; Indels 3; Gaps 0.
XX
XX      526 YWTFNFAKTGDPN 537
XX      |.....|
XX      430 YWTFNFAKTSDPN 501
XX
XX      RESCU... 61
XX      AAM57866
XX      ID      AAM57866 standard; Protein: 530 AA.
XX      AC      AAM57866;
XX      XX
XX      DT      23-SEP-1992 ('first entry')
XX      DE      C. fe'is esterase, nFEIc1987.
XX      XX
XX      KW      Esterase; flea; protective immune response; carboxylesterase; arthropod;
XX      KW      haemaphysagous ectoparasite infestation; nFEI01987.
XX      OS      Ctenocephalides felis.
XX      XX
XX      MN      WO9821324-A1.
XX      XX

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P3 22-MAY-1998.
 XX PF 10-NOV-1997; 97WQ-US20598.
 XX PR 12-NOV-1996; 96US-0747221.
 XX XX (HESK-) HESKA CORP.
 P2 Brandt KS, Silver GM, Wisniewski N;
 P1 WPI; 1998-297929/26.
 DR N-PSDB: AAU40762.
 XX
 FT New nucleic acid encoding carboxylesterase(s) from fleas - useful,
 PT e.g. in vaccines, for preventing infestation by haematophagous
 XX ectoparasites, particularly on cats and dogs
 PS Claim 2; Page 193-197; 230pp; English.
 XX
 CC This sequence is the flea esterase protein, nFE101947, of the invention.
 CC When administered to animals, the protein induces a protective immune
 CC (antibody) response against carboxylesterase (CE), so they, or
 CC compositions containing CE proteins, are used, therapeutically or as
 CC vaccines, to protect particularly mammals and birds, specifically cats
 CC and dogs, against haematophagous ectoparasite infestation (HEI),
 CC specifically fleas. More generally the compositions can be used to treat
 CC arthropods generally, including pests of agricultural crops, trees,
 CC scored goods etc., also those that are vectors of disease. Fragments of
 CC the DNA can be used as probes and primers for identification or
 CC production of nucleic acid. Antibodies against the protein can be used
 CC for passive immunisation; to screen expression libraries; to isolate the
 CC protein and to target cytotoxic compounds to HEI. The compounds
 CC containing CE are effective against both adult and larval stages. They
 CC target CEs, including juvenile hormone, that are involved in development,
 CC metamorphosis, feeding, digestion and reproduction.
 XX
 S0 Sequence 530 AA;
 XX
 QY 125 EDCLYDNLYVP 135
 XX |||||
 DB 81 EDCLYDNLYVP 91
 XX
 P3 RESULT 62
 XX AAW57867
 XX AC AAW57867; standard; Protein; 530 AA.
 XX DT 23-SEP-1998 (first entry)
 XX CE C. felis esterase, nFE101590.
 XX K4 Esterase; flea, protective immune response; carboxylesterase; arthropod;
 XX K4 haematophagous ectoparasite infestation; nFE101590.
 XX OS Ctenocephalides felis.
 XX PV WO3821324-A1.
 XX PD 22-MAY-1998.
 XX PF 10-NOV-1997; 97WQ-US20598.
 XX PR 12-NOV-1996; 96US-0747221.
 XX XX (HESK-) HESKA CORP.
 P2 Brandt KS, Silver GM, Wisniewski N;
 P1 WPI; 1998-297929/26.
 DR N-PSDB: AAU40762.
 XX
 FT New nucleic acid encoding carboxylesterase(s) from fleas - useful,
 PT e.g. in vaccines, for preventing infestation by haematophagous
 XX ectoparasites, particularly on cats and dogs
 PS Claim 2; Page 193-197; 230pp; English.
 XX
 CC This sequence is the flea esterase protein, nFE101947, of the invention.
 CC When administered to animals, the protein induces a protective immune
 CC (antibody) response against carboxylesterase (CE), so they, or
 CC compositions containing CE proteins, are used, therapeutically or as
 CC vaccines, to protect particularly mammals and birds, specifically cats
 CC and dogs, against haematophagous ectoparasite infestation (HEI),
 CC specifically fleas. More generally the compositions can be used to treat
 CC arthropods generally, including pests of agricultural crops, trees,
 CC scored goods etc., also those that are vectors of disease. Fragments of
 CC the DNA can be used as probes and primers for identification or
 CC production of nucleic acid. Antibodies against the protein can be used
 CC for passive immunisation; to screen expression libraries; to isolate the
 CC protein and to target cytotoxic compounds to HEI. The compounds
 CC containing CE are effective against both adult and larval stages. They
 CC target CEs, including juvenile hormone, that are involved in development,
 CC metamorphosis, feeding, digestion and reproduction.
 XX
 S0 Sequence 530 AA;
 XX
 QY 125 EDCLYDNLYVP 135
 XX |||||
 DB 81 EDCLYDNLYVP 91
 XX
 P3 RESULT 62
 XX AAW57867
 XX AC AAW57867; standard; Protein; 530 AA.
 XX DT 23-SEP-1998 (first entry)
 XX CE C. felis esterase, nFE101590.
 XX K4 Esterase; flea, protective immune response; carboxylesterase; arthropod;
 XX K4 haematophagous ectoparasite infestation; nFE101590.
 XX OS Ctenocephalides felis.
 XX PV WO3821324-A1.
 XX PD 22-MAY-1998.
 XX PF 10-NOV-1997; 97WQ-US20598.
 XX PR 12-NOV-1996; 96US-0747221.
 XX XX (HESK-) HESKA CORP.
 P2 Brandt KS, Silver GM, Wisniewski N;
 P1 WPI; 1998-297929/26.
 DR N-PSDB: AAU40762.
 XX
 FT New nucleic acid encoding carboxylesterase(s) from fleas - useful,
 PT e.g. in vaccines, for preventing infestation by haematophagous
 XX ectoparasites, particularly on cats and dogs
 PS Claim 2; Page 193-197; 230pp; English.
 XX
 CC This sequence is the flea esterase protein, nFE101947, of the invention.
 CC When administered to animals, the protein induces a protective immune
 CC (antibody) response against carboxylesterase (CE), so they, or
 CC compositions containing CE proteins, are used, therapeutically or as
 CC vaccines, to protect particularly mammals and birds, specifically cats
 CC and dogs, against haematophagous ectoparasite infestation (HEI),
 CC specifically fleas. More generally the compositions can be used to treat
 CC arthropods generally, including pests of agricultural crops, trees,
 CC scored goods etc., also those that are vectors of disease. Fragments of
 CC the DNA can be used as probes and primers for identification or
 CC production of nucleic acid. Antibodies against the protein can be used
 CC for passive immunisation; to screen expression libraries; to isolate the
 CC protein and to target cytotoxic compounds to HEI. The compounds
 CC containing CE are effective against both adult and larval stages. They
 CC target CEs, including juvenile hormone, that are involved in development,
 CC metamorphosis, feeding, digestion and reproduction.
 XX
 S0 Sequence 530 AA;
 XX
 QY 125 EDCLYDNLYVP 135
 XX |||||
 DB 81 EDCLYDNLYVP 91
 XX
 P3 RESULT 62
 XX AAW57867
 XX AC AAW57867; standard; Protein; 530 AA.
 XX DT 23-SEP-1998 (first entry)
 XX CE C. felis esterase, nFE101590.
 XX K4 Esterase; flea, protective immune response; carboxylesterase; arthropod;
 XX K4 haematophagous ectoparasite infestation; nFE101590.
 XX OS Ctenocephalides felis.
 XX PV WO3821324-A1.
 XX PD 22-MAY-1998.
 XX PF 10-NOV-1997; 97WQ-US20598.
 XX PR 12-NOV-1996; 96US-0747221.
 XX XX (HESK-) HESKA CORP.
 P2 Brandt KS, Silver GM, Wisniewski N;
 P1 WPI; 1998-297929/26.
 DR N-PSDB: AAU40762.
 XX
 FT New nucleic acid encoding carboxylesterase(s) from fleas - useful,
 PT e.g. in vaccines, for preventing infestation by haematophagous
 XX ectoparasites, particularly on cats and dogs
 PS Claim 2; Page 193-197; 230pp; English.
 XX
 CC This sequence is the flea esterase protein, nFE101947, of the invention.
 CC When administered to animals, the protein induces a protective immune
 CC (antibody) response against carboxylesterase (CE), so they, or
 CC compositions containing CE proteins, are used, therapeutically or as
 CC vaccines, to protect particularly mammals and birds, specifically cats
 CC and dogs, against haematophagous ectoparasite infestation (HEI),
 CC specifically fleas. More generally the compositions can be used to treat
 CC arthropods generally, including pests of agricultural crops, trees,
 CC scored goods etc., also those that are vectors of disease. Fragments of
 CC the DNA can be used as probes and primers for identification or
 CC production of nucleic acid. Antibodies against the protein can be used
 CC for passive immunisation; to screen expression libraries; to isolate the
 CC protein and to target cytotoxic compounds to HEI. The compounds
 CC containing CE are effective against both adult and larval stages. They
 CC target CEs, including juvenile hormone, that are involved in development,
 CC metamorphosis, feeding, digestion and reproduction.
 XX
 S0 Sequence 530 AA;
 XX
 QY 125 EDCLYDNLYVP 135
 XX |||||
 DB 81 EDCLYDNLYVP 91
 XX
 P3 RESULT 62
 XX AAW57867
 XX AC AAW57867; standard; Protein; 530 AA.
 XX DT 23-SEP-1998 (first entry)
 XX CE C. felis esterase, nFE101590.
 XX K4 Esterase; flea, protective immune response; carboxylesterase; arthropod;
 XX K4 haematophagous ectoparasite infestation; nFE101590.
 XX OS Ctenocephalides felis.
 XX PV WO3821324-A1.
 XX PD 22-MAY-1998.
 XX PF 10-NOV-1997; 97WQ-US20598.
 XX PR 12-NOV-1996; 96US-0747221.
 XX XX (HESK-) HESKA CORP.
 P2 Brandt KS, Silver GM, Wisniewski N;
 P1 WPI; 1998-297929/26.
 DR N-PSDB: AAU40762.
 XX
 FT New nucleic acid encoding carboxylesterase(s) from fleas - useful,
 PT e.g. in vaccines, for preventing infestation by haematophagous
 XX ectoparasites, particularly on cats and dogs
 PS Claim 2; Page 193-197; 230pp; English.
 XX
 CC This sequence is the flea esterase protein, nFE101947, of the invention.
 CC When administered to animals, the protein induces a protective immune
 CC (antibody) response against carboxylesterase (CE), so they, or
 CC compositions containing CE proteins, are used, therapeutically or as
 CC vaccines, to protect particularly mammals and birds, specifically cats
 CC and dogs, against haematophagous ectoparasite infestation (HEI),
 CC specifically fleas. More generally the compositions can be used to treat
 CC arthropods generally, including pests of agricultural crops, trees,
 CC scored goods etc., also those that are vectors of disease. Fragments of
 CC the DNA can be used as probes and primers for identification or
 CC production of nucleic acid. Antibodies against the protein can be used
 CC for passive immunisation; to screen expression libraries; to isolate the
 CC protein and to target cytotoxic compounds to HEI. The compounds
 CC containing CE are effective against both adult and larval stages. They
 CC target CEs, including juvenile hormone, that are involved in development,
 CC metamorphosis, feeding, digestion and reproduction.
 XX
 S0 Sequence 530 AA;
 XX
 QY 125 EDCLYDNLYVP 135
 XX |||||
 DB 81 EDCLYDNLYVP 91
 XX
 P3 RESULT 62
 XX AAW57867
 XX AC AAW57867; standard; Protein; 530 AA.
 XX DT 23-SEP-1998 (first entry)
 XX CE C. felis esterase, nFE101590.
 XX K4 Esterase; flea, protective immune response; carboxylesterase; arthropod;
 XX K4 haematophagous ectoparasite infestation; nFE101590.
 XX OS Ctenocephalides felis.
 XX PV WO3821324-A1.
 XX PD 22-MAY-1998.
 XX PF 10-NOV-1997; 97WQ-US20598.
 XX PR 12

XX WPI: 1998-297929/26.
 DR N-PSDB; AAV40764.
 XX
 PT New nucleic acid encoding carboxylesterase(s) from fleas - useful,
 PT e.g. in vaccines, for preventing infestation by haematophagous
 PT ectoparasites, particularly on cats and dogs
 XX
 PS Claim 1: Page 200-203; 230pp; English.

CC This sequence is the flea esterase protein, nfe:01590, of the invention.
 CC When administered to animals, the protein induces a protective immune
 CC (antibody) response against carboxylesterase (CE), so they, or
 CC compositions containing CE proteins, are used, therapeutically or as
 CC vaccines, to protect particularly mammals and birds, specifically cats
 CC and dogs, against haematophagous ectoparasite infestation (HPI).
 CC Specifically fleas. More generally the compositions can be used to treat
 CC arthropods generally, including pests of agricultural crops, trees,
 CC stored goods etc., also those that are vectors of disease. Fragments of
 CC the DNA can be used as probes and primers for identification or
 CC production of nucleic acid. Antibodies against the protein can be used
 CC for passive immunisation, to screen expression libraries, to isolate the
 CC protein and to target cytotoxic compounds to HEP. The compounds
 CC containing CE are effective against both adult and larval stages; they
 CC target CEs, including juvenile hormone, that are involved in development,
 CC metamorphosis, feeding, digestion and reproduction.

SC Sequence 530 AA;

Query Match 1.3%; Score 11; DB 29; Length 530;
 Best Local Similarity 100.0%; Pred. No. 0.036;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNIVP 135
 |||||
 DB 81 EDCLYLNIVP 91

RESULT 63
 ID ABB68593 standard; Protein: 1016 AA.
 XX
 AC ABB68593;
 XX
 DT 26-MAR-2002 (first entry);
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 32571.
 XX
 KM Drosophila developmental biology; cell signalling; insecticide;
 KM pharmaceutical.
 XX
 CS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PE 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2003; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEXE) FE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 CR WPI, 2001-656860/75.
 DR N-PSDB; ABL12696.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -

PS Disclosure; SEQ ID NO 32571; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL10511), expressed DNA
 CC sequences (ABL10840-ABL16175) and the encoded proteins
 CC (ABBS7737-ABBS7072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SC Sequence 1016 AA;

Query Match 1.3%; Score 11; DB 22; Length 1016;
 Best Local Similarity 100.0%; Pred. No. 0.066;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNIVP 135
 |||||
 DB 59 EDCLYLNIVP 69

RESULT 64
 ID ABB61204 standard; Protein: 537 AA.
 XX
 AC ABB61204;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 10404.
 XX
 KM Drosophila developmental biology; cell signalling; insecticide;
 KM pharmaceutical.
 XX
 CS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PE 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEXE) FE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 CR WPI, 2001-656860/75.
 DR N-PSDB; ABL05307.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -

PS Disclosure; SEQ ID NO 10404; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL10511), expressed DNA
 CC sequences (ABL10840-ABL16175) and the encoded proteins
 CC (ABBS7737-ABBS7072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 537 AA;
 SQ 1.2%; Score 10; DB 22; Length 537;
 Query Match: 100.0%; Pred. No. 0.41;
 Best Local Similarity: 100.0%;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

203 NVRLOITGFL 212
 178 NVRLOITGFL 167

RESULT 65
 AAO17545
 ID AAO17545 standard; Protein; 92 AA.
 AC AAO17545;
 DT 19-JUN-2002 (first entry)
 DE Human carboxylesterase-like enzyme #2.
 XX
 XX Human: carboxylesterase; organophosphorous compound; cancer;
 KM inflammation; chronic obstructive pulmonary disease; COPD; cyclostatic;
 KM extracellular matrix degradation; enzyme.
 XX
 XX Homo sapiens.
 OS WO200230969-A2.
 PN 18-APR-2002.
 PD
 XX 11-OCT-2002; 2001WO-EP11758.
 PF
 XX 13-OCT-2003; 2000US-239898P.
 PR 31-AUG-2001; 2001US-315947P.
 XX
 XX (PARB) BAYER AG.
 PA
 XX Zhu Z;
 PI
 XX MPI; 2002-416856/44.
 DR N-PSDB; AAU46412.
 XX
 XX New human carboxylesterase-like enzyme polypeptide, the regulation of
 PT which is useful for treating diseases due to organophosphorus
 P2 intoxication, cancer or chronic obstructive pulmonary disease -
 XX
 XX Claim 25; Fig 5; 92pp; English.
 PS
 XX The present invention provides the protein and coding sequences of a
 CC human carboxylesterase-like enzyme. The sequences can be used in the
 CC preparation of a medicament for modulating the activity of a
 CC carboxylesterase-like enzyme in a disease due to organophosphorus
 CC intoxication, cancer or chronic obstructive pulmonary disease (COPD). The
 CC present sequence is a human carboxylesterase-like enzyme of the
 CC invention.
 CC
 XX
 SQ Sequence 92 AA;
 Query Match 1.1%; Score 9; DB 23; Length 92;
 Best Local Similarity 100.0%; Pred. No. 0.92;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

125 EDCVLYNTY 133
 29 EDCVLYNTY 36

RESULT 66
 ABP69056
 ID ABP69056 standard; Protein; 266 AA.

AC ABP69056;
 XX
 XX 20-JAN-2003 (first entry)
 DT
 XX
 XX Human polypeptide SEQ ID NO 1:03.
 DE
 XX
 XX Human: genome mapping; gene therapy; food supplement; virus; fungus;
 KM cell-proliferative disorder; neurodegenerative disease; bacterial;
 KM Parkinson's disease; Alzheimer's disease; autoimmune disease;
 KM multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
 KM arthritis; cytostatic; immunomodulator; neotropic; neuroprotective;
 KM antiparkinsonian; antidiabetic; immunosuppressive; dermatocologic;
 KM haemostatic; vulnery; fungicide; antibacterial; vituocide; protozoacide;
 KM antiarthritic.
 XX
 XX Homo sapiens.
 OS
 XX WO200270539-A2.
 PN 12-SEP-2002.
 PD
 XX 05-MAR-2002; 2002WO-US05095.
 PF
 XX 05-MAR-2001; 2001US-0799451.
 PR
 XX (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Zhou P, Goodrich RM, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M,
 PI Wehrman T, Kang J, Wang D, Drmanac RT.
 XX
 DR MPI; 2002-759812/82.
 DR N-PSDB; ABZ11273.
 XX
 XX New polynucleotides comprising sequences assembled from expressed
 PT sequence tags (ESTs), useful for treating cell-proliferative,
 PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or
 P2 platelet or coagulation disorders -
 XX
 XX Claim 9; SEQ ID NO 1103; 1012pp + Sequence Listing; English.
 PS
 XX The invention relates to an isolated polynucleotide (I) comprising a
 CC nucleotide sequence selected from any of 948 sequences
 CC (ABZ1119-ABZ12066) or their mature protein coding portion, active domain
 CC coding protein or complementary sequences. The polynucleotides are useful
 CC for identifying expressed genes or for physical mapping of human genome.
 CC The encoded polypeptides (ABP68902-ABP69849) are useful as molecular
 CC weight markers, as a food supplement, for generating antibodies, in
 CC medical imaging, screening and diagnostic assays and for treating
 CC cell-proliferative disorders (cancer), neurodegenerative diseases
 CC (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple
 CC sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid
 CC disorders, platelet or coagulation disorders, wound, burns, incision,
 CC ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal,
 CC parasitic), arthritis, etc.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at http://wipo.int/pub/published_pat_sequences.
 CC
 XX
 SQ Sequence 266 AA;
 Query Match 1.1%; Score 9; DB 23; Length 266;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

125 EDCVLYNTY 133
 148 EDCVLYNTY 156

RESULT 67
 ABB61993
 ID ABB61993 standard; Protein; 507 AA.

```

XX AC ABB61993;
XX XX
XX DT 26-MAR-2002 (first entry)
XX XX
DE Drosophila melanogaster polypeptide SEQ ID NO 12771.
XX XX
XX KM Drosophila; developmental biology; cell signalling; insecticide;
XX KM pharmaceutical.
XX XX
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX XX
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US09231.
XX PR 23-MAR-2001; 2000US-191637P.
XX PR 11-JUL-2001; 2000US-0614150.
XX PA (PEKE ) FE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX DR WPI; 2001-656860/75.
XX DR N-PSDB; ABL01892.
XX XX
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions -
XX PS Disclosure; SEQ ID NO 12771; 21pp + Sequence Listing; English.
XX XX
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL01840-ABL01892), expressed DNA
XX CC sequences (ABL01840-ABL01892) and the encoded proteins
XX CC (ABB57737-ABB577072).
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pat_sequences.
XX SQ Sequence 507 AA;

Query Match 1.1%; Score 9; DB 22; Length 507;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 PWMVYTHGG 176
   |||||
Db 118 PWMVYTHGG 126

RESULT 68
ABB57789
ID ABB57789 standard; Protein; 541 AA.
XX
XX AC ABB57789;
XX XX
XX DT 26-MAR-2002 (first entry)
XX XX
XX DE Drosophila melanogaster polypeptide SEQ ID NO 159.
XX XX
XX KM Drosophila; developmental biology; cell signalling; insecticide;
XX KM pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.

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XX XX
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US09231.
XX PR 23-MAR-2001; 2000US-191637P.
XX PR 11-JUL-2001; 2000US-0614150.
XX PA (PEKE ) FE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX DR WPI; 2001-656860/75.
XX DR N-PSDB; ABL01892.
XX XX
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions -
XX PS Disclosure; SEQ ID NO 159; 21pp + Sequence Listing; English.
XX XX
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL01840-ABL01892), expressed DNA
XX CC sequences (ABL01840-ABL01892) and the encoded proteins
XX CC (ABB57737-ABB577072).
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pat_sequences.
XX SQ Sequence 541 AA;

Query Match 1.1%; Score 9; DB 22; Length 541;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 PWMVYTHGG 176
   |||||
Db 104 PWMVYTHGG 112

RESULT 69
AAV33146
ID AAV33146 standard; Protein; 543 AA.
XX
XX AC AAV33146;
XX DT 16-NOV-1999 (first entry)
XX XX
XX DE Rabbit liver carboxylesterase protein fragment.
XX XX
XX KM Carboxylesterase; rabbit; liver; tumour cell; chemotherapy; prodrug;
XX KM disease-specific responsive promoter; CR1-11; APC; resection;
XX KM recurrence; inhibition; bone marrow cell.
XX OS Oryctolagus cuniculus.
XX PN WO9942593-A1.
XX PD 26-AUG-1999.
XX PF 12-FEB-1999; 99WO-US03171.
XX PR 19-FEB-1998; 98US-0075258.
XX PA (STUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX PI Danks MK, Potter PM, Houghton PJ;
XX DR WPI; 1999-540311/45.

```

XX New carboxylesterase polypeptide for treatment of tumors -
 XX
 XX Claim 3; Page 61-65; 70pp; English.
 PS
 CC This invention describes a novel rabbit carboxylesterase polypeptide (I)
 CC capable of metabolizing a chemotherapeutic prodrug and its inactive
 CC metabolites into an active drug. The invention also describes a
 CC composition comprising (i) and a disease-specific responsive promoter.
 CC This composition is useful for sensitizing tumor cells to a
 CC chemotherapeutic prodrug (preferably CPT-11 or APC) by transfecting into
 CC tumor cells, and contacting the sensitized cells with a chemotherapeutic
 CC prodrug to inhibit growth of the tumor cells. The composition can also be
 CC administered to the site of tumor resection to inhibit tumor recurrence,
 CC and be administered to bone marrow cells to remove tumor cells. The
 CC products of the invention are useful for identifying drugs that are
 CC inactivated by a carboxylesterase enzyme, and are also useful for
 CC identifying compounds containing a COO-C ester linkage that are activated
 CC by a carboxylesterase enzyme. This sequence represents a rabbit liver
 CC carboxylesterase fragment which is described in the method of the
 CC invention.
 SO Sequence 543 AA:
 SX
 CY :25 EDCYLENLY 133
 D6 :|||||
 :114 EDCYLENLY 122
 RESULT 70
 ID AAO18272 standard: protein; 544 AA.
 XX AAO18272;
 AC AAO18272;
 XX 26-SEP-2002 (first entry)
 DE Recombinant porcine liver esterase protein subunit.
 XX
 KM P1g: esterase; enzyme; PLB; carboxylic acid; ester; organic synthesis;
 KM pro-stereogenic compound.
 XX Sus scrofa.
 OS Synthetic.
 XX WC0200248322-A2.
 PN 20-JUN-2002.
 PD 06-DEC-2001; 2001WO-EF14338.
 PF 12-DEC-2000; 2000DE-1061964.
 PR (DECS) DEGRASSA AG.
 XX Bornscheuer U, Musidlowska A, Schmidt-Dannert G, Lange S;
 Z1 WPI, 2002-547857/58;
 DR
 XX
 PT New recombinant porcine liver esterase subunit, useful for resolution
 of racemic carboxylic esters, is truncated at C-terminus -
 PS Claim 1; Page 3; 40pp; German.

CC present sequence is the esterase subunit of the invention.
XX
SQ Sequence 544 AA:
Query Match 1.1%; Score 9; DB 23; Length 544;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 125 EDCLYNMY 133
DE 97 EDCLYNMY 105
RESULT 71
ABP97364
IT ABP97364 standard; Protein; 562 AA.
XX
AC ABP97364;
XX
CT -0-MAY-2003 (first entry)
XX
FE Mouse acyl coenzyme A cholesterol acyltransferase-1.
XX
KM Mouse; murine; acyl coenzyme A cholesterol acyltransferase-1; ACAT;
KM chromosome 1; cholesterol metabolism; free sterol regulation;
KM cholesterol metabolism disorder; lipid metabolism disorder;
KM atherosclerosis; cardiovascular disease; cardiac; expression inhibition;
KM antisense therapy; enzyme.
XX
OS Mus musculus.
XX
PN MO2003012144-A1.
XX
PD -3-FEB-2003.
XX
PF 17-JUL-2002; 2002MO-US22696.
XX
PR 01-AUG-2001; 2001US-0920394.
XX
PA (ISIS-1) ISIS PHARM INC.
XX
PI Crooke RM, Graham MJ, Lemonidis KM;
DR MP-1: 2003-239532/23.
CR N-PSDB; A5274890.
XX
PT New antisense oligonucleotides targeted to a nucleic acid encoding acyl
PT coenzyme A cholesterol acyltransferase-1, useful for treating a
PT disease/condition involving abnormal lipid or cholesterol metabolism,
PT e.g. atherosclerosis -
XX
PS Disclosure; Page 101-104; 117pp; English.
XX
CC This sequence represents murine acyl coenzyme A cholesterol
CC acyltransferase-1. Acyl coenzyme A cholesterol acyltransferase (ACAT)
CC enzymes catalyse the synthesis of cholesterol esters from free
CC cholesterol and fatty acyl-CoA, and are also involved in regulating the
CC concentration of cellular free sterols. The murine acyl coenzyme A
CC cholesterol acyltransferase-1 gene is located on chromosome 1. The
CC invention relates to antisense oligonucleotides targeted to the human
CC or mouse acyl coenzyme A cholesterol acyltransferase-1 gene, which
CC inhibit its expression. A series of oligonucleotides (AB274897-AB274942)
CC were designed to target different regions of the human or murine acyl
CC coenzyme A cholesterol acyltransferase-1 RNA, and were analysed for their
CC effect on mRNA levels by quantitative real-time PCR. The oligonucleotides
CC of the invention are useful for the prevention and treatment of
CC conditions associated with acyl coenzyme A cholesterol acyltransferase-1,
CC such as disorders involving abnormal lipid or cholesterol metabolism,
CC e.g., atherosclerosis or cardiovascular disease. They are also useful in
CC research and diagnostics for modulating the expression of acyl coenzyme
CC A cholesterol acyltransferase-1.
XX
XX Sequence 562 AA;

Query Match 1.1%; Score 9; DB 24; Length 562;
 Best Local Similarity 100.0%; Pred. No. 4.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNIY 133
 DB 115 EDCLYLNIY 123

RESULT 72
 ABB60215

ID ABB60215 standard; Protein; 564 AA.

XX ABB60215;

XX 26-MAR-2002 (first entry);

XX Drosophila melanogaster polypeptide SEQ ID NO 7437.

XX Drosophila developmental biology; cell signalling; insecticide;

KW pharmaceutical.

XX Drosophila melanogaster.

XX MO260171c42-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WC-US09233.

XX 23-MAR-2000; 2000US-191637E.

XX 21-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams X, Li FWD, Myers EW;

XX WPI; 2001-656662/75.

XX N-FSD3; ABL04319.

XX New isolated nucleic acid detection reagent for detecting 1000 or more

XX genes from Drosophila and for elucidating cell signalling and cell-cell

XX interactions -

XX Disclosure; SEQ ID NO 7437; 21pp - Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent

XX capable of detecting 1000 or more genes from Drosophila. The invention is

XX useful in developmental biology and in elucidating cell signalling and

XX cell-cell interactions in higher eukaryotes for the development of

XX insecticides, therapeutics and pharmaceutical drugs. The invention

XX discloses genomic DNA sequences (ABU16176-ABU35111), expressed DNA

XX sequences (ABU37737-ABU72072).

XX The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WFO

XX at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 564 AA;

XX Query Match 1.1%; Score 9; DB 22; Length 564;
 Best Local Similarity 100.0%; Pred. No. 4.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 PMVYIHGG 176
 DB 120 PMVYIHGG 128

RESULT 73

AAV33145
 ID AAV33145 standard; Protein; 565 AA.

XX AAV33145;
 XX 16-NOV-1999 (first entry);
 XX

XX Rabbit liver carboxylesterase protein.

XX Carboxylesterase; rabbit; liver; tumour cell; chemotherapy; prodrug;

XX disease-specific responsive promoter; CRT-11; APC; resection;

XX recurrence; inhibition; bone marrow cell.

XX Oryctolagus cuniculus.

XX Key Location/Qualifiers

XX Msc-difference 74 /note="Encoded by TTC"

XX MO9942593-A1.

XX 26-AUG-1999.

XX 12-FEB-1999; 99WO-US03171.

XX 19-FEB-1998; 98US-0075258.

XX (SCUD-) ST JUDE CHILDREN'S RES HOSPITAL.

XX Danks WK, Potter PX, Houghton PJ;

XX WPI; 1999-540311/45.

XX N-FSD3; AA209683.

XX New carboxylesterase polypeptide for treatment of tumors -

XX Disclosure; Fig 4; 70pp; English.

XX This invention describes a novel rabbit carboxylesterase polypeptide (1)

XX capable of metabolizing a chemotherapeutic prodrug and its inactive

XX metabolites into an active drug. The invention also describes a

XX composition comprising (1) and a disease-specific responsive promoter.

XX This composition is useful for sensitizing tumor cells to a

XX chemotherapeutic prodrug (preferably CRT-11 or APC) by transfecting into

XX tumor cells, and contacting the sensitized cells with a chemotherapeutic

XX prodrug to inhibit growth of the tumor cells. The composition can also be

XX administered to the site of tumor resection to inhibit tumor recurrence,

XX and be administered to bone marrow cells to remove tumor cells. The

XX products of the invention are useful for identifying drugs that are

XX inactivated by a carboxylesterase enzyme, and are also useful for

XX identifying compounds containing a COOC ester linkage that are activated

XX by a carboxylesterase enzyme. This sequence represents a rabbit liver

XX carboxylesterase which is described in the method of the invention.

XX Sequence 565 AA;

XX Query Match 1.1%; Score 9; DB 20; Length 565;
 Best Local Similarity 100.0%; Pred. No. 4.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNIY 133
 DB 114 EDCLYLNIY 122

RESULT 74
 AAB08202
 ID AAB08202 standard; Protein; 566 AA.

XX AAB08202;

XX 04-DEC-2000 (first entry)

XX Amino acid sequence of a rabbit liver esterase 3 designated R-E-3.

KW Rabbit; liver; esterase; RfE-3; pyridine herbicide;
 KM pyridine resistant plant; herbicide tolerance; herbicide resistance.
 XX
 OS Oryctolagus cuniculus.
 XX
 PN US6107549-A.
 XX
 PD 22-AUG-2003.
 XX
 PF 09-MAR-1999; 99US-0264737.
 XX
 PR 10-MAR-1998; 98US-0077377.
 XX
 PA (MONS; WCN5A;70 CO.
 XX
 PI Feng FCC; Ruff TG;
 XX
 DR WPI; 2000-579555/54.
 DR N-PDE; AAA63884.
 XX
 PT Recombinant polynucleotide molecule for generating pyridine resistant
 PT transgenic plants, comprises plant functional promoter operably linked
 PT to polynucleotide sequence encoding esterase.
 XX
 PS Claim 20; Column 31-36; 31pp; English.
 XX
 CC The present sequence represents a rabbit liver esterase, designated
 CC RfE-3. The esterase catalyses the hydrolysis of a pyridine herbicide
 CC compound. The esterase is linked to a plant functional promoter and
 CC a 3' non-translated region that functions in plant cells to cause the
 CC polydenylation of the 3' end of the RNA molecule produced by promoter.
 CC The esterase construct is useful for production of pyridine resistant
 CC transgenic plant. The esterase construct is also useful for genetic
 CC manipulation of plants and confers herbicide tolerance and herbicide
 CC resistance to the plants.
 XX
 SQ Sequence 566 AA;
 XX
 QY 125 EDCYLYNLY 133
 DB 115 EDCYLYNLY 123
 XX
 RESULT 75
 AAAB73263
 ID AAB73263 standard; protein; 566 AA.
 XX
 AC AAB73263;
 XX
 DT 16-MAY-2001 (first entry)
 XX
 DE Human triacylglycerol hydrolase, TGH.
 XX
 KM Human; TGH; triacylglycerol hydrolase; carboxylesterase; EST-3; WLDL;
 KM very low density lipoprotein; atherosclerosis; hypercholesterolaemia;
 KM hyperbetalipoproteinaemia; non-insulin dependent diabetes mellitus;
 KM coronary arterial disease; peripheral vascular disease; pancreatitis;
 KM obesity; mixed dyslipidaemia; cerebro-vascular disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200116158-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 24-AUG-2000; 2000MC-EP04262.
 XX
 PR 26-AUG-1999; 99GB-0020334.
 XX

PA (GLAX) GILAX GROUP LTD.
 PA (YVAL-1) UNIV ALBERTA.
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 PI Borg-Capra CS, Lehner RJ, Vance DE;
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 DR WPI; 2001-235119/24.
 XX
 PT Identifying compounds for treating elevated circulating levels of
 PT triglyceride, very low density lipoprotein/low density
 PT lipoprotein-cholesterol and ApoB-100, comprises identifying
 PT triacylglycerol hydrolase inhibitors.
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 PS Claim 2; fig 1; 26pp; English.
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 CC The present sequence is human triacylglycerol hydrolase (TGH). This
 CC protein has previously been known as carboxylesterase EST-1. It is
 CC thought that TGH may participate in the mobilisation of triacylglycerides
 CC for assembly into very low density lipoproteins (VLDL). The present
 CC invention relates to a method for identifying compounds which will be
 CC useful in the treatment of conditions resulting from elevated circulating
 CC levels of: triglycerides, apoB-100, and/or VLDL/LDL-cholesterol. The
 CC method comprises determining whether the compound inhibits TGH activity.
 CC Inhibitors of TGH are useful for treating atherosclerosis,
 CC hypercholesterolaemia, hyperbetalipoproteinaemia, non-insulin dependent
 CC diabetes mellitus (NIDDM), coronary arterial disease, peripheral vascular
 CC disease, pancreatitis, obesity, mixed dyslipidaemia and cerebro-vascular
 CC disease.
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 SQ Sequence 566 AA;
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 DB 114 EDCYLYNLY 122
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